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Result No.	Query			ID	Description
	Score	Match	Length		
1	4508	100.0	835	1	NLG2 HUMAN
2	4415.5	97.9	836	1	NLG2 RAT
3	2876	63.8	840	1	NLG1 HUMAN
4	2809	62.3	843	1	NLG1 MOUSE
5	2773.5	61.5	825	1	NLG3 MOUSE
6	2771	61.5	843	1	NLG3 RAT
7	2750	61.0	848	1	NLG3 HUMAN
8	2746	60.9	848	1	NLG3 RAT
9	2713.5	60.2	816	1	NLG4 HUMAN
10	2678.5	59.4	816	1	NLG4 MOUSE
11	859	19.1	574	1	CHLE HORSE
12	858	19.0	581	1	CHLE RABIT
13	855	19.0	602	1	CHLE HUMAN
14	852	18.9	614	1	CHES MOUSE
15	846.5	18.8	614	1	ACFS RAT
16	841.5	18.7	613	1	ACFS BOVIN
17	841	18.7	611	1	ACFS FELCA
18	837	18.6	603	1	CHLE MOUSE
19	836.5	18.6	566	1	EST1 PIG
20	830	18.4	557	1	SASS ANAPL
21	830	18.4	581	1	ACFS BUNFA
22	828.5	18.4	742	1	BAL HUMAN
23	827.5	18.4	614	1	ACFS HUMAN
24	823.5	18.3	562	1	ES22 MOUSE
25	819	18.2	561	1	EST3 RAT
26	819	18.2	612	1	BAL RAT
27	817	18.1	586	1	EST1 HUMAN
28	812.5	18.0	586	1	ACFS TORCA
29	807	17.9	584	1	ACFS RABIT
30	804.5	17.8	634	1	ACFS BRARE
31	800.5	17.8	590	1	ACFS TORMA
32	797	17.7	549	1	EST1 RAT
33	793.5	17.6	561	1	EST4 RAT

RESULT 1	NCBI	STANDARD;	PRT;	835 AA.
ID	HLG2_HUMAN			
AC	Q8NEZ4; Q9P211;			
DT	15-SEP-2003 (Rel. 42, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Neuregulin 2 precursor.			
GN	NLGN2 OR KIAA1366.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=12669065;			
RA	Jamain S., Quach H., Beranour C., Rastam M., Colineaux C.,			
RA	Gillberg T., Soderstrom H., Giros B., Leboyer M., Gillberg C.,			
RA	Bourgeron T., Nyden A., Philippe A., Cohen D., Chabane N.,			
RA	Mouron-Gimeoni M.C., Brice A., Sponheim E., Spurkland I.,			
RA	Skjeldal O.H., Coleman M., Pearl P.L., Cohen I.L., Tsouris J.,			
RA	Zappella M., Menchetti G., Pompella A., Aschauer H., Van Maldergem L.,			
RT	"Mutations of the X-linked genes encoding neurologins NLGN3 and NLGN4			
RT	are associated with autism";			
RL	Nat. Genet. 34:27-29 (2003)			
RL	[2]			
RP	SEQUENCE OF 285-835 FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=20181126; PubMed=10718198;			
RA	Negase T., Kikuno R., Ishikawa K.-I., Hirotsawa M., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XVI.			
RT	the complete sequences of 150 new cDNA clones from brain which code			
RT	for large proteins in vitro.";			
RL	DNA Res. 7:65-73 (2000).			
RL	[3]			
RP	INTERACTION WITH DLG4.			
RX	PubMed=9278515;			
RA	Irie M., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,			
RA	Takai Y., Rosahl T.W., Suedhof T.C.;			
RT	"Binding of neurologins to PSD-95";			
RL	Science 277:1511-1515 (1997).			
RL	[4]			
RP	FUNCTION			
RX	PubMed=10892652;			
RA	Scheiffele P., Fan J., Choeh J., Petter R., Serafini T.;			
RT	"Neuregulin expressed in nonneuronal cells triggers presynaptic			
RT	development in contacting axons";			
RL	Cell 101:657-669 (2000).			
CC	1- FUNCTION: Neuronal cell surface protein thought to be involved in			
CC	cell-cell interactions by forming intercellular junctions through			
CC	binding to beta-neurexins. Seems to play role in formation or			
CC	maintenance of synaptic junctions. In vitro, triggers the de novo			
CC	formation of presynaptic structures.			
CC	1- SUBUNIT: Interacts with neuroligin 1-beta, neuroligin 2-beta and			
CC	neuroligin 3-beta [By similarity]. Probably interacts through its C-			
CC	terminus with DLG4/PSD-95 third PDZ domain.			

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -----
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 CC -----
 DR EMBL: AF376802; AAM46111.1; -;
 DR EMBL: AB037787; BAA92604.1; -;
 DR HSSP: P21836; 1MAA.
 DR Genew: HGNC:14290; NLGN2.
 DR MIM: 606479; -;
 DR InterPro: IPR002018; Carbesterase.
 DR InterPro: IPR000460; Neuroligin.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PRO1090; NEUROLOGIN.
 DR PROSITE: PS00941; CARBOXYLESTERASE B_2; 1.
 KW Cell adhesion; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 14
 FT CHAIN 15 835
 FT DOMAIN 15 677
 FT TRANSMEM 678 698
 FT DOMAIN 699 835
 FT DISULFID 106 141
 FT DISULFID 317 328
 FT DISULFID 487 521
 FT CARBOHYD 98 98
 FT CARBOHYD 136 136
 FT CARBOHYD 522 522
 FT SEQUENCE 835 AA; 90819 MW; 359938630193EF87 CRC64;
 SQ
 Query Match
 Best Local Similarity 100.0%; Score 4508; DB 1; Length 835;
 Matches 835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWLLALCLVLAGAQRGGGPGGAPGGPGLGLSGLEERFPVNTAYGRVGRVRLNN 60
 DB 1 MWLLALCLVLAGAQRGGGPGGAPGGPGLGLSGLEERFPVNTAYGRVGRVRLNN 60
 QY 61 ELIGPVNQLGVYATPPLGARRFQPEAPASWPGVRNATLTPACPNLHGALPAIMLP 120
 DB 61 ELIGPVNQLGVYATPPLGARRFQPEAPASWPGVRNATLTPACPNLHGALPAIMLP 120
 QY 121 VWFDTNLEAAATYVQSEDCLYLNLVYPTEDGPLTKKRDEATLNPPTDIRDPKXPVM 180
 DB 121 VWFDTNLEAAATYVQSEDCLYLNLVYPTEDGPLTKKRDEATLNPPTDIRDPKXPVM 180
 QY 181 LFLHGSYMEGTGNMFDGSLAAYGNVATLNYELVGLSTGDAQAKNGYGLDQIQ 240
 DB 181 LFLHGSYMEGTGNMFDGSLAAYGNVATLNYELVGLSTGDAQAKNGYGLDQIQ 240
 QY 241 ALRWLSENIAHFGGPPERITIFSGAGASCYNLLILSHHSEGLFQKALAQSGTAISSNSV 300
 DB 241 ALRWLSENIAHFGGPPERITIFSGAGASCYNLLILSHHSEGLFQKALAQSGTAISSNSV 300
 QY 301 NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARHYAIGPVVDGDDV 360
 DB 301 NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARHYAIGPVVDGDDV 360
 QY 361 PDPEILMQCGEFLNVDMLIGNVQCEGLKFVEDSAESDGVSAFDFTVSNFVDNLYGY 420
 DB 361 PDPEILMQCGEFLNVDMLIGNVQCEGLKFVEDSAESDGVSAFDFTVSNFVDNLYGY 420
 QY 421 PEGKDVLRITIKFMYTDWADRNGEMRRKTLIALFTDQWVAPAVATAKLHADYQSPYVF 480
 DB 421 PEGKDVLRITIKFMYTDWADRNGEMRRKTLIALFTDQWVAPAVATAKLHADYQSPYVF 480
 QY 481 YTFYHHCQAEGRPEWADAAGDELVYFGVPMVGATDLFPNFSKNDVWLSAVVMTYTN 540

DB 481 YTFYHHCQAEGRPEWADAAGDELVYFGVPMVGATDLFPNFSKNDVWLSAVVMTYTN 540
 QY 541 FAKTGDNPQVQDQKFKHTKRNREEVVWVKFNSEKQYLIHGLKPRVDNRANKVAF 600
 DB 541 FAKTGDNPQVQDQKFKHTKRNREEVVWVKFNSEKQYLIHGLKPRVDNRANKVAF 600
 QY 601 WLELVPHLNLHNLTELTFTTTRLPYATRWPPPPAGAGPTRRPPPPATLPPPEPEPGR 660
 DB 601 WLELVPHLNLHNLTELTFTTTRLPYATRWPPPPAGAGPTRRPPPPATLPPPEPEPGR 660
 QY 661 AYDRPFGDSRDYSTELSVTVAGSILFLNLIILAFALYVYKRRROELRCRRLSPGGSGS 720
 DB 661 AYDRPFGDSRDYSTELSVTVAGSILFLNLIILAFALYVYKRRROELRCRRLSPGGSGS 720
 QY 721 GVFGGGLLPAAAGRELPPPEELVSLQKRGGVGADPAELRPACPPDYTLALRAPDDV 780
 DB 721 GVFGGGLLPAAAGRELPPPEELVSLQKRGGVGADPAELRPACPPDYTLALRAPDDV 780
 QY 781 PLLAPGALTLLPSGLGPPPPPPPSLHPGPPPPPPPTATSHNTLPHPHSTTRV 835
 DB 781 PLLAPGALTLLPSGLGPPPPPPPSLHPGPPPPPPPTATSHNTLPHPHSTTRV 835
 RESULT 2
 NLG2 RAT STANDARD; PRT; 836 AA.
 AC Q62888;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuroligin 2 precursor.
 GN NLGN2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). SEQUENCE OF N-TERMINUS, TISSUE
 RP SPECIFICITY, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN 2-BETA AND
 RP NEUREXIN 3-BETA.
 RC TISSUE=Forebrain;
 RX MEDLINE=96162010; PubMed=8576240;
 RX Ichtchenko K., Nguyen T., Suedhof T.C.;
 RA "Structures, alternative splicing, and neuroligin binding of multiple
 RT neuroligins";
 RL J. Biol. Chem. 271:2676-2682(1996).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX PubMed=11329178;
 RA Gilbert M., Smith J., Roskams A.J., Auld V.J.;
 RT "Neuroligin 3 is a vertebrate gliotactin expressed in the olfactory
 RT ensheathing glia, a growth-promoting class of macroglia";
 RL Glia 34:151-164(2001).
 CC -!- FUNCTION: Neuronal cell surface protein thought to be involved in
 CC cell-cell interactions by forming intercellular junctions through
 CC binding to beta-neurexins. Seems to play role in formation or
 CC maintenance of synaptic junctions. In vitro, triggers the de novo
 CC formation of presynaptic structures (By similarity).
 CC -!- SUBUNIT: Interacts with neuroligin 1-beta isoforms 3/Beta 4B5A and
 CC 4/Beta 4B5B. Interacts with neuroligin 2-beta isoforms 3/Beta 4B5A and
 CC 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with
 CC neuroligin 3-beta. Probably interacts through its C-terminus with
 CC DLG4/PSD-95 third PDZ domain (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q62888-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q62888-2; Sequence=VSP_007533;
 CC -!- TISSUE SPECIFICITY: Expressed in brain, spinal chord and dorsal
 CC root ganglion.

CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC
 CC EMBL; U41662; AAA97870.1; -;
 CC DR HSP; P37967; 10E3.
 CC DR InterPro; IPR002018; CarboxylesteraseB.
 CC DR InterPro; IPR000460; Neurotrophin.
 CC DR InterPro; IPR000379; Ser estersite.
 CC DR Pfam; PF00135; Coesterase_1.
 CC DR PRINTS; PR01090; NEUROLOGIN.
 CC DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 CC KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
 CC Alternative splicing.
 CC SIGNAL 1 14
 CC CHAIN 15 836 PROBABLE.
 CC DOMAIN 15 678 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 679 693 POTENTIAL.
 CC DOMAIN 700 836 CYTOPLASMIC (POTENTIAL).
 CC DISULFID 106 141 BY SIMILARITY.
 CC DISULFID 317 328 BY SIMILARITY.
 CC FT CARBOHYD 487 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPLIC 153 169 Missing (in isoform 2).
 CC FT FTID; VSP_007533.
 CC SEQUENCE 836 AA; 90961 MW; 1AD51CB1BE4BFCF CRC64;
 CC
 CC Query March 97.98; Score 4415.5; DB 1; Length 836;
 CC Best Local Similarity 98.38; Pred. No. 1.4e-238;
 CC Matches 822; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
 CC
 CC QY 1 MWLLALCLVGLAQRGGGPGGAGPGGLGSLGSEGRFPVNTAYGRVGRRLNN 60
 CC DB 1 MWLLALCLVGLAQRGGGPGGAGPGGLGSLGSEGRFPVNTAYGRVGRRLNN 60
 CC QY 61 EILGPVVOFLGVVPATPLGARFPQPEAPSPGVRNATLTPACPNLHGLPALMLP 120
 CC DB 61 EILGPVVOFLGVVPATPLGARFPQPEAPSPGVRNATLTPACPNLHGLPALMLP 120
 CC QY 121 VWFDTNLEAAATVYQNSDCLNLYVPTDGDPLTKRDEATLNPPDTRDGGKPYM 180
 CC DB 121 VWFDTNLEAAATVYQNSDCLNLYVPTDGDPLTKRDEATLNPPDTRDGGKPYM 180
 CC QY 181 LFLHGGSYMEGTGNMFGSVLAAYGNVIVATNLYRGLVGLSTGQAAGNYGLDQIQ 240
 CC DB 181 LFLHGGSYMEGTGNMFGSVLAAYGNVIVATNLYRGLVGLSTGQAAGNYGLDQIQ 240
 CC QY 241 ALRWLSNIAHFGDPERITIFSGAGASCNLLILSHSEGLFQKALQSGTAISSWSV 300
 CC DB 241 ALRWLSNIAHFGDPERITIFSGAGASCNLLILSHSEGLFQKALQSGTAISSWSV 300
 CC QY 301 NYQPLKVTLLAAKVGQRDESAVCLARKSRELVDDQVOPARYHIAFGVWDGVV 360
 CC DB 301 NYQPLKVTLLAAKVGQRDESAVCLARKSRELVDDQVOPARYHIAFGVWDGVV 360
 CC QY 361 PDDPEILMQQGEFLNYDMLIGNGEGIKFVEDSAESDGVSAADFTVSNFVDNLGY 420
 CC DB 361 PDDPEILMQQGEFLNYDMLIGNGEGIKFVEDSAESDGVSAADFTVSNFVDNLGY 420
 CC QY 421 PEGKDVLRITIKMYTDWADRNGEMRKTLALFTDQHWAPAVATAKLHAYQSPVYF 480
 CC DB 421 PEGKDVLRITIKMYTDWADRNGEMRKTLALFTDQHWAPAVATAKLHAYQSPVYF 480
 CC QY 481 YTFYHHCQAEGRPEWADAAGDELPPYGVGMVAGATDLFCNFSKNDVMSAVVMTWTN 540

DB 481 YTFYHHCQAEGRPEWADAAGDELPPYGVGMVAGATDLFCNFSKNDVMSAVVMTWTN 540
 QY 541 FAKTGDNDQNPVQDTKEIHTKPNRFEVWVSKNSKEQYVHLGLKPRVDRNYRANKVAF 600
 DB 541 FAKTGDNDQNPVQDTKEIHTKPNRFEVWVSKNSKEQYVHLGLKPRVDRNYRANKVAF 600
 QY 601 WLELVPHLNLHTELTFTTTLRLPPYATRWPPRPPA-GAPOTRRPPPPATLPPPEPEPGP 659
 DB 601 WLELVPHLNLHTELTFTTTLRLPPYATRWPPRPPA-GAPOTRRPPPPATLPPPEPEPGP 660
 QY 660 RAYDRFPGDSRDYSTELSVTVVAGASLFLNLAFAALYYKRRRQELRCRLSPPGSG 719
 DB 661 RAYDRFPGDSRDYSTELSVTVVAGASLFLNLAFAALYYKRRRQELRCRLSPPGSG 720
 QY 720 SGVPGGGPLPAAGRELPPPEELVSLQKRGVGGADPAEALPACPPDYTLARRAPDD 779
 DB 721 SGVPGGGPLPAAGRELPPPEELVSLQKRGVGGADPAEALPACPPDYTLARRAPDD 780
 QY 780 VPLLAPGALTLLPSGLGPPPPPPPSLHPGPPPPPPPTATSHNNTLPHPHSTTRV 835
 DB 781 VPLLAPGALTLLPSGLGPPPPPPPSLHPGPPPPPPPTATSHNNTLPHPHSTTRV 836
 RESULT 3
 NLG1_HUMAN STANDARD; PRT; 840 AA.
 ID NLG1_HUMAN Q9N2Q7; Q9N2Q2;
 AC Q9N2Q7; Q9N2Q2;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neurotrophin 1 precursor.
 GN NLGN1 OR KIAA1070.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Negase T., Ishikawa K.-I., Hirose M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:197-205 (1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Ductum;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Whiting M., Madan A., Young J.W., Green E.D., Dickinson M.C.,
 RA Blakesley R.W., Touchman A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE OF 315-823 FROM N.A.
 RC TISSUE=Embryo;

RA Isogai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwavanagi T., Ninomiya K.,
RT "NEDO human cDNA sequencing project";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CONCEPTUAL TRANSLATION (ISOFORM 1).
RA Roehrborn B.;
RL Unpublished observations (MAY-2003).
RN [5]
RP INTERACTION WITH DLG4.
RX PubMed:9278515;
RA Irie W., Hata K., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,
RA Takai Y., Rosahl T.W., Suedhof T.C.;
RT "Binding of neurologins to PSD-95";
RL Science 277:1511-1515(1997).
RN [6]
RP FUNCTION
RX PubMed:10892652;
RA Scheiffele P., Fan J., Choih J., Fetter R., Serafini T.;
RT "Neurologin expressed in nonneuronal cells triggers presynaptic
RT development in contacting axons";
RL Cell 101:657-669(2000).
CC -!- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell interactions by forming intercellular junctions through
CC binding to beta-neurexins. Seems to play role in formation or
CC maintenance of synaptic junctions. In vitro, triggers the de novo
CC formation of presynaptic structures. May be involved in
CC specification of excitatory synapses.
CC -!- SUBUNIT: Interacts with neuroligin 1-beta, neuroligin 2-beta and
CC neuroligin 3-beta (By similarity). Interacts through its C-terminus
CC with DLG4/PSD-95 third PDZ domain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Enriched in
CC synaptic plasma membranes and clustered in synaptic clefts and
CC postsynaptic densities (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8N207-1; Sequence=Displayed;
CC Note=No experimental confirmation available;
CC Name=2;
CC IsoId=Q8N207-2; Sequence=VSP_007527;
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
CC -----
CC EMBL; AB028993; BAA83022.1; -;
CC EMBL; BC032555; AAH32555.1; -;
CC EMBL; AK074522; BAC11039.1; ALT_INIT.
CC HSP; P21836; 1MAA.
CC Genew; HGNC:14291; NLGN1.
CC MIM; 600568; -;
CC InterPro; IPR002018; Carboxylesterase.
CC InterPro; IPR000460; Neurologin.
CC InterPro; IPR000379; Ser esterase.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR01090; NEUROLOGIN.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Cell adhesion; Glycoprotein; Signal; Transmembrane;
KW Alternative splicing.
KW SIGNAL 1 45 POTENTIAL.
FT CHAIN 46 840 NEUROLOGIN 1.
FT DOMAIN 46 694 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 695 715 POTENTIAL.

FT DOMAIN 716 840 CYTOPLASMIC (POTENTIAL).
FT DISULFID 117 153 BY SIMILARITY.
FT DISULFID 339 350 BY SIMILARITY.
FT DISULFID 509 543 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 544 544 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 165 181 Missing (in isoform 2).
FT CONFLICT 711 711 /FTid=VSP_007527.
FT SEQUENCE 840 AA; 93835 MW; A3FB21716F62DB29 CRC64;
SQ
Query Match 63.8%; Score 2876; DB 1; Length 840;
Best Local Similarity 63.5%; Pred. No. 6.e-153;
Matches 556; Conservative 98; Mismatches 134; Indels 88; Gaps 16;
QY 1 MWLLAL-CLVLAGAORGGGPGGAGPGGGLGLSLG-----LTLMLGCLLQAGHVLSQLDDVDLVAI 46
DB 12 VWRVAVACLV-----HRLGAP-----LTLMLGCLLQAGHVLSQLDDVDLVAI 57
QY 47 AYGRVRGRVRELNNEILGPVVFGLVPPYATPPIGARRFQPPPEAPASWPGVNRNATTLPPAC 106
DB 58 NFGKIRGIRKELNNEILGPVVFGLVPPYATPPIGARRFQPPPEAPASWPGVNRNATTLPPAC 117
QY 107 PON-LHGALPAIMLPVWFTDNLAAATVYQNOSEDCLYLNLYVPTEDGPLTKKRDATLN 165
DB 118 PQNIIDRLPEVWLPVWFTDNLVSSYVQDQSDCLYLNLYVPTEDGPLTKKRDATLN 177
QY 166 PPDTDIRDP-GKKPVMFLHGGSYMEGTGNMFGSVLAAYGNVIVATLNYRLGVGLFLST 224
DB 178 PPDTDIRDSGRPEVMVYIHGGSYMEGTGNLYDGSVLSYGNVIVITVNYRLGVGLFLST 237
QY 225 GDQAAGKNGYLLDQIQALRWLSENIHFGDDPRITIFSGAGASCNNLLILSHHE--- 281
DB 238 GDQAAGKNGYLLDQIQALRWLSENIHFGDDPRITIFSGAGASCNNLLILSHHE--- 297
QY 282 -----GLFOKAIAQSGTAISMSVNVQPLKYTRLLAAKVGCDREDSAAVECLRKPSR 335
DB 298 WSNSTKGLFORIAQSGTALSSWAVSFQPAKYARMLATKVCNVSDTVELVECLQKPYK 357
QY 336 ELVDQDVQARYHIAFGPVVDGVDPPDEILMQGFEFLNYDMLIGNOGEGLKFFVDSA 395
DB 358 ELVDQDVQARYHIAFGPVVDGVDPPDEILMQGFEFLNYDMLIGNOGEGLKFFVENIV 417
QY 396 ESDGYSASAFDTVSNFVDNLGYPEKQDVLRETIKEMVTDWADRDNGEMRKKTLALF 455
DB 418 DSDDGISASDFDFAVSNFVDNLGYPEKQDVLRETIKEMVTDWADRDNGEMRKKTLALF 477
QY 456 TDHQWAPAVATAKLHAYQSPVYFYTFYHCOAQRPEWADAAGDELFPYFVGPMVGA 515
DB 478 TDHQWAPAVATAKLHAYQSPVYFYTFYHCOAQRPEWADAAGDELFPYFVGPMVGA 537
QY 516 TDLPPCNFKNYDMLSAVMYTNFAKTDGPNQVPQDTKFIHTKPNRFEFVWWSKFS 575
DB 538 TDLPPCNFKNYDMLSAVMYTNFAKTDGPNQVPQDTKFIHTKPNRFEFVWWSKFS 597
QY 576 KEQQLYHLGLKPRVDRNRYANKVAFLELVPHLNLH--TELFTTTTTLPPFYATRPWPRP 633
DB 598 KDQLYLHLGLKPRVDRNRYANKVAFLELVPHLNLH--TELFTTTTTLPPFYATRPWPRP 657
QY 634 PAGAGTTRPPPPATLPPPEPEPEPPRAYDRPFGSDRYSTELSVTVAVGASLLFNILA 693
DB 658 KNSVPVTSAPPTAKQDDPKQQSP-----FSDQORDYSTELSVTVAVGASLLFNILA 710
QY 694 FAALYVKRDRQRQELRCRLSPGSGSGVPGGGLLPAAGRELPPPEELVSLQKRGGV 753
DB 711 FAALYVKRDRQRQELRCRLSPGSGSGVPGGGLLPAAGRELPPPEELVSLQKRGGV 755
QY 754 GAD-----PAE-ALRPACPPDYTLARRAPDDVELLAPGALTLLPSGLGPPPPPPPPS 805
DB 756 DLDHECESIHPHEVWLRACPPDYTLARRAPDDVELLAPGALTLLPSGLGPPPPPPPPS 810


```
Db 233 GVLGFLSTGDQAQKNGYGLLDLQALRWTSSENIFFGGDPLRITVFGSAGGSCVNLITL 292
QY 277 SHSE-----GLFQKAIASQGTASSVNVYQPLKYTRLLAAKYGCCREDSSAEAVE 327
Db 293 SHYSEGNRNSNTKGLFORAIAQSGTALSSWAFQPAKYARILATKYGCNVSDTVLVE 352
QY 328 CLRKRSPRELVDQVQPARHYHAFGVVDGVDVDDPELMOGGEFLYVMDLIGNQEG 387
Db 353 CLQKPKYKELVDQVQPARHYHAFGVVDGVDVDDPELMOGGEFLYVMDLIGNQEG 412
QY 388 LKFVEDSAESDEGVSAFDFTVSNFVNDLYGPEGKVLRETIFKMTYTDWADRNGSMR 447
Db 413 LKFVENIVSDSGVSAFDFTVSNFVNDLYGPEGKVLRETIFKMTYTDWADRNPETR 472
QY 448 RKTLLALFTDQHWAPAVATAKLHADYQSPVYVTFYHHCOAGRPWADAAGDELIV 507
Db 473 RKTLLALFTDQHWAPAVATAKLHNSGFTYFYAFYHHCQTDQVPAWADAAGDEVIV 532
QY 508 FGVPVMGATDLPFCNFKNDVMSLVAVMTYTNFAKTGDPNPQVQDTKFIHTKPNREE 567
Db 533 LGIPMTGTELPFCNFKNDVMSLVAVMTYTNFAKTGDPNPQVQDTKFIHTKPNREE 592
QY 568 VVWSKFNSEKQYLHIGLPRVDNRANKVAFWELVPHLNLH--TELFTTTTLRPPY 625
Db 593 VAWTRYSQDQLYLHIGLPRVKEHYRANKVNLVLELPHLNLNDISQYTTTKVP-- 650
QY 626 ATRWPPRPAGAPGTRRRPPAT-----LPPEPEPGPRAYDRFPDGSRDYSTELSVT 679
Db 651 STDITLRP-----TKNSTPTVSAFPAKQDDPKQOSP-----FSVDQDYSTELSVT 699
QY 680 VAVGASLLFLNTLAFALYKDRQELRRLSPFGSGGVPGGGLLPAAGRELPE 739
Db 700 IAVGASLLFLNTLAFALYKDRQELRRLSPFGSGGVPGGGLLPAAGRELPE 747
QY 740 ELVLSIQLXRGGVGAD-----PAB-ALRPACSPDYTLALRAPDDVPILLACALTL 791
Db 748 EELMSLQMKH-----TDLHCECSIHHEVVRVACSPDYTLAWRSPPDIPMLPTNTIMI 804
QY 792 PSLGOLPPPPPPSLHFGFPFPPPTATSHNTLPHP-----HSTTRV 835
Db 805 PNTI-----PGIQLTFTNF-----TGGQNNTLPHPHPHSHSTRV 843

RESULT 5
NLG3_MOUSE
AC Q8BYM5; Q8BXK4;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuroigin 3 precursor (Gliotactin homolog).
GN NLG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus, and Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osaoto N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogani A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
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RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [2]

TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RP PubMed=11329178;
RX Gilbert M., Smith J., Roakams A.J., Auld V.J.;
RT "Neuroigin 3 is a vertebrate gliotactin expressed in the olfactory
RT ensheathing glia, a growth-promoting class of macroglia."
RL Glia 34:151-164 (2001).
CC -|- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell-interactions by forming intercellular junctions through
CC binding to beta-neurexins. May play a role in formation or
CC maintenance of synaptic junctions. May also play a role in glia-
CC glia or glia-neuron interactions in the developing peripheral
CC nervous system.
CC -|- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and
CC neuexin 3-beta, and probably through its C-terminus with
CC DLG4/PSD-95 third PDZ domain (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -|- TISSUE SPECIFICITY: Expressed in olfactory bulb and olfactory
CC epithelium. Found in olfactory ensheathing glia but not in
CC olfactory neurons, and in developing peripheral glia.
CC -|- DEVELOPMENTAL STAGE: Detected at embryonic day E17 and postnatal
CC day P1 in retinal astrocytes, spinal chord astrocytes and Schwann
CC cells of the dorsal root ganglion.
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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CC -----
DR ENBL; AK039018; BAC30207.1; -
DR ENBL; AK044438; BAC31918.1; -
DR MGD; MGI:2444609; A230085M13Rik.
DR InterPro; IPR002018; CarboxylesteraseB.
DR Pfam; PF00135; Coesterase_1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Cell adhesion; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 34
FT CHAIN 35 825
FT DOMAIN 35 686
FT TRANSMEM 687 707
FT DOMAIN 708 825
FT DISULFID 103 138
FT DISULFID 317 328
FT DISULFID 487 521
FT CARBOHYD 95 95
FT CARBOHYD 522 522
FT CONFLICT 459 459
FT SEQUENCE 825 AA; 91175 MW; 3BF17F889B0A44CE CRC64;

Query Match 61.5%; Score 2773.5; DB 1; Length 825;
Best Local Similarity 64.8%; Pred.No. 3.3e-147;
Matches 531; Conservative 98; Mismatches 132; Indels 59; Gaps 14;
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QY 42 PVNTAYVRGVRRELNNEILGVVQFLGVPVATPPLGARRFOPPEAPASPGVGNATT 101
DB 39 PTNTHTFGKLGARVPLPSEILGVQVQYGLVPAAPPIGEKFLPEPPPPSGSGINATH 98
QY 102 LPACQNLHGLALPALMPWFNTDNLEAATYVQVQSECLYNLYVPEDGFLPKRDE 161
DB 99 FPPVCPQNIHTAVPEVWMLPWFNTANLDIVATYIQEPEDEDCLYNLYVPTDGGAKQGE 158
QY 162 ATLN---PPDTRDRGKPKVMLFLGGSGMEGTGMFGSGLAAVGNIVATLVNRLGV 218
DB 159 DLADNDGDEDEDIRDSGAKPVMYIIGGSGMEGTGMIDGSLVLAGVNVITLVNRLGV 218
QY 219 LGFLSTGDOAAKNYGLLDQIQALRWLSNIAHFQGGDPRITIFGSGAGASCVLLTLSH 278
DB 219 LGFLSTGDOAAKNYGLLDQIQALRWLSNIAHFQGGDPRITIFGSGAGASCVLLTLSH 278
QY 279 HSEGLFQKALQAGTALSSVNYQPKYTRLLAAKVGCDREDSAEVCEIARKEPSREL 338
DB 279 HSEGLFQKALQAGTALSSVNYQPKYTRLLAAKVGCDREDSAEVCEIARKEPSREL 338
QY 339 DQVQPARVHIAFGPVVGDVDPDEILMQGGEFLNYDMLGVNQEGELKTFVDSASE 398
DB 339 EQDIQPARVHIAFGPVVGDVDPDEILMQGGEFLNYDMLGVNQEGELKTFVDSASE 398
QY 399 DGVSAGAFDTNFDNLYGPEGKDVLRRTIKFMYTDWADRDNGEMRKILLALFTDH 458
DB 399 DGVSAGAFDTNFDNLYGPEGKDVLRRTIKFMYTDWADRDNGEMRKILLALFTDH 458
QY 459 QWVAPAVATKLAHADYQSPVFTYVHHQOAGRPEDWADAAGDELPPYVGVPMVGCATDL 518
DB 459 QWVAPAVATKLAHADYQSPVFTYVHHQOAGRPEDWADAAGDELPPYVGVPMVGCATDL 518
QY 519 FPCNFKNDVMSAVVMTYTNFAKTGDPNPQVQDTKFIHTKPNRFEVWVKNSKEK 578
DB 519 FPCNFKNDVMSAVVMTYTNFAKTGDPNPQVQDTKFIHTKPNRFEVWVKNSKEK 578
QY 579 QYHLGKPRVRNRYANKVAFWELVPHLNLHTELF---TTTTLPP-----YATRWPP 631
DB 579 LYHLGKPRVRNRYANKVAFWELVPHLNLHTELF---TTTTLPP-----YATRWPP 631
QY 632 RPPAGAGTRRRPPPPATLPPEPEPEPRAYDRFPQDS-----RDYSTELSVTVA 681
DB 632 RPPAGAGTRRRPPPPATLPPEPEPEPRAYDRFPQDS-----RDYSTELSVTVA 681
QY 682 VGASLLFLNTLFAALYKRDQERLRLSPGSGSGVPGGGPLLPAAARELPPEE 741
DB 682 VGASLLFLNTLFAALYKRDQERLRLSPGSGSGVPGGGPLLPAAARELPPEE 741
QY 691 VGASLLFLNTLFAALYKRDQERLRLSPGSGSGVPGGGPLLPAAARELPPEE 739
DB 691 VGASLLFLNTLFAALYKRDQERLRLSPGSGSGVPGGGPLLPAAARELPPEE 739
QY 742 LVSLQLKRGSGV-----GADPAALRPACPPDYTLALRAPDVPVLLAPGALTLPGLG 796
DB 742 LVSLQLKRGSGV-----GADPAALRPACPPDYTLALRAPDVPVLLAPGALTLPGLG 796
QY 797 PPPPPPPSLHFGPPPPPPPTATSHNNT-LPHPHSHSTRV 835
DB 797 PPPPPPPSLHFGPPPPPPPTATSHNNT-LPHPHSHSTRV 835
QY 796 ---VGLQTLHPYNTF-----AAGENSTGLPHSHSTRV 825
DB 796 ---VGLQTLHPYNTF-----AAGENSTGLPHSHSTRV 825
```

RESULT 6

NLG1 RAT

ID NLG1 RAT

AC Q62765

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Neurotrophin 1 precursor (Neurotrophin I).

GN NLG1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), PARTIAL SEQUENCE.

CHARACTERIZATION, AND INTERACTION WITH NEUREXIN 1-BETA.

TISSUE=Brain;

MEDLINE=95254653; PubMed=7736595;

Ichchenko K., Hata Y., Nguyen T., Ullrich B., Missler M., Moomaw C., Suedhof T.C.;

"Neurotrophin 1: a splice site-specific ligand for beta-neurexins.";

Cell 81:435-443(1995).

[2]

INTERACTION WITH NEUREXIN 1-BETA, AND FUNCTION.

MEDLINE=97467410; PubMed=9325340;

Nguyen T., Suedhof T.C.;

"Binding properties of neurotrophin 1 and neurexin 1beta reveal function as heterophilic cell adhesion molecules.";

J. Biol. Chem. 272:26032-26039(1997).

[3]

BLOCKAGE OF N-TERMINUS, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN 2-BETA AND NEUREXIN 3-BETA.

MEDLINE=96162010; PubMed=8576240;

Ichchenko K., Nguyen T., Suedhof T.C.;

"Structures, alternative splicing, and neurexin binding of multiple neurotrophins.";

J. Biol. Chem. 271:2676-2682(1996).

[4]

TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.

PubMed=9927700;

Song J.-Y., Ichchenko K., Suedhof T.C., Brose N.;

"Neurotrophin 1 is a postsynaptic cell-adhesion molecule of excitatory synapses.";

Proc. Natl. Acad. Sci. U.S.A. 96:1100-1105(1999).

[5]

TISSUE SPECIFICITY.

PubMed=11329178;

Gilbert M., Smith J., Roskams A.J., Auld V.J.;

"Neurotrophin 3 is a vertebrate gliotactin expressed in the olfactory ensheathing glia, a growth-promoting class of macroglia.";

Glia 34:151-164(2001).

CC -!- FUNCTION: Neuronal cell surface protein thought to be involved in cell-cell-interactions by forming intercellular junctions through binding to beta-neurexins. Seems to play role in formation or maintenance of synaptic structures. In vitro, triggers the de novo formation of presynaptic structures (By similarity). May be involved in specification of excitatory synapses.

CC -!- SUBUNIT: Interacts with neurexin 1-beta isoforms 3/Beta 4B5A and 4/Beta 4B5B. Interacts with neurexin 2-beta isoforms 3/Beta 4B5A, 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with corresponding neurexin 3-beta isoforms. Interacts through its C-terminus with DLG4/PSD-95 third PDZ domain (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Enriched in synaptic plasma membranes and clustered in synaptic clefts and NMDAR1/glutamate (NMDA) receptor subunit zeta 1.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;

CC Name=1;

CC IsoId=Q62765-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q62765-2; Sequence=VSP_007531; VSP_007532;

CC Note=No experimental confirmation available;

CC Name=3;

CC IsoId=Q62765-3; Sequence=VSP_007532;

CC Name=4;

CC IsoId=Q62765-4; Sequence=VSP_007531;

CC -!- TISSUE SPECIFICITY: Expressed in brain, almost exclusively in neurons, and spinal chord.

CC -!- DEVELOPMENTAL STAGE: Expression is low in embryonic brains (E12-E16) but increases dramatically after birth (postnatal days P0-P3) and reaches a plateau during the period when most synapses are formed (P5-P8).

CC -!- PTM: N- and O-glycosylated.

CC -!- PTM: The N-terminus is blocked.

CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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 CC -----
 DR EMBL; U22952; AAA85720.1; --
 DR HSP; P37967; 1OE3
 DR InterPro; IPR002018; CarboxesteraseB.
 DR InterPro; IPR000460; Neurotrophin.
 DR InterPro; IPR000379; Ser_estr_ site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR01090; NEUROLOGIN.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
 KW Alternative splicing.
 FT SIGNAL 1 45
 FT CHAIN 46 843
 FT DOMAIN 46 697
 FT TRANSMEM 698 718
 FT DOMAIN 719 843
 FT DISULFID 117 153
 FT DISULFID 172 181
 FT DISULFID 342 353
 FT DISULFID 512 546
 FT CARBOHYD 109 109
 FT CARBOHYD 303 303
 FT CARBOHYD 343 343
 FT CARBOHYD 547 547
 FT VARSPLIC 165 184
 FT VARSPLIC 298 306
 FT SEQUENCE 843 AA; 94294 MW; 90A18540245B789D CRC64;
 SQ
 Query Match 61.5%; Score 2771; DB 1; Length 843;
 Best Local Similarity 61.1%; Pred. No. 4.6e-147;
 Matches 546; Conservative 100; Mismatches 133; Indels 114; Gaps 21;
 QY 1 MW-----LLALCLVLGAGAQGGGPGGPGGPGGLGLGSLG-----LTLCLGLCLQTFHVLSQLDQD 52
 DB 7 MWPNVYRAMACVV-----HKGSGAP-----LTLCLGLCLQTFHVLSQLDQD 52
 QY 42 PVNTAYGRVGRVRENNELIPVQVQVGVYATPTTGARFQPEAPASGPGVGRNAT 101
 DB 53 PLVTTNFGKIRGKIKELNNEILGPVILQVGYAPPTGEHRFQPEPSPSWDIRNATQ 112
 QY 102 LPPACPN-LHGALPALMLPVMTNLEAAATVQNSQEDCLYLNLYPTEDGPTKKRD 160
 DB 113 FAPVCQNIIDGLPEVMLPVMTNLDVVSIVQDSQEDCLYLNLYPTEDGPTKKRD 169
 QY 161 EATLNPPDT-----DIRDP-GKKPMLFLHGSYMEGTGNMFDGSLVLAAYGNVIVATLN 213
 DB 170 KECARPGKIKRKGDIRSGGPKPVWYIHGSGYMEGTGNLYDGSVLASYGNVIVITVN 229
 QY 214 YRLGVGLSTGDOAKGNVGLDIOALRWLSNIAHFGGDPERITFGSGAGACVNL 273
 DB 230 YRLGVGLSTGDOAKGNVGLDIOALRWLSNIAHFGGDPERITFGSGAGACVNL 289
 QY 274 LILSHSE-----GLFQKAIQSGTAISSWSVNTQPLKTYRLLAAYGCCREDSDAE 324
 DB 290 LTLSHYSEGNRWSNSTKGLFQRAIAGSGTALSMVAVSQPAKYARILATKVCNVSDIVE 349
 QY 325 AVECLARKSRELVDQVOPARYHIAFGVVDGVDVDDPEILMQGDFLNYDMIGVNG 384
 DB 350 LVECLQKPEYKELVDQVOPARYHIAFGVVDGVDVDDPEILMQGDFLNYDMIGVNG 409
 QY 385 GEGLEKVEDSDESDGVSASAFDFTVSNFVDNLYGYPEGKVLRTIKFMTYDADRNG 444
 DB 410 GEGLEKVENIVDSGVSASDFDFAVSNFVDNLYGYPEGKVLRTIKFMTYDADRNG 469
 QY 445 EMERKTLALFTDQHWAPAVATAKLHADYQSVVYTFYTHHQAEGRPWADAAGDEL 504

DB 470 ETRKTKLLALFTDQHWAPAVATAKLHADYQSVVYTFYTHHQAEGRPWADAAGDEL 529
 QY 505 PYFVGVMVATDLPFCNFKNDVMSAVVMTYNTWTFNFAKTGDPNQVPQDTKFIHTKPNR 564
 DB 530 PYVLGIPMIGTPELFCNFKNDVMSAVVMTYNTWTFNFAKTGDPNQVPQDTKFIHTKPNR 589
 QY 565 PEEVWSKFNSEKQYLIHGLKPRVDRNRYRANKVAFWLELVPHLNLH--TEFTTTTREL 622
 DB 590 FEEVATRYSKQQLYLIHGLKPRVKEHYRANKVNLWLELVPHLNLNDISQVSTTTTKV 649
 QY 623 PPVATRWPPPPAGAPGTRPPPPAT-----LPPEPEPPGPRAYDRFPDGRDYSTEL 676
 DB 650 P--STDITLAP-----TRKNSIPVSAFTAKQDDPKQPPSP-----FVSDQDYSYTEL 696
 QY 677 SVTVAGASLLFLNLAFALYKRRDRRQELRRRLSPGGSGSGVGGGGLLPAGREL 736
 DB 697 SVTVAGASLLFLNLAFALYKRRDRRQELRRRLSPGGSGSGVGGGGLLPAGREL 745
 QY 737 PPEELVSLQKRGGVGAD-----PAB-ALRPACPPDYTLALRRAPDDVPLAPGAL 788
 DB 746 -PEEINSLQKH---TDLDECESIHPHEVVLRTACPPDYTLARRSPDDVPLMTNTI 801
 QY 789 TLLPSGGLGPPPPPPSLHPFGPPPPPTATSHNNTLPHP-----HSTRV 835
 DB 802 TMTPTNTI-----FGIQPLHTFNTF-----TGGQNTLPHPHPHSHSTRV 843
 RESULT 7
 ID NLG3 HUMAN STANDARD; PRT; 848 AA.
 AC Q9NZ94; Q9NZ95; Q9NZ96; Q9NZ97; Q9P248;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neurotrophin 3 precursor (Gluotactin homolog).
 GN NLG3 OR NL3 OR KIAA1480.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 EN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=2021756; PubMed=10767552;
 RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Ginns E.I.;
 RT "The structure and expression of the human neurotrophin-3 gene."
 RL Gene 246:303-310(2000).
 EN [2]
 RP SEQUENCE OF 12-848 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20277482; PubMed=10819331;
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XVII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 7:143-150(2000).
 EN [3]
 RP SEQUENCE OF 410-848 FROM N.A.
 RA Isogai T., Ota T., Nishikawa T., Hayaishi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Maehuo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 EN [4]
 RP INTERACTION WITH DLG4.
 RX PubMed=9278515;
 RA Irie M., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,
 RA Takai Y., Rosahl T.W., Suedhof T.C.;
 RT "Binding of neurotrophins to PSD-95."
 RL Science 277:1511-1515(1997).
 EN [5]

NLG3_RAT
 ID NLG3_RAT STANDARD; PRT; 848 AA.
 AC Q62889;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuroligin 3 precursor (Glycactin homolog).
 GN NLG3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID:10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4). BLOCKAGE OF N-TERMINUS,
 RP TISSUE SPECIFICITY, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN
 RP 2-BETA AND NEUREXIN 3-BETA.
 RC TISSUE=Forebrain;
 RA Ichchenko K., Nguyen T., Suedhof T.C.;
 RT "Structures, alternative splicing, and neurexin binding of multiple
 RT neuroligins."; J. Biol. Chem. 271:2676-2682(1996).
 RL J. Biol. Chem. 271:2676-2682(1996).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX PubMed=1329178;
 RA Gilbert M., Smith J., Roskams A.J., Auld V.J.;
 RT "Neuroligin 3 is a vertebrate glycoprotein expressed in the olfactory
 RT ensheathing glia, a growth-promoting class of macroglia.";
 RL Glia 34:151-164(2001).
 CC -!- FUNCTION: Neuronal cell surface protein thought to be involved in
 CC cell-cell interactions by forming intercellular junctions through
 CC binding to beta-neurexins. May play a role in formation or
 CC maintenance of synaptic junctions. May also play a role in glia-
 CC glia or glia-neuron interactions in the developing peripheral
 CC nervous system.
 CC -!- SUBUNIT: Interacts with neuroligin 1-beta isoforms 3/Beta 4B5A and
 CC 4/Beta 4B5B. Interacts with neuroligin 2-beta isoforms 3/Beta 4B5A,
 CC 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with
 CC corresponding neuroligin 3-beta isoforms. Probably interacts through
 CC its C-terminus with DLG4/PSD-95 third PDZ domain (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoID=Q62889-1; Sequence=Displayed;
 CC Name=2;
 CC IsoID=Q62889-2; Sequence=VSP_007535, VSP_007536;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoID=Q62889-3; Sequence=VSP_007536;
 CC Name=4;
 CC IsoID=Q62889-4; Sequence=VSP_007535;
 CC -!- TISSUE SPECIFICITY: Expressed in brain, spinal cord and dorsal
 CC root ganglion.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC
 CC EMBL; U41663; AAA9781.1; -
 CC HSSP; P21836; 1MAA.
 CC InterPro; IPR002018; CarboxylesteraseB.
 CC InterPro; IPR000460; Neuroligin.
 CC Pfam; PF00135; COesterase; 1.
 CC PRINTS; PR01090; NEUROLIGIN.
 CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
 KW Alternative splicing.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 848 NEUROLIGIN 3.
 FT DOMAIN 38 709 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 710 730 POTENTIAL.
 FT DOMAIN 731 848 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 141 BY SIMILARITY.
 FT DISULFID 340 351 BY SIMILARITY.
 FT DISULFID 510 544 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 153 172 Missing (in isoform 2 and isoform 4).
 FT VARSPLIC 173 192 Missing (in isoform 2 and isoform 3).
 FT VARSPLIC 192 192 Missing (in isoform 2 and isoform 3).
 FT VARSPLIC 192 192 Missing (in isoform 2 and isoform 3).
 SQ SEQUENCE 848 AA; 93888 MW; 7520653B3253E750 CRC64;
 Query Match 60.9%; Score 2746; DB 1; Length 848;
 Best Local Similarity 61.1%; Pred. No. 1,le-145;
 Matches 538; Conservative 101; Mismatches 138; Indels 104; Gaps 18;
 QY 1 MWLLALCLVGLAGAQKGGGPGGAPGGGLGSLGSEERFPVNTAYGRVGRRELNN 60
 DB 26 LWFLSLVL--RSTQ-----APA-----FTVNTFFGKRGARVPLES 60
 QY 61 EILGPPVQFLGVPTATPLGARRFQPEAPSPGVRNATTLPPACPNLHGALPAIMLP 120
 DB 61 EILGPPVQFLGVPTATPLGARRFQPEAPSPGVRNATTLPPACPNLHGALPAIMLP 120
 QY 121 VFTDNLAAATVQNSQEDCLYLNLYPTD-----GPTFKKED 160
 DB 121 VFTANLDIVATYIQPNEDCLYLNLYPTDVKRISKECARPNKKICRKGSGAKQK 180
 QY 161 EATLN--SPDTIRDPKPKVWLFHGSGYMEGTCNMFDSGLAAYGNVIVATLNRYLG 217
 DB 181 EDLADNDEDEDIRSGAKPVWYIHGSGYMEGTCNMFDSGLAAYGNVIVATLNRYLG 240
 QY 218 VLGFSLTGQAQKNGYGLLDQALRWLSENIAHFGDPERITIFGSGAGACVNLILLS 277
 DB 241 VLGFSLTGQAQKNGYGLLDQALRWLSENIAHFGDPERITIFGSGAGACVNLILLS 300
 QY 278 HHSEGLFQKAIQSGTAISWSVNYQPLKYTRLLAAKVCDEDSAEAVECLRRKESREL 337
 DB 301 HHSEGLFQKAIQSGTAISWSVNYQPLKYTRLLAAKVCDEDSAEAVECLRRKESREL 360
 QY 338 VDODVOPARYHIAFGVVDGDDVDDPEILMQGGEFLNYDMLGYNQGLKFVEDSAES 397
 DB 361 VEQDIQARYHIAFGVVDGDDVDDPEILMQGGEFLNYDMLGYNQGLKFVEDSAES 420
 QY 398 EDGVSASAFDTVSNFVDNLYGYPEGKDVLRITKPMYTDWADRDNGEMRRTLLALFTD 457
 DB 421 EDGVSAGTDFYSVSNFVDNLYGYPEGKDVLRITKPMYTDWADRDNGEMRRTLLALFTD 480
 QY 458 HQWVAFAVATAKLHADYQSPVYVYTHHCOAEGREPWADAAGDELVYVFGVPMVGATD 517
 DB 481 HQWVEFSVTVADLHARYGPTFYAFYHHCQSLMKPWSADAAGDELVYVFGVPMVGATD 540
 QY 518 LFFCNFSKNDVMSLVAVMTYTNFAKTGDPNFPQDTKFIHTKPNRFEVVMKFSKSE 577
 DB 541 LFFCNFSKNDVMSLVAVMTYTNFAKTGDPNFPQDTKFIHTKPNRFEVVMKFSKSE 600
 QY 578 KQYLHLGLKPRVDNTRANKVAFWLEVLPHNLHTELF---TTTTLRPP-----YATRP 630
 DB 601 QLYLHLGLKPRVDNTRANKVAFWLEVLPHNLHTELF---TTTTLRPP-----YATRP 659
 QY 631 PRPPAGAGTTRPPPPATLPPPEPEPGPRAYDRFPDGS-----RDYSTELSVTV 680
 DB 660 RRPNGKWTSTKRP-----AISPAYSINENAFSGWN---GDQDAGFLLVENPRDYSTELSVTV 712
 QY 681 AVGASLLFLNLIAFAALYYKRRRQELCRRLSPGGSGSGVGGGLLPAGARELPPESE 740
 DB 713 AVGASLLFLNLIAFAALYYKRRRQELCRRLSPGGSGSGVGGGLLPAGARELPPESE 761

Takai Y., Rosahl T.W., Suedhof T.C.;
RT "Binding of neurotrogins to PSD-95.";
RL Science 277:1511-1515(1997).
RN [5]
RP INTERACTION WITH DLG4, AND TISSUE SPECIFICITY.
RX PubMed=11369786;
RA Bolliger M.F., Frei K., Winterhalter K.H., Gloor S.M.;
RT "Identification of a novel neuroligin in humans which binds to PSD-95
and has a widespread expression.";
RL Biochem. J. 356:581-588(2001).
CC -I- FUNCTION: Putative neuronal cell surface protein involved in cell-cell-interactions.
CC -I- SUBUNIT: Interacts through its C-terminus with DLG4/PSD-95 third PDZ domain.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: Expressed at highest levels in heart.
CC and expressed at lower levels in liver, skeletal muscle and pancreas and at very low levels in brain.
CC -I- DISEASE: Defects in NLGN4 may be the cause of X-linked autism [MIM:300425], a pervasive developmental disorder (PDD), prototypically characterized by impairments in reciprocal social interaction and communication, restricted and stereotyped patterns of interests and activities, and the presence of developmental abnormalities by 3 years of age.
CC -I- DISEASE: Defects in NLGN4 may be the cause of Asperger syndrome (AS), a form of childhood autism.
CC -I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR ENBL; AF376803; AAW46112.1; -;
DR ENBL; AB033086; BAA86574.1; ALT_INIT.
DR HMBL; BC034018; AAH34018.1; -;
DR HGSP; P21836; LMAA.
DR Genew; HGNC:14287; NLGN4.
DR MTM; 300427; -;
DR MM; 300425; -;
DR InterPro; IPR002018; CarbesteraeB.
DR InterPro; IPR000460; Neuroligin.
DR InterPro; IPR000379; Ser_estr_site.
DR Pfam; PF00135; Coesterase_1.
DR PRINTS; PR01090; NEUROLIGIN
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Cell adhesion; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 43
FT CHAIN 44 816
FT DOMAIN 44 676 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 677 697 POTENTIAL.
FT DOMAIN 698 816 CYTOPLASMIC (POTENTIAL).
FT DISULFID 110 145 BY SIMILARITY.
FT DISULFID 306 317 BY SIMILARITY.
FT DISULFID 476 510 BY SIMILARITY.
FT CARBOHYD 102 102 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 511 511 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 816 AA; 91915 MW; EA1320D690F76BBD CRC64;

Query Match 80.2%; Score 2713.5; DB 1; Length 816;
Best Local Similarity 63.8%; Pred. No. 7e-144;
Matches 520; Conservative 96; Mismatches 139; Indels 63; Gaps 13;

QY 38 EEFPVVNTAYGVRRVGRVRELNNELIGPVVFGLGVYATPPPLGARFQPPEAPSWPGVR 97
DB 42 QAQYPVNTNYGKIRGLRPLNELIGPVQEYLGVYASPPTGERFRQPPESSWTGIR 101

QY 98 NATTLPPACPQN-HGALPAIMLVPMFTDNLEAAATVQNQSDECIYLNLYVTEDGPLT 156
DB 102 NTTFQAACVPQHLDERSLLHDMLPIWFTANLDTLMTYVDQNDSDCIYLNLYVTED --- 157

QY 157 KKDEATLNPPDTRDP-GKPVMLFLHGSGYMEGTGMMFDGSLVLAAYGNVIVATLNYR 215
 Db 158 -----DHDQNSKKPVVYTHGSGYMEGTGMMFDGSLVLAAYGNVIVATLNYR 204
 QY 216 LGVGLSTGDAQAAGNYGLLQICALLRWLSNIAHFGDGPRIITFGSGAGASCWILLI 275
 Db 205 LGLGLSTGDAQAAGNYGLLQICALLRWLSNIAHFGDGPRIITFGSGAGASCWILLI 264
 QY 276 LSHHSEGLFQKAIASGTAISSWVNYQPLKTRLLAAKVGCDREDSAEAVECLRRKPSR 335
 Db 265 LSHYSEGLFQKAIISGTAISSWVNYQPAKTRILADKVGCMMLDITDVMVECLRNKNYK 324
 QY 336 ELVDQDVQFARVHIAFGPVGDGVDDPEILLMOQGEFLNMDLGVNQGSLGFVEDSA 395
 Db 325 ELIQTITPATVHIAFGPVGDGVDDPEILLMOQGEFLNMDLGVNQGSLGFVEDGIV 384
 QY 396 ESDGVSAFDTVSNFVNDLYGYPEGKVLRETIFKMYTDMADRDNGEMRKTLLALF 455
 Db 385 DNEGDGVTNDFSVSNFVNDLYGYPEGKDLRETIFKMYTDMADRDNGEMRKTLLALF 444
 QY 456 TDHOMVAPAVATAKLHADYQSPVYEVTVHCOAGREPEWADAAGDELPTVFGVPMVGA 515
 Db 445 TDHOMVAPAVATAKLHADYQSPVYEVTVHCOAGREPEWADAAGDELPTVFGVPMVGA 504
 QY 516 TDLFFCNFSKNDVMSAVVMTYTNFAKTGDPNPQDTKFIHTKPNRFEVVVSKFNS 575
 Db 505 TELFCNFSKNDVMSAVVMTYTNFAKTGDPNPQDTKFIHTKPNRFEVVVSKFNS 564
 QY 576 KEKQVHLGLKPRVDNRANKVAFWELVPLHLNHLTELF-----TTTTRLP 625
 Db 565 KDQLYLHGLKPRVDNRANKVAFWELVPLHLNHLN-EIFQYVSTTTKVPDPMTGFFY 623
 QY 626 ATRWPPRPAG-A-POTRPPPPATLPPPEPEPEP---GPRVDRFPDGRSDYSTLSVTVA 681
 Db 624 GTR---RSPAKWPTTKPATPANPKSKDPKHTGPDVTVLIEKXDYSTLSVTVA 680
 QY 682 VGASLLFLNLAFAALYKRRDRQELRCRLSPGGSGGVGGPGLLPAAAGRELPEEE 741
 Db 681 VGASLLFLNLAFAALYKRRDRQELRCRLSPGGSGGVGGPGLLPAAAGRELPEEE 728
 QY 742 LVSLOLQK---GGGVGADPAEALRACPPDYTLALRAPDDVPLAPGALTLLPSGLP 797
 Db 729 LMSLOKQLEHDECELSQADHTLRLTCTPDYTLRLRSPDDIFLMTPTNITMPTLTG 788
 QY 798 PPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV 835
 Db 789 MQP-----LHTFNTF-----SGGQNSTLPHGHSTTRV 816
 RESULT 10
 NLGY HUMAN
 ID NLGY HUMAN STANDARD; PRT; 816 AA.
 AC Q8NFZ3; Q9Y2F8;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuroigin 4, y linked precursor (Neuroigin y).
 GN NLGN4Y OR KIAA0951.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX PubMed=12669065;
 RA Jamin S., Quach H., Betancur C., Rastam M., Colineaux C.,
 RA Gillberg I.C., Soderstrom H., Gjos B., Leboyer M., Gillberg C.,
 RA Bourgeron T., Nyden A., Philippe A., Cohen D., Chabane N.,
 RA Mouron-Simeoni M.C., Brice A., Sponheim E., Spurkland I.,
 RA Skjeldal O.H., Coleman M., Pearl P.L., Cohen I.L., Tsilouris J.,
 RA Zappella M., Menchetti G., Pompella A., Aschauer H., Van Maldergem L.;
 RT "Mutations of the X-linked genes encoding neuroigins NLGN3 and NLGN4

RT are associated with autism.";
 RL Nat. Genet. 34:27-29(2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=99246063; PubMed=10231032;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:63-70(1999).
 CC -I- FUNCTION: Putative neuronal cell surface protein involved in cell-
 CC cell-interactions.
 CC -I- SUBUNIT: Interacts through its C-terminus with DLG4/PSD-95 third
 CC PDZ domain (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8NFZ3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8NFZ3-2; Sequence=VSP_007537;
 CC Note=No experimental confirmation available;
 CC -I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC
 CC EMBL; AF376804; AAM46113.1; --
 CC EMBL; AB023168; BAA76795.1; --
 CC InterPro; IPR002018; Carboxylesterase.
 CC InterPro; IPR000460; Neuroigin.
 CC InterPro; IPR000379; Ser esters_site.
 CC Pfam; PF00135; Coesterase; 1.
 CC PRINTS; PR01090; NEUROIGIN.
 CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 CC Cell adhesion; Glycoprotein; Signal; Transmembrane;
 CC Alternative splicing.
 FT SIGNAL 1 43
 FT CHAIN 44 816
 FT DOMAIN 44 676
 FT TRANSMEM 677 697
 FT DOMAIN 698 816
 FT DISULFID 110 146
 FT DISULFID 306 317
 FT DISULFID 476 510
 FT CARBOHYD 511 511
 FT VARSPIC 1 168
 FT SEQUENCE 816 AA; 92020 MW; FB68910773B1BBF6 CRC64;
 QY 38 ERFVNTAYGRVGRVRELNNEILGPVQPLGVYATPPLGARRFQPPAPASWPGVR 97
 Db 42 QAQYVVTNTYKIQGLRTPLPSEILGPVYASPTTGERFQPPSPSSWTGIR 101
 QY 98 NATTLPPACPNL-HGALPAIMLPVMTDNLFAATYVQNSQEDCLNLYVPTDGLT 156
 Db 102 NATQSAVCPQHLDERFLHMLPFWFTSLDTLMTYVQDQNECLNLYVPMED---- 157
 QY 157 KKRDEATLNPPDTRDP-GKPVMLFLHGSGYMEGTGMMFDGSLVLAAYGNVIVATLNYR 215
 Db 158 -----DIHQNSKKPVVYTHGSGYMEGTGMMFDGSLVLAAYGNVIVATLNYR 204
 Query Match 59.4%; Score 2678.5; DB 1; Length 816;
 Best Local Similarity 62.7%; Pred. No. 6.2e-142;
 Matches 513; Conservative 101; Mismatches 141; Indels 63; Gaps 13;

DE (Choline esterase II) (Butyrylcholine esterase)
GN (Pseudocholinesterase).
OS BCHE OR CHEL.
OS Homo sapiens (Human).
OC Sakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP MEDLINE=90212557; PubMed=2322535;
RX Arpagaus M., Kott M., Varsis K.P., Bartels C.F., la Du B.N.,
RA Lockridge O.;
RA "Structure of the gene for human butyrylcholinesterase. Evidence for
RT a single copy.";
RT Biochemistry 29:124-131(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Fetal;
RX MEDLINE=87231856; PubMed=3035536;
RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreq H.;
RT "Isolation and characterization of full-length cDNA clones coding for
RT cholinesterase from fetal human tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=88016155; PubMed=3477799;
RA McTiernan C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,
RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.;
RT "Brain cDNA clone for human cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN [4]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Zeebman B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN SEQUENCE OF 29-602.
RP TISSUE=Plasma;
RX MEDLINE=87109144; PubMed=3542989;
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RA Johnson L.L.;
RT "Complete amino acid sequence of human serum cholinesterase.";
RL J. Biol. Chem. 262:549-557(1987).
RN [6]
RN DISULFIDE BONDS.
RX MEDLINE=88007487; PubMed=3115973;
RA Lockridge O., Adkins S., la Du B.N.;
RT "Location of disulfide bonds within the sequence of human serum
RT cholinesterase.";
RL J. Biol. Chem. 262:12945-12952(1987).
RN [7]
RN REVIEW.
RX MEDLINE=89149759; PubMed=3067729;

RA Lockridge O.;
RT "Structure of human serum cholinesterase.";
RL Bioessays 9:125-128(1988).
RN [8]
RN VARIANT ATYPICAL GLY-98.
RX MEDLINE=89128896; PubMed=2915989;
RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA van der Spek A.F.L., Lockridge O., la Du B.N.;
RT "Identification of the structural mutation responsible for the
RT dibucaine-resistant (atypical) variant form of human serum
RT cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN [9]
RN VARIANT ILE-358.
RX MEDLINE=96287386; PubMed=8680411;
RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA Moriwaki K.;
RT "Mutations of human butyrylcholinesterase gene in a family with
RT hypocholinesterasemia.";
RL Hum. Mutat. 6:349-351(1995).
CC -|- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -|- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED
CC OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A
CC DISULFIDE BOND.
CC -|- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -|- DISEASE: MUTANT ALLELES OF CHE1 ARE RESPONSIBLE FOR
CC HYPOCHOLINESTERASEMIA RESULTING IN SUKAMETHONIUM SENSITIVITY.
CC HOMozyGous PERSONS SUSTAIN PROLONGED APNEA AFTER ADMINISTRATION
CC OF THE MUSCLE RELAXANT SUKAMETHONIUM IN CONNECTION WITH SURGICAL
CC ANESTHESIA.
CC -|- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; M32391; AAA99296.1; -;
CC EMBL; M32389; AAA99296.1; JOINED.
CC EMBL; M32390; AAA99296.1; JOINED.
CC EMBL; M16541; AAA98113.1; -;
CC EMBL; M16474; AAA52015.1; -;
CC EMBL; BC018141; AAH18141.1; -;
CC PIR; A33769; ACU.
CC PDB; 1EHO; 08-AUG-01.
CC PDB; 1EHQ; 08-AUG-01.
CC Genew; HGNC:983; BCHE.
CC MIM; 177400; -;
CC GO; GO:0004104; F:cholinesterase activity; TAS.
CC InterPro; IPR002018; CarboxylesteraseB.
CC InterPro; IPR000997; Cholinesterase.
CC InterPro; IPR000379; Ser_setra_site.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLINESTERASE.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Hydrolase; Serine esterase; Glycoprotein; Signal; Disease mutation;
CC Polymorphism; 3D-structure.
FT SIGNAL 1 28
FT CHAIN 29 602 CHOLINESTERASE.
FT ACT SITE 226 226
FT ACT SITE 353 353 BY SIMILARITY.
FT ACT SITE 466 466 BY SIMILARITY.
FT DISULFID 93 120
FT DISULFID 280 291
FT DISULFID 428 547
FT DISULFID 599 599 INTERCHAIN.

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FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .)
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .)
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .)
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .)
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .)
FT CARBOHYD 369 369 N-LINKED (GLCNAC. . .)
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .)
FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .)
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .)
FT CARBOHYD 98 98 D -> G (IN ATYPICAL FORM, DIBUCAINE-
FT VARIANT REGISTANT; dbsNP:1799807).
FT VARIANT /FTID=VAR 002360.
FT VARIANT T -> M (IN FLUORIDE-1).
FT VARIANT /FTID=VAR 002361.
FT VARIANT L -> I (IN HYPOCHOLINESTERASEMIA).
FT VARIANT /FTID=VAR 002362.
FT VARIANT G -> V (IN FLUORIDE-2).
FT VARIANT /FTID=VAR 002363.
FT VARIANT A -> T (IN K VARIANT; WITH REDUCED ENZYME
FT VARIANT ACTIVITY; dbsNP:1803274).
FT VARIANT /FTID=VAR 002364.
FT SEQUENCE 602 AA; 68418 MW; C9836409D9057F27 CRC64;
Query Match 19.0%; Score 855; DB 1; Length 602;
Best Local Similarity 32.5%; Pred. No. 1.3e-40;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;
QY 2 WLLALCLVGLAGQRCGGGPGGAPGGLGSLGEERFPVVNTAYGVGRVRELNNE 61
Db 15 WFLLLCWL-----IGKSHTEDDIIATKNGKVRG---MMLT 47
QY 62 IL-GPVVQFLGVYATPPLGAREFOPPEAPASWPGVGNATTLPPAQPNLHGALPAIMLP 120
Db 48 VFGGTVAFLGIFYAQPPLGLRFLFKPKFQSLKWSDIWNAIKYANSCCNIDQSPFGFHS 107
QY 121 VMTDNLAAATVQVQNSDECLVNLVYPTEDGPLTKKSDATLNPDPFDIDRDKPKPYM 180
Db 108 EMNPNPTDL-----SEDCLYNLVWIPAP-----KPKNATVL 138
QY 181 LFLHGSGYMEGTGNM--FDGSLVLAAGNIVATNLVRLGLVGLFLS-TGDAQAKGNVGLLD 237
Db 139 IWIYGGFTGTSLSLVYDGKFLARVERVIVSMNTRVGALGFLAPGNFPAQNGNGLFD 198
QY 238 QIQALRWLSNIAHFQGDPERITIFGAGASCWNLLILSHHSEGLFQKAIQAQSGTAISS 297
Db 199 QQLALQWQKNIAAFQGNPKSVTLFGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSYN--YQPLKYTLIAAKVCGDREDSAEVCLRKPSRELVDQVQARY-----HIAF 351
Db 259 WAVTSYEARNRTNLAKLTGCSRENETIILKLRNKPQOEILLNEAFVVPVYGTFLSVNF 318
QY 352 GPVVDGVDVDPDPEILMQQGEFLNYDMLIGVNOGELKTEVEDSAE--SDGVSASAFDFT 409
Db 319 GPTVDGDLTMDPDLLELLELQFKTKQLVGVNKGDEGTAFLVYGAFGFSKDNNSI----IT 374
QY 410 VSNFVNLL-YGYPEGKDVLRRTIKFWYTOWARDNGEMRKTLALLFTDHWQWAVATA 468
Db 375 RKPFQGLKTFPFQSEFSGESILFTYTDVDDQDRPENREALGDVGVGYNFICALEFT 434
QY 469 KLHADYQSPVYFTFYHHCQAEGRPEWADAAGDELPPYVFGVPMVGATDLFFCNFSKNDV 528
Db 435 KKPSEWGNNAFFYFPHRSKLPWPBWGMVMEGYEIEFVGLPLERRD-----NTYKAE 489
QY 529 MLSAVVWYVNTNFAKTGDPNPQVPQDTKTHTKPNRFEVWVKFNSKEQYLHGLK-P 587
Db 490 ILSRSIVKRWANFAKYGNFNETQNNST-----WPVFKSTEQKYLTLNTEST 536
QY 588 RVRDNYRANKVAFWLELVP 606
Db 537 RIMTKLRAQOCREWTSTFFP 555

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RESULT 14

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ACES MOUSE
ID ACES MOUSE STANDARD; PRT; 614 AA.
AC P21836;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
OS ACHE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=90380429; PubMed=2400605;
RA Machinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
RT of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=129/SV;
RX MEDLINE=21138439; PubMed=11239002;
RA Wilson M.D., Riener C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.P.;
RT "Comparative analysis of the gene-dense ACHE/TFP2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL Nucleic Acids Res. 29:1352-1365(2001).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RX MEDLINE=96067648; PubMed=8521480;
RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
RT the complex.";
RL Cell 83:503-512(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=99115643; PubMed=9915834;
RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
RT occluding loop in a tetrameric assembly.";
RL J. Biol. Chem. 274:2963-2970(1999).
CC -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -!- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE
CC LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
CC MONOMERS AND DIMERS TO COLLAGE-TAILED AND HYDROPHOBIC-TAILED
CC FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING
CC PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
CC MEMBRANES. IN THE COLLAGE-TAILED FORMS, ISOFORM T SUBUNITS ARE
CC ASSOCIATED WITH A SPECIFIC COLLAGEN, COLQ, WHICH TRIGGERS THE
CC FORMATION OF ISOFORM T TETRAMERS, FROM MONOMERS AND DIMERS (BY
CC SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=P21836-1; Sequence=Displayed;
CC Name=H;
CC IsoId=P21836-2; Sequence=Not described;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES EXCEPT
CC ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF ACHE
CC PREDOMINATES.
CC -!- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
CC CHOLINESTERASE, WITH A COLLAGE-LIKE PART DISULFIDE-BONDED TO THE
CC CATALYTIC PART, A DIFFERENT GLOBULAR TYPE OF CHOLINESTERASE
CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
CC ERYTHROCYTES.
CC -!- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
CC SOLUBLE FORM OF ACHE.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----

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EMBL; X56518; CAA39867.1; -
 EMBL; AF312033; AAK28816.1; -
 PIR; JH0314; JH0314.
 PDB; 1MAH; 03-APR-96.
 PDB; 1MAA; 20-APR-99.
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 PDB; 1C2O; 19-JAN-00.
 PDB; 1J06; 04-FEB-03.
 PDB; 1J07; 04-FEB-03.
 PDB; 1NEM; 04-FEB-03.
 PDB; 1NSR; 04-FEB-03.
 MGD; MGI:87876; Ache.
 GO; GO:0045202; C:synaptic junction; IDA.
 InterPro; IPR002018; Carboxylesterase.
 InterPro; IPR000997; Cholinesterase.
 InterPro; IPR000379; Ser esterase.
 Pfam; PF00135; Coesterase; 1.
 PRINTS; PR00878; CHOLINESTERASE.
 PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 Neurotransmitter degradation; Glycoprotein; Alternative splicing;
 3D-structure.
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Db 294 GNDTELIACTRAQDLVDHEWHLVQESIFRFSFVVDGDFSLDTPALINTGDFQ 353
QY 375 NYDMLIGNVQSGELKFV-----EDSAESEDGVSASAFDTVSNFVDNLYGYPEGKDVLR 429
Db 354 DLQVLGVVQKDEGSYFLVYVGFSGKDNESLISRAQFLAGVR-----IGVPGASDLAAE 407
QY 430 TIKFWYTOWADRDNGEMERKILLALFTDHWAPAVATAKLHADYQSPVYTYTHHCQA 489
Db 408 AVLHYHTLWHPEDTHLRDAMSAAVGVHNVCPVQAQAGLAAQAGARVYAYIFEHRAST 467
QY 490 EGRPEWADAADDELYVFGVPMVGATDLFCNFSKNDVMSAVVMTYTNFAKTGDPNQ 549
Db 468 LTMPLMVGPHGYEYEFGLPLDPS-----LNYTBERIQAQLMKXWTNFAKTGDPND 522
QY 550 PVPQTKIHKPNRPFBEVWSKFNKSKQYLHGLKP-RVYDNYRANKVAFWLELVPHL 608
Db 523 --PRDSK-----SPQ-----WFPYTAAQYVSLNLKPLEVRGLRAQTCAPMNRFLP-- 568
QY 609 HNLHTELETTITRLPPYATRW 629
Db 569 -----KLISATDTLDEAEQW 584

RESULT 15
ACES_RAT
ID ACES_RAT STANDARD; PRT; 614 AA.
AC P37136;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN ACHE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM T).
RX MEDLINE=93107932; PubMed=8417155;
RA Legay C., Bon S., Vernier P., Cussen F., Massoulie J.;
RT "Cloning and expression of a rat acetylcholinesterase subunit;
RT generation of multiple molecular forms and complementarity with a
RT Torpedo collegenic subunit.";
RL J. Neurochem. 60:337-346 (1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS H AND R).
RX MEDLINE=93114454; PubMed=8417973;
RA Legay C., Bon S., Massoulie J.;
RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
RT acetylcholinesterase.";
RL FEBS Lett. 315:163-166 (1993).
CC -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-
CC TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES
CC OF KNOWN ACHE FORMS.
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=3;
CC Name=T;
CC Name=H;
CC IsoId=P37136-1; Sequence=Displayed;
CC IsoId=P37136-2; Sequence=VSP_001458;
CC Name=R;
CC IsoId=P37136-3; Sequence=VSP_001459;
CC Note=May be not functional;
CC -!- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND
CC MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT
CC LIVER.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; SS0879; AAB24586.1; -
CC EMBL; X70140; CAA49717.1; -
CC EMBL; X70141; CAA49718.1; -
CC PIR; JH0811; JH0811.
CC HSP; P21836; IMAA.
CC InterPro; IPR002018; Carboxylesterases.
CC InterPro; IPR000997; Cholinesterase.
CC InterPro; IPR000379; Ser estersite.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLINESTRASE.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
CC Neurotransmitter degradation; Glycoprotein; Alternative splicing.
CC SIGNAL 1 31 POTENTIAL.
CC CHAIN 32 614 ACETYLCHOLINESTERASE.
CC ACT_SITE 234 234 BY SIMILARITY.
CC ACT_SITE 365 365 BY SIMILARITY.
CC ACT_SITE 478 478 BY SIMILARITY.
CC DISULFID 100 127 BY SIMILARITY.
CC DISULFID 288 303 BY SIMILARITY.
CC DISULFID 440 560 BY SIMILARITY.
CC DISULFID 611 611 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 296 296 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 381 381 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 495 495 N-LINKED (GLCNAC...) (POTENTIAL).
CC VARSPLIC 575 614 DTLEAEQWKAERFRWSSYVHWKQFDHSHKQRCSDL
CC -> ATEVPCTSPAHGAAPRPGFALSLSLFLFLHSG
CC LRMW (in isoform H).
CC /FTIQ-VSP 001458.
CC FT VARSPLIC 575 614
CC DTLEAEQWKAERFRWSSYVHWKQFDHSHKQRCSDL
CC isoform R)
CC /FTIQ-VSP 001459.
CC SEQUENCE 614 AA; 68196 MW; 2EAE7D46282E7C0 CRC64;
Query Match 18.8%; Score 846.5; DB 1; Length 614;
Best Local Similarity 33.0%; Pred. No. 4.1e-40;
Matches 205; Conservative 98; Mismatches 235; Indels 83; Gaps 17;
QY 31 LGLSIGLEERFP---VNTAYGRVGRVRELNNEILGPVQFLGVPYATPPLGARFQPP 87
Db 25 LGGGARAEGRDPQLLVVRVGGQIGIRLKAPG---GPVSAPLGIPIFAAPPVGSRRFPP 81
QY 88 EAPASWPGVRNATLPPACPNLHGALPAIMLPVMTDNLAAATVQNQSDCLYLNLY 147
Db 82 EPRKPSGLDATTQNVCYQVDTLYPGFEGTEWNPREL-----SEDCLYLVNW 133
QY 148 VTEOPLTKGDEATLPPDITDIPGKPVMLFHGGSYMEGTGM--PDGSLVLAAYG 205
Db 134 TTPY-----RPTSPTPLIWIYGGFGYSGASSLDVYDGRFLAQVE 173
QY 206 NVIVATLNYRLVGLFGLS-TGDOAAKNGVGLDQALRWLSENIAHFSGDPERITFGS 264
Db 174 GTVLVSMYRVGTGFLALPGSREAPGVNGLDQELALQWQENIAAEGDPMSTLGE 233
QY 265 GAGACVNLILSHSEGLFKATAQSGTAISSMSV--NYQFLKYTRLLAAKVGCD---- 318
Db 234 SAGAAVGMHILSLPSRLFRAVLQSGTPNGPNATVSAGEARRATLLARLVGPPGGA 293
QY 319 REDSAEAEVCLRRKPSRELVDQD---VQPARYHIAFGVVDGVVDPPDPEILMQQBEFL 374
Db 294 GGNDELISCLNTRPAQLVDHEWHLVQESIFRFSFVVDGDFSLDTPALINTGDFQ 353
QY 375 NYDMLIGNVQSGELKFV-----EDSAESEDGVSASAFDTVSNFVDNLYGYPEGKDVLR 429

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Db 354 DLOVLGVWVWDEGSYFLVYGVPGFSKDNESLISRAQFLAGVR-----ICVPOASDLAAE 407
Qy 430 TIKFMYTDMADRDNGEMRRKTLALPTDHOVAPAVATAKLHADYQSPVYFYTFYHHCOA 489
Db 408 AVVLHYTDNLHPEDPAHLRDAMSAVVGDHNVVCPVAQLAGRLAAQGARVYAYIFEHRAST 467
Qy 490 EGRPEWADAAHGDELPHYVGVPMVGATDLEPCNFSKNDVMSAVVMYTWNTFAKTGDPNQ 549
Db 468 LTWPLMNGVPHGYEIEFIFGLPLDPS-----LNYTVEERIFAQRLAQYWTNFARTGDPND 522
Qy 550 PVPQDTKFIHTKPNRPEEVVWSKFSKSKOYLHGLKP-RVRDNYRANKVAFWLELVPHL 608
Db 523 --PRDSK-----SPR-----WPPYTTAAQQYVSINLKPLEVRRLRAQTCAFWNRFLP-- 568
Qy 609 HNLHLELFTTTTTLPPYATEW 629
Db 569 -----KLSATDTLDEAERQW 584

Search completed: February 13, 2004, 13:12:38
Job time : 19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: February 13, 2004, 13:09:47 ; Search time 46 Seconds
(without alignments)
4684.216 Million cell updates/sec

Title: US-09-934-323-2

Perfect score: 4508
Sequence: 1 MWLLALCLVLGLAGAQGGGG.....PPTATSHNTLPHPHSTTRV 835

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4508	100.0	835	4 Q8NFZ4	Q8nfz4 homo sapien
2	4415.5	97.9	836	11 Q62888	Q62888 rattus norv
3	2986	66.2	550	4 Q9P211	Q9p211 homo sapien
4	2773.5	61.5	825	11 Q8BYM5	Q8bym5 mus musculu
5	2771	61.5	843	11 Q62765	Q62765 rattus norv
6	2770	61.4	828	4 Q9NZ94	Q9nz94 homo sapien
7	2765.5	61.3	823	4 Q9UPT2	Q9upt2 homo sapien
8	2763	61.3	828	4 Q9NZ97	Q9nz97 homo sapien
9	2750	61.0	848	4 Q9NZ95	Q9nz95 homo sapien
10	2746	60.9	848	11 Q62889	Q62889 rattus norv
11	2713.5	60.2	816	4 Q8NW44	Q8nw44 homo sapien
12	2713.5	60.2	817	4 Q9ULG0	Q9ulg0 homo sapien
13	2678.5	59.4	816	4 Q8NFZ3	Q8nfz3 homo sapien
14	2344	52.0	682	4 Q9P248	Q9p248 homo sapien
15	2287	50.7	648	4 Q9VZF8	Q9vzf8 homo sapien
16	1999	44.3	558	4 Q9NZ96	Q9nz96 homo sapien

Q8n2q7 homo sapien
Q8bxr4 mus musculu
Q8ncd0 homo sapien
Q9ngk5 drosophila
Q9vic5 drosophila
Q9nl9 equus cabal
Q9vic7 drosophila
Q9nld1 gorilla gor.
Q9vdp5 drosophila
Q8row5 mus musculu
Q46421 macaca fasc
Q9jkc1 rattus norv
Q77540 oryctolagus
Q87582 sus scrofa
Q62760 felis silve
Q8row7 mus musculu
Q9up41 homo sapien
Q62761 panthera ti
P70104 cavia porce
Q6e88 homo sapien
Q90xk8 gallus gall
Q95n05 canis fami
Q16398 homo sapien
Q64571 rattus norv
Q8i034 felis silve
Q76998 brachiosto
Q8tdz9 homo sapien
Q9uk77 homo sapien
Q8ism4 anopheles g

ALIGNMENTS

RESULT 1

Q8NFZ4
ID Q8NFZ4 PRELIMINARY; PRT; 835 AA.
AC Q8NFZ4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Neurologin 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jamain S., Quach H., Fellous M., Bourgeron T.,
RT "Evolution and expression of the human neurologin family, including
RT two primate specific members on the X and Y chromosomes.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF376802; AAM46111.1; --
DR InterPro; IPR002018; CarboxesteraseB.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR002965; P rich extensn.
DR InterPro; IPR000379; Ser est:s_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PRINTS; PR01217; PRICHEXTENSIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 835 AA; 90819 MW; 359938630193EF87 CRC64;

Query Match 100.0%; Score 4508; DB 4; Length 835;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLLALCLVLGLAGAQGGGGPGGPGGLGSLGEERFPVNTAYGRVGRVRELN 60

Db 1 MWLLALCLVLGLAGAQGGGGPGGPGGLGSLGEERFPVNTAYGRVGRVRELN 60

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QY 61 EILGPVVQFLGVFYATPPLGARRFQPEAPASWPGVGNATLTPPACQNLHGAIPALMLP 120
Db 61 EILGPVVQFLGVFYATPPLGARRFQPEAPASWPGVGNATLTPPACQNLHGAIPALMLP 120
QY 121 VWTNDLEAAATVYQNSDCLYLNLYVPTDGLTKKDEATLAPPDTHIDPQKPKVM 180
Db 121 VWTNDLEAAATVYQNSDCLYLNLYVPTDGLTKKDEATLAPPDTHIDPQKPKVM 180
QY 181 LFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAKNGYGLDQIQ 240
Db 181 LFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAKNGYGLDQIQ 240
QY 241 ALRWLSENIAHFGDPERITIFSGAGASCNVLILSHSEGLFQKAIQSGTAISSWSV 300
Db 241 ALRWLSENIAHFGDPERITIFSGAGASCNVLILSHSEGLFQKAIQSGTAISSWSV 300
QY 301 NYOPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARHYIAFGPVVDGVDV 360
Db 301 NYOPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARHYIAFGPVVDGVDV 360
QY 361 PDDPEILMQQGEFLNYDMLIGNVQGEGLKFVEDSAESDGVSAFDFTVSNFVNDLYGY 420
Db 361 PDDPEILMQQGEFLNYDMLIGNVQGEGLKFVEDSAESDGVSAFDFTVSNFVNDLYGY 420
QY 421 PEGKDLVRETIKFMYTDWADRDNGEMRRKTLTLLALFTDHWVAPAVATAKLHADYQSPVVF 480
Db 421 PEGKDLVRETIKFMYTDWADRDNGEMRRKTLTLLALFTDHWVAPAVATAKLHADYQSPVVF 480
QY 481 YTFYHHCQAEGRPEWADAAGHDELPIYVFGVMVGTDLFPFCNFSKNDVMSAVVMTYWTN 540
Db 481 YTFYHHCQAEGRPEWADAAGHDELPIYVFGVMVGTDLFPFCNFSKNDVMSAVVMTYWTN 540
QY 541 FAKTGPNQVPQDTKFIHTKPNRFEEVWWSKFNSEKQYLIHGLKPRVDNYRANKVAF 600
Db 541 FAKTGPNQVPQDTKFIHTKPNRFEEVWWSKFNSEKQYLIHGLKPRVDNYRANKVAF 600
QY 601 WLELVPHLNLHTELTFTTTLRPPYATRWPPRPPACAGCTRRPPPPATLPPPEPEPGPR 660
Db 601 WLELVPHLNLHTELTFTTTLRPPYATRWPPRPPACAGCTRRPPPPATLPPPEPEPGPR 660
QY 661 AYDRFPGSDSDYSTELSVTVAVGASLLFNILAFALYYKRRDRQELRCRLSPGSGGS 720
Db 661 AYDRFPGSDSDYSTELSVTVAVGASLLFNILAFALYYKRRDRQELRCRLSPGSGGS 720
QY 721 GVPGGGPLLPAAGRELPPPEELVSLQKGGGVGADPAEALRPACPDYTLALRRAPDDV 780
Db 721 GVPGGGPLLPAAGRELPPPEELVSLQKGGGVGADPAEALRPACPDYTLALRRAPDDV 780
QY 781 PLLAPGALTLLPSGLGPPPPPPPSLHFGPPPPPPPTATSHNNTLPHPHSTTRV 835
Db 781 PLLAPGALTLLPSGLGPPPPPPPSLHFGPPPPPPPTATSHNNTLPHPHSTTRV 835

RESULT 2
Q62888 PRELIMINARY; PRT; 836 AA.
ID Q62888
AC Q62888;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Neurologin 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=forebrain;
RX MEDLINE=96162010; PubMed=8576240;
RA Ichtchenko K., Nguyen T., Sudhof T.C.;
RT "Structures, alternative splicing, and neurexin binding of multiple
RT neurologins.";
RL J. Biol. Chem. 271:2676-2682 (1996).
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CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; U41662; AAA97870.1; -.
DR HSP; P37967; IOE3.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PRO1090; NEUROLIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Hydrolase.
SQ SEQUENCE 836 AA; 90961 MW; 1AD51CB1BE4BF9CF CRC64;

Query Match 97.9%; Score 4415.5; DB 11; Length 836;
Best Local Similarity 98.3%; Pred. No. 8.2e-318;
Matches 822; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 1 MWLLALCLVLAGAQRGGGPGGAPGGGLGSLGEERFPVNTAYGVRGVRRELN 60
Db 1 MWLLALCLVLAGAQRGGGPGGAPGGGLGSLGEERFPVNTAYGVRGVRRELN 60
QY 61 EILGPVVQFLGVFYATPPLGARRFQPEAPASWPGVGNATLTPPACQNLHGAIPALMLP 120
Db 61 EILGPVVQFLGVFYATPPLGARRFQPEAPASWPGVGNATLTPPACQNLHGAIPALMLP 120
QY 121 VWTNDLEAAATVYQNSDCLYLNLYVPTDGLTKKDEATLNPDDTDIRDPKPKVM 180
Db 121 VWTNDLEAAATVYQNSDCLYLNLYVPTDGLTKKDEATLNPDDTDIRDPKPKVM 180
QY 181 LFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAKNGYGLDQIQ 240
Db 181 LFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAKNGYGLDQIQ 240
QY 241 ALRWLSENIAHFGDPERITIFSGAGASCNVLILSHSEGLFQKAIQSGTAISSWSV 300
Db 241 ALRWLSENIAHFGDPERITIFSGAGASCNVLILSHSEGLFQKAIQSGTAISSWSV 300
QY 301 NYOPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARHYIAFGPVVDGVDV 360
Db 301 NYOPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARHYIAFGPVVDGVDV 360
QY 361 PDDPEILMQQGEFLNYDMLIGNVQGEGLKFVEDSAESDGVSAFDFTVSNFVNDLYGY 420
Db 361 PDDPEILMQQGEFLNYDMLIGNVQGEGLKFVEDSAESDGVSAFDFTVSNFVNDLYGY 420
QY 421 PEGKDLVRETIKFMYTDWADRDNGEMRRKTLTLLALFTDHWVAPAVATAKLHADYQSPVVF 480
Db 421 PEGKDLVRETIKFMYTDWADRDNGEMRRKTLTLLALFTDHWVAPAVATAKLHADYQSPVVF 480
QY 481 YTFYHHCQAEGRPEWADAAGHDELPIYVFGVMVGTDLFPFCNFSKNDVMSAVVMTYWTN 540
Db 481 YTFYHHCQAEGRPEWADAAGHDELPIYVFGVMVGTDLFPFCNFSKNDVMSAVVMTYWTN 540
QY 541 FAKTGPNQVPQDTKFIHTKPNRFEEVWWSKFNSEKQYLIHGLKPRVDNYRANKVAF 600
Db 541 FAKTGPNQVPQDTKFIHTKPNRFEEVWWSKFNSEKQYLIHGLKPRVDNYRANKVAF 600
QY 601 WLELVPHLNLHTELTFTTTLRPPYATRWPPRPPA-GAPCTRRPPPPATLPPPEPEPGP 659
Db 601 WLELVPHLNLHTELTFTTTLRPPYATRWPPRPPA-GAPCTRRPPPPATLPPPEPEPGP 660
QY 660 RAYDRFPGSDSDYSTELSVTVAVGASLLFNILAFALYYKRRDRQELRCRLSPGSGG 719
Db 661 RAYDRFPGSDSDYSTELSVTVAVGASLLFNILAFALYYKRRDRQELRCRLSPGSGG 720
QY 720 SGVFGGGPLLPAAGRELPPPEELVSLQKGGGVGADPAEALRPACPDYTLALRRAPDD 779
Db 721 SGVFGGGPLLPAAGRELPPPEELVSLQKGGGVGADPAEALRPACPDYTLALRRAPDD 780
QY 780 VPLLAPGALTLLPSGLGPPPPPPPSLHFGPPPPPPPTATSHNNTLPHPHSTTRV 835
Db 781 VPLLAPGALTLLPSGLGPPPPPPPSLHFGPPPPPPPTATSHNNTLPHPHSTTRV 836
```

RESULT 3

Q9P211 PRELIMINARY; PRT; 550 AA.
 AC Q9P211; 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Hypothetical protein KIAA1366 (fragment).
 GN KIAA1366.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCSI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirokawa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 CC -/- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; AB037787; BA92604.1; -;
 DR HSSP; P21836; 1MAA.
 DR Genew; HGNC:14290; NLGN2.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR InterPro; IPR000460; NeuroLigin.
 DR InterPro; IPR002965; P-rich_extensn.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR01090; NEUROLIGIN.
 DR PRINTS; PR01217; PRICHEXTENGN.
 GW Hypothetical protein; Hydrolase.
 NT NON_TER
 IT 1
 Q SEQUENCE 550 AA; 60734 MW; 5B09C3E23233618F1 CRC64;

Query Match 66.2%; Score 2986; DB 4; Length 550;
 Best Local Similarity 100.0%; Pred. No. 2.3e-212;
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

286 KAIAQSGTAISSWNYQPLKYLTRLLAAKVGCDREDSAEAECLRRKPSRELVDQVPA 345
 1 KAIAQSGTAISSWNYQPLKYLTRLLAAKVGCDREDSAEAECLRRKPSRELVDQVPA 60
 346 RVHIAFGPVVDGVDPEILMQQGEFLNYDMLIGVNGQEGKLFVEDSAEEDGVSA 405
 61 RVHIAFGPVVDGVDPEILMQQGEFLNYDMLIGVNGQEGKLFVEDSAEEDGVSA 120
 406 FQFTVSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNGEMRKTLLALFTDHWVAPV 465
 121 FQFTVSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNGEMRKTLLALFTDHWVAPV 180
 466 ATAKLHADYQSPVYFTFYHHCQASGRPEWADAAGDELPLYVFGVPMVGATDLPFCNFSK 525
 181 ATAKLHADYQSPVYFTFYHHCQASGRPEWADAAGDELPLYVFGVPMVGATDLPFCNFSK 240
 526 NDVMSAVVMTYNTNPAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNKEKQYLHIGL 585
 241 NDVMSAVVMTYNTNPAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNKEKQYLHIGL 300
 586 KPRVRDNYEANKVAFWLELVPHLNHLTELFTTTTLRPPYATRWPRPPAGPTRRPP 645
 301 KPRVRDNYEANKVAFWLELVPHLNHLTELFTTTTLRPPYATRWPRPPAGPTRRPP 360
 646 PATLPEPEPEGPRAYDFPGDSRDYSTELSVTVAVGASLLFLNLAFAALYKRRDRQ 705
 361 PATLPEPEPEGPRAYDFPGDSRDYSTELSVTVAVGASLLFLNLAFAALYKRRDRQ 420
 706 ELRCRLSPFGSGSGVPGGGLLPAAGRELPPBELVSLQKRGGVGADPAEALRPAC 765
 421 ELRCRLSPFGSGSGVPGGGLLPAAGRELPPBELVSLQKRGGVGADPAEALRPAC 480
 766 PDYTLALRRAPDDVPLAPGALTLLPSGLGPPPPPPPSLHPFGPPPTATSHNNT 825

Db 481 PPDYTLALRRAPDDVPLAPGALTLLPSGLGPPPPPPPSLHPFGPPPTATSHNNT 540
 QY 826 LPHPHSTTRV 835
 Db 541 LPHPHSTTRV 550
 RESULT 4
 Q8BYMS
 ID Q8BYMS PRELIMINARY; PRT; 825 AA.
 AC Q8BYMS;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE NEUROLIGIN 3 isoform HNL3 homolog.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCSI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK039018; BAC30207.1; -;
 SQ SEQUENCE 825 AA; 91175 MW; 3BF17F889B0A44CE CRC64;

Query Match 61.5%; Score 2773.5; DB 11; Length 825;
 Best Local Similarity 84.8%; Pred. No. 2.2e-196;
 Matches 531; Conservative 98; Mismatches 132; Indels 59; Gaps 14;

QY 42 PVNTAYGRVGRVREINNEILGVPVQFLGVPYATPPLGARFPQPEAPSWFQVRNATT 101
 Db 39 PTVNTHEKLGARVPLPSSELLGVPVQYLGVPYAAPIGEKRLPPEPPPSWSGIRNATH 98
 QY 102 LPACPNLHGLAPALMPLVWFTDNLEAAATYVQNOSECLYLNLYPTDGLTKRDE 161
 Db 99 FPPVPCQNIHTAVPEVMLPVWFTANLDIVATYIQEBNEPCLXNLNVYPTDGGSGAKQGE 158
 QY 162 ATLN---PDDTDRDPKPKVMLFHHGSGMGTGNMFDGSLAAAYGNVIVATLNVRLGV 218
 Db 159 DLADNCGDEDEDIRDSGAKPVVYIHHGSGMGTGNMIDGSLVLSYGNVIVITLNVRGV 218
 QY 219 LGFLSTGDOAAKNGYGLLDQIQALRWLSENIAHFGDGPERRITIFGSGAGASCNLLILSH 278
 Db 219 LGFLSTGDOAAKNGYGLLDQIQALRWLSENIAHFGDGPERRITIFGSGIGASCNLLILSH 278
 QY 279 HSGELFQKATAQSGTAISSWNYQPLKYTRLLAAKVGCDREDSAEAECLRRKPSREL 338
 Db 279 HSGELFQALIQSGSALSSWAVNYQVKTSLADKVCNVLDTVDVMDCLQRKSAKELV 338
 QY 339 DQDQPARVHIAFGPVVDGVDPEILMQQGEFLNYDMLIGVNGQEGKLFVEDSAE 398
 Db 339 EQDQPARVHIAFGPVVDGVDPEILMQQGEFLNYDMLIGVNGQEGKLFVEDVDPE 398
 QY 399 DGVSAFADFTVSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNGEMRKTLLALFTDH 458
 Db 399 DGVSGTDFDYSVSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNPETRRKTLVALFTDH 458
 QY 459 QWVAPAVATAKLHADYQSPVYFTFYHHCQASGRPEWADAAGDELPLYVFGVPMVGATD 518
 Db 459 QWVPSVTTADLEARYGSPYFYAFVHHQCSLMKPAWSDAAGHDEVPYVFGVPMVGPTDL 518
 QY 519 FPCNFSKNDVMSAVVMTYNTNPAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNKEK 578
 Db 519 FPCNFSKNDVMSAVVMTYNTNPAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNKEK 578
 QY 579 QYHLHIGLKPRVRDNYEANKVAFWLELVPHLNHLTELFTTTTLRPP-----YATRWPP 631

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Db 579 LYHIGLGRVDRHRAKVAFWKHLVPHLNLH-DMFHYTSTTTTKVPPDTHSHSHTR 637
Qy 632 RPPAGAGTRRRPPPPATUPPEPEPPGPRAYDRPPGDS-----RDYSTELSVTA 681
Db 638 RPNKGTWSTKRP-----AISPAYSNENAPGSWN---GDQDAGLLVENVPRDYSTELSVTA 690
Qy 682 VGASLLPLNLAFALYKRDQRQLCRRLSPPGSGSGVPGGGLLPAAGRELPEEE 741
Db 691 VGASLLPLNLAFALYKRDQRQLCRRLSPPGSGSGVPGGGLLPAAGRELPEEE 739
Qy 742 LVSLQLKRGVY-----GADPABALRACPPDYTLALRAPPDVLPLAPGALTLPSGLG 796
Db 740 LAALQV---GPHHSCEAGPPEDTLRLTALPDYTLTLRSPPDPLTPNTIMPNL- 795
Qy 797 PPPPPPPSLHPPGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 835
Db 796 ---VGLQTLHPYNTF-----AAGFNSTGLPHSHSHSTRV 825

RESULT 5
Q62765 PRELIMINARY; PRT; 843 AA.
AC Q62765;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neuroigin I.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95254653; PubMed=7736595;
RA Ichtchenko K., Hata Y., Nguyen T., Ullrich B., Missler M., Moonaw C.,
RA Suchof J.C.;
RT "Neuroigin I: a splice site-specific ligand for beta-neurexins.";
RL Cell 81:435-443(1995).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; U22952; AAA85720.1; -.
DR HSSP; P37967; IQE3.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000460; Neuroigin.
DR InterPro; IPR000379; Sex_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 843 AA; 94294 MW; 90A18540245B789D CRC64;

Query Match 61.5%; Score 2771; DB 11; Length 843;
Best Local Similarity 61.1%; Pred No. 3, 5e-196;
Matches 546; Conservative 100; Mismatches 133; Indels 114; Gaps 21;

Qy 1 MW-----LLALCLVGLAGQGGGPGGAPGGLGLGSLG-----EERF 41
Db 7 MFNPNYVRAMACW-----HRGSGAP-----LTLCLLGLLQCTFFVLSQKLDVD 52
Qy 42 PVNTAYGRVGRVRLNNEILGPVQFLGVYATPPLGARRFQPPAPASWPGVRNAT 101
Db 53 PLVTTFNGKIRGKRELNNEILGPVQFLGVYATPPLGARRFQPPAPASWPGVRNAT 112
Qy 102 LPPACQON-LHAGALPAIMLPWNTONLEAATYVQNSQEDCLYLNLYPTEDGFLTKRD 160
Db 113 FAPVCPQNTIDGRLPEWLPVNTNLDVSSYVQDSQEDCLYLNLYPTEDGFLTKRD 169
Qy 161 EATINPPDT-----DIRDP-GKKFVMLFLHGGSWMECTGNMFGSVLAAYGNVIVATLN 213
Db 170 KECARPGKKICRKGDIRSGGKPKWVYIHGGSWMECTGNMFGSVLAAYGNVIVATLN 229
Qy 214 YRLGVGLFSTGDAQAKNGYGLDQIALRWLSENIAHFQGGDPERITFGSGAGASCVNL 273

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Db 230 YRLGVGLFSTGDAQAKNGYGLDQIALRWLSENIAHFQGGDPERITFGSGAGASCVNL 289
Qy 274 LIISHSE-----GLFQKAIAGSGTAISWSVNYOPLKYTRLLAAKVCGRDSDAE 324
Db 290 LTLSHSEGNRNSNKTGLFQRAIAQSGTALSWSVSPQAKYARILATKVCNVDSTVE 349
Qy 325 AVECLRRKPSRELVDQVOPARYHIAFGVPVDDVDDPEILMOQGGFLNLMIGVQ 384
Db 350 LVECLQKKPKYELVDQVOPARYHIAFGVPVDDVDDPEILMOQGGFLNLMIGVQ 409
Qy 385 GEGLKVFEDSAGSASADFTVSNFVDMNLVYPPGKOVLRITIKFMTYDWDNRNG 444
Db 410 GEGLKVFENVDSDGVSASDFDFAVSFVDMNLVYPPGKOVLRITIKFMTYDWDNRNP 469
Qy 445 EMRRKTLALLFTDQWVAPAVATADLHNSFGSFTFYAFYHHCQTDQVPAWADAAGDEV 504
Db 470 ETRRKTLLALLFTDQWVAPAVATADLHNSFGSFTFYAFYHHCQTDQVPAWADAAGDEV 529
Qy 505 PYVFGVPMVGCATDLFCNFSKNDVMSAVMTYTNFAKTGDPNQPQDTKFIHTKENR 564
Db 530 PYVGLGPMIGTFLFCNFSKNDVMSAVMTYTNFAKTGDPNQPQDTKFIHTKENR 589
Qy 565 FEEVMSKFSKQYLHLGLKPRVDRNDRANKVAFWLELPHLNLH--TELFTTTTL 622
Db 590 FEEVATRYSKQQLYHLGLKPRVDRNDRANKVAFWLELPHLNLHNDISQYTSITTKV 649
Qy 623 PPVATRWPPPPAGAPGTRPPPPAT-----LPPEPEPGPRAYDRPGSDRYSDEL 676
Db 650 P--STDITLAP-----TRNSTPVTSAFTAKQDDPKQSP-----FSDQRDYSDEL 696
Qy 677 SVTVAGASLLPLNLAFALYKRDQRQLCRRLSPPGSGSGVPGGGLLPAAGREL 736
Db 697 SVTVAGASLLPLNLAFALYKRDQRQLCRRLSPPGSGSGVPGGGLLPAAGREL 745
Qy 737 PPEBELVSLQKRGVY-----PAE-ALRACPPDYTLALRAPPDVLPLAPGAL 788
Db 746 -PPEEIMSLQKH---TDLDHCESESHPHEVVRACPDYTLANRSPDDVPLMTPTNTI 801
Qy 789 TLPSPGLGPPPPPPPPSPPLHPPGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 835
Db 802 TMIPNTI-----FGIQPLTFNTF-----TGQNNTLPHPHPHSHSHSTRV 843

RESULT 6
Q62765 PRELIMINARY; PRT; 828 AA.
AC Q62765;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neuroigin 3 isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Ginns E.I.;
RT "The structure and expression of the human neuroigin-3 gene.";
RL Gene 246:303-310(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF217413; AAF71232.1; -.
DR HSSP; P21836; IMAA.
DR Genew; HGNC:14289; NLGN3.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000460; Neuroigin.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.

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SQ SEQUENCE 828 AA; 91570 MW; B72E4F3472678692 CRC64;
 Query Match 61.4%; Score 2770; DB 4; Length 828;
 Best Local Similarity 62.6%; Pred. No. 4.1e-196;
 Matches 539; Conservative 101; Mismatches 142; Indels 78; Gaps 16;
 QY 1 MWLLALCLVLAGAORGGGGGGGPGGLGSLGEERFPVNTAYGRVGRVRLNN 60
 DB 26 LWFSLAL--RSTQ-----APA-----PTVNTFFKLGARVFLPS 60
 QY 61 EILGPVQVLGVNYATPPICAGARRFOPPEAPSPGVRNATLTPACPNLHGALPALMLP 120
 DB 61 EILGPVQVLGVNYATPPICAGARRFOPPEAPSPGVRNATLTPACPNLHGALPALMLP 120
 QY 121 VMTFDNLEAAATVQVQSDCLYLNLVPTDGLTKKRDEATLN---PPDTRDRPQKK 177
 DB 121 VMTFANDIVATYIQPNEDCLYLNVVPTDGSAGKQSGEDLADNDDDEDLDSGAK 180
 QY 178 PVMFLHGGSYMEGTGMFTDGGVLAAYGNVIVATLNYRLVGLFSLTGDQAAGNYGLLD 237
 DB 181 FNVVYIHGGSYMEGTGMFTDGGVLAAYGNVIVATLNYRLVGLFSLTGDQAAGNYGLLD 240
 QY 238 QIQALRWLSNIAHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIQSGTAISS 297
 DB 241 QIQALRWLSNIAHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIQSGTAISS 300
 QY 298 MSVNYQPLKXVTLAAKVCDDREDAEVECLRRKPSRELVDQVQARVHAFGPVVDG 357
 DB 301 WANYQPLKXVTLAAKVCDDREDAEVECLRRKPSRELVDQVQARVHAFGPVVDG 360
 QY 358 DVVPDDPEILMQGGEFLNYDMLIGNVQGEGLKFVEDSAESDGVSAFAFTVSNFVDNL 417
 DB 361 DVVPDDPEILMQGGEFLNYDMLIGNVQGEGLKFVEDGVVDPEDVSGTDFDYSVNFVDNL 420
 QY 418 YGYPEGKVLRETIKEMVTDADRONGBRKTLLALFTDHWNPAPAVATAKHADYQSP 477
 DB 421 YGYPEGKVLRETIKEMVTDADRONGBRKTLLALFTDHWNPAPAVATAKHADYQSP 480
 QY 478 VYPTFYHHCQAGREPEWADAAGDELPIYFGVPMVGTDLFPCNFKNDVMSAVVMTY 537
 DB 481 TYPTFYHHCQAGREPEWADAAGDELPIYFGVPMVGTDLFPCNFKNDVMSAVVMTY 540
 QY 538 WTNFATGDPNVPQDTKFIHTKRNREEVWVSKFNKSKOYLHIGLKPRVDRNVEANK 597
 DB 541 WTNFATGDPNVPQDTKFIHTKRNREEVWVSKFNKSKOYLHIGLKPRVDRNVEANK 600
 QY 598 VAFWELVPHLNLHTELF---TTTTRLPP---YATRWPRPPAGAGTRPPPPATLP 650
 DB 601 VAFWELVPHLNLHTELF---TTTTRLPP---YATRWPRPPAGAGTRPPPPATLP 659
 QY 651 PE-----PEPEGPRAVDRFPDGRDYSTELSVTVAVAGSLFLNLAFALYKRD 703
 DB 660 NENAGSWNGDQDAGPLVE---NPRDYSTELSVTVAVAGSLFLNLAFALYKRD 715
 QY 704 RQELRCRLSPGGSGVGGGGLPPLAAGRELPEBELVSLQKRGV---GADPA 758
 DB 716 RQELRCRLSPGGSGVGGGGLPPLAAGRELPEBELVSLQKRGV---GADPA 761
 QY 759 EALRPACPDYTLARRAPDDVPLAPALTLPSGLCPPPPPPSLHPFGPPPPPPPT 818
 DB 762 DTLRLTALPDYTLARRAPDDVPLAPALTLPSGLCPPPPPPSLHPFGPPPPPPPT 810
 QY 819 ATSHNNT-LPHPSHTTV 835
 DB 811 AAGFNSTGLPHSHSTTV 828

RESULT 7

Q9UPT2

ID Q9UPT2

AC Q9UPT2

DT 01-MAY-2000

DT 01-MAY-2000

DT 01-MAY-2000

DT 01-MAY-2000

01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 Hypothetical protein KIAA1070 (Neurologilin 1).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
 Tanaka A., Kotani H., Nomura N., Ohara O.,
 "Prediction of the coding sequences of unidentified human genes. XIV.
 The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro."
 RNA Res. 6:197-205(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ductum;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; AB028993; BA83022.1;
 DR EMBL; BC032555; AAH32555.1;
 DR HSPF; F21836; IMAA.
 DR Genew; HGNC:14291; NLGN1.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR InterPro; IPR000460; Neurologilin.
 DR InterPro; IPR000379; Ser esters_site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR01090; NEUROLOGILIN.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hypothetical protein; Hydrolase
 SQ SEQUENCE 823 AA; 92000 MW; EA9328F9801CB8A8 CRC64;

Query Match 61.3%; Score 2765.5; DB 4; Length 823;
 Best Local Similarity 61.5%; Pred. No. 8.7e-196;
 Matches 539; Conservative 98; Mismatches 134; Indels 105; Gaps 17;
 QY 1 MWLLAL-CLVLAGAORGGGGGGGPGGLGSLG-----LTLNMLGCLLAGHVLSQKLDVDPVAT 46
 DB 12 VWRVMACLV-----HRLGAP-----LTLNMLGCLLAGHVLSQKLDVDPVAT 57
 QY 47 AYGRVGRVRELNEILGPVQVPLGYATPPLGARRFOPPEAPSPGVRNATLTPAC 106
 DB 58 NFGKIRGKIKELNEILGPVQVPLGYATPPLGARRFOPPEAPSPGVRNATLTPAC 117
 QY 107 PQN-LHGALPAIMLPVWFTDNLEAAATVQVQSDCLYLNLVPTDGLTKKRDEATLN 165
 DB 118 PQNLIIDGRLEPVMPLPWFTNLDVSSVYQDQSEDCLYLNLVPTDGLTKKRDEATLN 164
 QY 166 PPDTDIRDP-GKYPVMLFLHGGSYMEGTGMFTDGGVLAAYGNVIVATLNYRLVGLFSLT 224
 DB 165 ----DIDSGGPPVWVYIHGGSYMEGTGMFTDGGVLAAYGNVIVATLNYRLVGLFSLT 220
 QY 225 GDQAAGNYGLLDLQIQALRWLSNIAHFGGDPERITIFGSGAGASCVNLLILSHHSE--- 281
 DB 221 GDQAAGNYGLLDLQIQALRWLSNIAHFGGDPERITIFGSGAGASCVNLLILSHHSE--- 280
 QY 282 -----GLFQKAIQSGTAISSVNYQPLKXVTLAAKVCDDREDAEVECLRRKPSR 335
 DB 281 WSNSTKGLFORALQSGTALSSWVSFQAKARMLATKVCNWSVDIVELVECLQKPKYK 340
 QY 336 ELVDQDVQPARVHAFGPVVDGVPDDPEILMQGGEFLNYDMLIGNVQGEGLKFVEDSA 395
 DB 341 ELVDQDVQPARVHAFGPVVDGVPDDPEILMQGGEFLNYDMLIGNVQGEGLKFVEDSA 400
 QY 396 ESDGVSASAFDFTVSNFVDNLVGYPEGKVLRETIKEMVTDADRONGBRKTLLALF 455
 DB 401 DSDGVSASAFDFTVSNFVDNLVGYPEGKVLRETIKEMVTDADRONGBRKTLLALF 460
 QY 456 TDRQWAPAVATAKHADYQSPVYFTFYHHCQAGREPEWADAAGDELPIYFGVPMVGA 515

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Db 461 TDQWQWPAVATADLHNGFSGTFFYAFYHCTDQVPAWADAAHGDGDEYVYVIGLPMIGP 520
QY 516 TDLFFCNFSKNDVMSLVMTYTNFAKTGDPNPQVPQDTKFIHTKPNRPFEEVWWSKENS 575
Db 521 TELFFCNFSKNDVMSLVMTYTNFAKTGDPNPQVPQDTKFIHTKPNRPFEEVWWSKENS 580
QY 576 KEKQYVHGLKPRVDNRANKVAFWELVPHLHNLH--TELFTTTTTLRPPVATRWPPRP 633
Db 581 KDQVLYHGLKPRVKEHYRANKVNLWELVPHLHNLHNDISQVSTTTTKVPSDITFRPTR 640
QY 634 PAGAGTRRRPPPPATLPEPEPEPEPRAYDRFPGDGRDYSSTELSVTVAVGASLLFNILA 693
Db 641 KNSVPTVSFAFTAKQDQFQKQSP-----FSDQDYSSTELSVTVAVGASLLFNILA 693
QY 694 FAALYKKDRQELRCRLSPGSGSGVPGGGLPAPAGRELPPPEELVLSQLKRGGV 753
Db 694 FAALYKKDRHVDHRCSPQRTTNDLTHA-----QEEIIMSLQMKH--T 738
QY 754 GAD-----PAB-ALRPACPDYTLALRRAPDDVLLAPGALTILPSGLGPPPPPPPS 805
Db 739 DUDHCEBIHVEHVLRTACPDYTLAWRRSPDDVPLMTPTITMIPNTI-----FGIQP 793
QY 806 LHPGFPFPPTATSHNNLPHP-----HSTRV 835
Db 794 LHTFNTF-----TGGQNTLPHPHPHSHSTRV 823

RESULT 8
Q9NZ95 ID Q9NZ95 PRELIMINARY; PRT; 828 AA.
AC Q9NZ95;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-WAR-2002 (TREMELrel. 20, Last annotation update)
DE Neuroigin 3 isoform HNL3.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Ginns E.I.;
RT "The structure and expression of the human neuroigin-3 gene.";
RL Gene 246:303-310(2000)
CC 1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF217411; AAF71230.1; -.
DR HSSP; P37967; IQE3.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neuroigin.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 828 AA; 91554 MW; A896C059326780AA CRC64;

Query Match 61.3%; Score 2763; DB 4; Length 828;
Best Local Similarity 62.5%; Pred. No. 1.3e-195;
Matches 536; Conservative 101; Mismatches 143; Indels 78; Gaps 16;

QY 1 MWLLALCVLAGAQGGGGGPGGGLGLGSLGEERFPVNTAYGVRVREANN 60
Db 26 LWFSLAL--RSTQ-----APA-----PTVTHFGKLRGARVPLPS 60
QY 61 EILGPVQFLGVFYATPLGARRFQPPAPASWPGVNRATLTPACQNLHGALPAILP 120
Db 61 EILGPVDQVLYGVFAAFTIGKRFPLPPPPPSWSGIERNATHFFPVPQNIHTAVPEVMLP 120
QY 121 VNFNTNLAAATVYQNSQEDCLYLNLYVPTEDGLTKKRDEATLN---PDDTDIRPGKK 177
Db 121 VNFNTNLDAIVYIGPNECDCLYLNLYVPTEDGSGAKKQGEDLADNDGDEDEDIRSGAK 180

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QY 178 PVMFLHGGSYMEGTGCMFDSVLAAYGNVIVATINRLGVLSGLSTGDOAAKNGYGLD 237
Db 181 PVMVYHGGSYMEGTGCMFDSVLAAYGNVIVATINRLGVLSGLSTGDOAAKNGYGLD 240
QY 238 QIQALRWSENIAHFGDPERITITFGSAGASCYNLLILSHHSEGLFKQIAQSGTAISS 297
Db 241 QIQALRWSENIAHFGDPERITITFGSAGASCYNLLILSHHSEGLFKQIAQSGTAISS 300
QY 298 WSNYTOPLKYTLLAAKVGCDREDSAEVCELRKSPRELVDQVQARYHIAFGPVVVG 357
Db 301 WAVNYQVYKITSLLADKVGCVNLDVTVDWCDLRQSAKELVEQDIQARHVAFGPIDG 360
QY 358 DVVPDPEILMOQGFYANLMLIGNVQSEGKLFVEDSAESDGVSAFAFTVTSNFDNL 417
Db 361 DVIPDPEILMEQGFYANLMLIGNVQSEGKLFVEDSAESDGVSAFAFTVTSNFDNL 420
QY 418 YGVPEGKQVLRITIKFMYTDWADRNGEMRKTLIALFTDHWVAPAVATAKLHAYQSP 477
Db 421 YGVPEGKQVLRITIKFMYTDWADRNGEMRKTLIALFTDHWVAPAVATAKLHAYQSP 480
QY 478 VIFYPTFHCOAGREPEWADAAHGDDELPIYFVGVPMVGATDLPFCNFKNDVMSAVMTY 537
Db 481 TYFYAFYHHCQSLMKPAWSDAAHGDDEVEYFVGVPMVGATDLPFCNFKNDVMSAVMTY 540
QY 538 WTNPAKTGDPNPQVPQDTKFIHTKPNRPFEEVWWSKENSKEQYLIHGLKPRVDNRANK 597
Db 541 WTNPAKTGDPNPQVPQDTKFIHTKPNRPFEEVWWSKENSKEQYLIHGLKPRVDNRANK 600
QY 598 VAPWLELVPHLHNLHTELFTTTTTLRPP-----YATEWPPRPAGAGTERRPPPATLP 650
Db 601 VAPWLELVPHLHNLHTELFTTTTTLRPP-----YATEWPPRPAGAGTERRPPPATLP 659
QY 651 PE-----PEPEPGFRAYDRPPGSDRYSSTELSVTVAVGASLLFNILAFAALYKRRD 703
Db 660 NENAQSGWNGDQDAGPLLE-----NPRDYSSTELSVTVAVGASLLFNILAFAALYKRRD 715
QY 704 RQELRCRLSPGSGSGVPGGGLPAPAGRELPPPEELVLSQLKRGGV-----GADPA 758
Db 716 RROEPLRQSPORGAGA-----PELGAA-----PEBELAALQD---GPTHCEAGAPFH 761
QY 759 EALRPACPDYTLALRRAPDDVLLAPGALTILPSGLGPPPPPPPPSLHFGPPPPPPPT 818
Db 762 DTLRLTALPDYTLALRRAPDDVLLAPGALTILPSGLGPPPPPPPPSLHFGPPPPPPPT 810
QY 819 ACSHNT-LPHEHSTRV 835
Db 811 AAGFNSTGLPHSHSTRV 828

RESULT 9
Q9NZ95 ID Q9NZ95 PRELIMINARY; PRT; 848 AA.
AC Q9NZ95;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Neuroigin 3 isoform.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Ginns E.I.;
RT "The structure and expression of the human neuroigin-3 gene.";
RL Gene 246:303-310(2000)
CC 1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR HSSP; P21836; IMAA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neuroigin.

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Db 541 LFCNFKNDVMSAVVNTWTFNFAKTGDDNKVPQDTKEIHTKANRFEVAVSKYNPRD 600
 QY 578 KOYLHIGLKRVRDNYRANKVAFWLELVPHLHNLHTELF---TTTTRLP---YATRW 630
 Db 601 QLYLHIGLKRVRDHYRATKVAFWKHLVPHLYNLH-DMFYHTSTTTKVPDPDTHSSHIT 659
 QY 631 PRPAGAPGTRPPPPATLPEPEPECPRAYDRFPGDS-----RDYSTELSVTV 680
 Db 660 RRPNGKWTSTKRP---AISPAVSNENAPGSWN---GDQDAGPLLVENPRDYSTELSVTI 712
 QY 681 AVASLFLNLILAFALYLYRDRRQELRCRLSPGGSGGVPGGGLPPLPAAGRELPPPEE 740
 Db 713 AVASLFLNLVLAFAALYLYRDRRQELRCRLSPGGSGGVPGGGLPPLPAAGRELPPPEE 761
 QY 741 ELVSLQIKRGGV-----GADPAELRPACPPDYTLALRAPDVLAPGALTLLPSGL 795
 Db 762 ELAALQL---GPTHCEAGAPPHDTLRLTALPDYTLTLRSPDDIPLMTPTNTIPIENSL 818
 QY 796 GPPPPPPPSLHPFGPPPPPPPTATSHNNT-LPHPHSTTRV 835
 Db 819 -----VGLQLHPTNTF-----AAGFNSIGLPSHSTTRV 848

RESULT 11
 Q8NOW4
 ID Q8NOW4 PRELIMINARY; PRT; 816 AA.
 AC Q8NOW4
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Neurologin X.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA Janain S., Quach H., Fellous M., Bourgeron T.;
 RT "Evolution and expression of the human neurologin family, including
 RT two primate specific members on the x and y chromosomes.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; BC034018; AAH34018.1;
 DR EMBL; AF376803; AAM46112.1;
 DR InterPro; IPR002018; CarbesteraseB.
 DR InterPro; IPR000460; Neurologin.
 DR Pfam; PF00135; Coesterase_1.
 DR PRINTS; PR01090; NEUROLOGIN.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE. 816 AA; 91915 MW; EA1320D690F76BBD CRC64;
 Query Match 60.2%; Score 2713.5; DB 4; Length 816;
 Best Local Similarity 63.6%; Pred. No. 6e-192;
 Matches 520; Conservative 96; Mismatches 139; Indels 63; Gaps 13;

QY 38 EEFPPVNTAYGVRGVRRLNNEILGPVVQFLGVPIATPPGARRFQPEAPASWPGVR 97
 Db 42 QAQYPVVNTYNGIRGLRTPLEILGPVEQVLGVPIATPPGARRFQPEAPASWPGVR 101
 QY 98 NATLPPACQNL-HGALPAILMPPVMTDNLAAATYVQNSGDCILNLYVPTEDGLPT 156
 Db 102 NTTQFAACVCPQLDERSLLHDMLPINFNTANLDTMTYVQDQEDCLNLYVPTED 157
 QY 157 KKDEATLNPDPDTRDP-GKPKVMLFLHGSGYMEGTGMFGSLAAYGNVIVATLNYR 215
 Db 158 -----DIHQNSKKFWMYVIRGGSGYMEGTGMFGSLAAYGNVIVITINX 204

QY 216 LGVLGFLSTGDOAAKNGYGLLDQIQALRWLSENIAHFGDPERITIFSGAGASCNLLI 275
 Db 205 LGILGFLSTGDOAAKNGYGLLDQICALRWIENVGAFGDPRVTIFSGAGASCNLLI 264
 QY 276 LSHHSEGLFQKAIQAQSGTAISSWNTQPLKYITLLAAKVGCCDREDSAEAVECLRRPSR 335
 Db 265 LSHYSEGLFQKAIQSGTALSSWNTQPAKYITLLADKVGCCNMLDITDMVECLRNKYNK 324
 QY 336 ELVDQDVQARYHIAFGVVDGVDVVDPPPEILMOQGEFLNMLIGVNOGSLGKFVEDSA 395
 Db 325 ELIQTIPTAYHIAFGVVDGVDVVDPPPEILMOQGEFLNMLIGVNOGSLGKFVEDSA 384
 QY 396 ESEGVASASADFTVSNFVNLGYPEGKQVLRITIKFMTYDADRNGENRRTKILALF 455
 Db 385 DNEGVTENDDFSVNFVNLGYPEGKQVLRITIKFMTYDADRNGENRRTKILALF 444
 QY 456 TDHQWAPAVATAKHAHDYQSPVYFYFHHCOAGREPEWADAAGDELPPVFGVPMVGA 515
 Db 445 TDHQWAPAVATAKHAHDYQSPVYFYFHHCOAGREPEWADAAGDELPPVFGVPMVGA 504
 QY 516 TDLPCNPKNDVMSAVVNTWTFNFAKTGDDNKVPQDTKEIHTKANRFEVAVSKYNP 575
 Db 505 TELFSCNPKNDVMSAVVNTWTFNFAKTGDDNKVPQDTKEIHTKANRFEVAVSKYNP 564
 QY 576 KEKOYLHIGLKRVRDNYRANKVAFWLELVPHLHNLHTELF---TTTTRLP---PY 625
 Db 565 KDQYLHIGLKRVRDHYRATKVAFWLELVPHLHNLHTELF---TTTTRLP---PY 623
 QY 626 ATRWPPPPAGA-FGTRPPPPATLPEPEPEP---GPRAYDRPFGSDRSTELSVTVA 681
 Db 624 GTR---RSPAKIWTTKRPAITPANNPKSKDPKHTGPDITVLIETKDYSTELSVTIA 680
 QY 682 VGASILLNLILAFALYLYRDRRQELRCRLSPGGSGGVPGGGLPPLPAAGRELPPPEE 741
 Db 681 VGASILLNLILAFALYLYRDRRQELRCRLSPGGSGGVPGGGLPPLPAAGRELPPPEE 728
 QY 742 LVSLQLKLR---GGVGADPAELRPACPPDYTLALRAPDVLAPGALTLLPSGLP 797
 Db 729 IMSLQMKLEHDEHCESLQAHDTLRLTCTPPDYTLTLRSPDDIPLMTPTNTIPIENSL 788
 QY 798 PPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV 835
 Db 789 MQP-----LHTFNTF-----SGGQNSTLPHGHSTTRV 816

RESULT 12
 Q9ULG0
 ID Q9ULG0 PRELIMINARY; PRT; 817 AA.
 AC Q9ULG0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein KIAA1260 (Fragment).
 GN KIAA1260.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=20039619; PubMed=10574462;
 RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:337-345 (1999).
 CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; AB033086; BAA86574.1;
 DR HSSP; P21836; IMAA.
 DR InterPro; IPR002018; CarbesteraseB.
 DR InterPro; IPR000460; Neurologin.

DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B
KW Hypothetical protein; Hydrolase.
FT NON TER 1

Query March	60.2%	Score 2713.5	DB 4	Length 817
Best Local Similarity	63.6%	Pred. No. 6.1e-192		
Matches 520	Conservative 96	Mismatches 139	Indels 63	Gaps 13
Qy	38	EERPPVNTAYGRVGRVRRLENNILGPVVOFLGVVATPPLGARFRQPPEAPASWPGVR	97	
Db				
Db	43	QAQYPVNTVNYGKIEGRTPLPNEILGPVEQYLGVPASPTGERRTQPPPEPSSWTGIR	102	
Qy	98	NATTLPPACPNL-HGALPAIMLPVWFNDLLEAAATYVQNSECLYLNLYVPTDGLT	156	
Db				
Db	103	NTTOFAAVCPQHLDERSLIHDLPIWFETANDLTNTVYVQDQNECLYLNLYVPTD---	158	
Qy	157	KKRDEATLNPDDTDIRDP-GKKPVMLFLHGGSYMEGTGNMGDGSVLAAAGNVIVATLN	215	
Db				
Db	159	-----DIHQNSEKKPVMTVYHGGSYMEGTGNMGDGSILASYGNVIVITIN	205	
Qy	216	LGVLGLSTGDQAAKNGYGLLDQIALRWLSENTAHFGDGPERRITIFSGAGASCVNLLI	275	
Db				
Db	206	LGILGLSTGDQAAKNGVGLLDQIALRWIEENVGAFGGDKPRTVIFSGAGASCVSLLT	265	
Qy	276	LSHSEGLFQKATAQSGTATSSSNVYQPLKYITPELLAAKYGCCREDSDAEAVECLRRP	335	
Db				
Db	266	LSHSEGLFQKATIIQSGTALSSMAVNYQPAKYTRILADKVGCCNMLDITDMVECLRN	325	
Qy	336	ELVDQDVQPARYHIAFGPVVDGDDVPDDPELLMQGGEFLYNDMLIGNVQCEGLKFV	395	
Db				
Db	326	ELIQOTTIPATYHIAFGPIDGDIVDDPQILMEQGEFLYNDMLIGNVQCEGLKFVD	385	
Qy	396	ESEDCVGSARDFFTVSNFVNLYGYPGKQVLRRTIKFMTDADRNGEMRKTLIALF	455	
Db				
Db	386	DNEGVTENDPDFSVSNFVNLYGYPGKQDTRRTIKFMTDADKKNPRTKRKTLVAF	445	
Qy	456	TDHOWAPAVATAKLHADYQSPVYFYFHHCOAEGREPWADAAHGDELPVFGVPMVGA	515	
Db				
Db	446	TDHOWAPAVATADLHAQYQSPYFYFYHCOSEMKPWSADSAHGDEVPYVIGPMIGP	505	
Qy	516	TDLPFCNFSKNDVMSLVAMVMTYNTNFAKTGDPNPQVPQDTKFHTKENRFEVVM	575	
Db				
Db	506	TELFSCNFSKNDVMSLVAMVMTYNTNFAKTGDPNPQVPQDTKFHTKENRFEVVA	565	
Qy	576	KEKOYLHIGLKPRVDNRYANKAVFLELVPHLNHLNLTFLF-TTTLPLP-----	625	
Db				
Db	566	KDKOYLHIGLKPRVDHRYATKAVFLELVPHLNHLN-LFQVVSITTKVPDPDMSFP	624	
Qy	626	ATRWPPPPAGA-FGTRRRPPPPATLPEPPEP-----GPRAYDRFPDSDRSTY	681	
Db				
Db	625	GTR---RSPAKIWPTTKRPAITPANNPKSKDPHKTGPDFTVLTLETKRDYSTELS	681	
Qy	682	VGASLLELNTLAFNALYYKEDRQELRCRLSPGSGSGVPGGGLLPAAGRELPEEE	741	
Db				
Db	682	VGASLLELNTLAFNALYYKDKRHTHRPSPQRNTNDIAH-----IQNEE	729	
Qy	742	LVSLQLKR-----GGGVGADPAEARLPCPDYTLALRAPDDVPLLAGALTLPS	797	
Db				
Db	730	IMSLQMKLEHDECESLQADHTLRLCTCPDYTLTLERSPDDPLMTPTNITMIPNLT	789	
Qy	798	PPPPPPSLHPGFPFPPPPPTATSHNNTLDPHPSHTTRV	835	
Db				
Db	790	MQP-----LHTNFTF-----SGGCSNLPHGHSSTRV	817	

RESULT 13
Q8NFZ3
ID Q8NFZ3 PRELIMINARY; PRT; 816 AA.
AC Q8NFZ3;

DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Neurologlin Y.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Jaman S., Quach H., Fellous M., Bourgeron T.;
RT	"Evolution and expression of the human neurologlin family, including
RT	two primate specific members on the X and Y chromosomes.";
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR	EWEL; AF376804; AAM46113.1; --
DR	InterPro; IPR002018; CarbesteraseB.
DR	InterPro; IPR000460; Neurologlin.
DR	InterPro; IPR000379; Ser_estrs_site.
DR	Pfam; PF00135; Coesterase_1.
DR	PRINTS; PR01090; NEUROLIGIN.
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW	Hydrolase.
SQ	SEQUENCE. 816 AA; 92020 MW; PB68910773B1BBF6 CRC64;
Query Match	59.4%; Score 2678.5; DB 4; Length 816;
Best Local Similarity	62.7%; Pred. No. 2.4e-189;
Matches	513; Conservative 101; Mismatches 141; Indels 63; Gaps 13;
QY	38 EERFFPVNTAYGVRGVRRLENNELIGPVVQFLGVGYATPPLGARFPQPPEAPASFGVGR 97
DB	: :
QY	42 QAGYPVVNTNGKIQGLRTPLESEIIGPVVEYLGVGYASPTTGERRFQPPESSWTGIR 101
DB	: :
QY	98 NATTLPPACPNL-HGALPAIMLVFWFTDNLAAATTVQNQSDDCLYMLYVTEBGPLT 156
DB	: :
QY	102 NATQFAVCFOHLDERFLHDMLPWFETTSLDLTMTVYQDNEDCLYMLYIVPMED--- 157
DB	: :
QY	157 KKXDEATLNPPTDIIRD-GKKPVMLFLGGSWMEGTGMFQGSVLAAAGNVIVATINLR 215
DB	: :
QY	158 -----DIHEQNSKKPVMYIHGGSWMEGTGNMIDGSIASLVGNVIVITINYR 204
DB	: :
QY	216 LGVLGLSTGDQAAGNYGLLDIQIALRWLSLENIAHFQGDPERITTFSGGAGASCVMLLI 275
DB	: :
QY	205 LGVLGLSTGDQAAGNYGLLDIQIALRWLEENVGAFGDPKRVTIFSGGAGASCVSLLT 264
DB	: :
QY	276 LSHSSEGLFKQAIQSGTAISWSVNYQLKTRLLAAKVGCDDREDSAAVECLRKPSPR 335
DB	: :
QY	265 LSHYSSEGLFKQAIQSGTALSNAVNYQAKYTRILADKVGCGNMDDTTDMVCELNKNKYK 324
DB	: :
QY	336 ELVDQDVQPARVHAIFGPVVDGVPDPPEILMQQGEFLNYDMLIGNOQEGLFKFVEDSA 395
DB	: :
QY	325 ELIIQTITPATYHIAFGPIDGVIDPDPIQLMEQGEFLNYDMLGVNQEGLFKFDGIV 384
DB	: :
QY	396 ESDDGVSASAFDETGVSNFDVNLGYPGEKDUVRETIKFMYTOWARDNGEMRKTLIALP 455
DB	: :
QY	385 DNDGGVTNPDFDFSVNFVNLYGYPEGKDTLRETIKFMYTOWADKENPETERTKLVALP 444
DB	: :
QY	456 TDHQWAPAVATAKLHADYQSPVYFYTFHHCOAQRPEWADAAGHDELPLYFGVPMVGA 515
DB	: :
QY	445 TDHQWAPAVATADLHAQYGSTYFYAFVHHQSEMKPSKADSAGHDEVYFVFIEMIWP 504
DB	: :
QY	516 TDLPPCNFNKDVMLSAVMTYWNINPAKTGDGNQVPVQDKTKFIHTKPNRFEVYVMSKFNFS 575
DB	: :
QY	505 TELFSCNFKNDVMLSAVMTYWNINPAKTGDGNQVPVQDKTKFIHTKPNRFEVYVMSKYNP 564
DB	: : : : : : : : : : ~~~~~~
QY	576 KEKOYLHI GLKPRVRDNRANKVAFWLELVPHLNLHTELFI-----PY 625
DB	: : : : : : : : : : ~~~~~~
QY	565 KOOLYLIHGLKPRVRDNRANKVAFWLELVPHLNLNL-EIPQVYSTTKVKPPEDMTSPFY 623
DB	: : : : : : : : : : ~~~~~~
QY	626 ATRWPRRPAGA-PGTRRPPPPATLPPPEPEPEP-----GPRAYDRFPGQSDRYSTELSVTVA 681
DB	: : : : : : : : : : ~~~~~~
QY	624 GFR----RSPAKTWPTTKRPAITPANPKHSKDHPKTKPEDTTVLIETKDYSTELSVTVA 680
DB	: : : : : : : : : : ~~~~~~

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QY 682 VGASLLFLNIIAALYKRRROELRCRLSPGGSGGVPGGPIILPAAGRELPEEE 741
Db 681 VGASLLFLNIIAALYKRRROELRCRLSPGGSGGVPGGPIILPAAGRELPEEE 728
QY 742 LVSLQKKE---GGGAGDPAEALRACPPDYITLALRAPDDVLLAPGALTLLPSGLP 797
Db 729 IMSLQMKLEHDEHCESIQANDTLRLICPPDYITLARSDDIPFMTPTNITWIPNLMG 788
QY 798 PPPPPPSLHPGPPPPPTATSHNNVLPHPHSTTRV 835
Db 789 MQP-----LHTFKTF-----SGGQNSTNLPHGHSTTRV 816

RESULT 14
Q9P248 PRELIMINARY; PRT; 682 AA.
AC Q9P248;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein KIAA1480 (Fragment).
GN KIAA1480
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human
RT genes.XVII.The complete sequences of 100 new cDNA clones from brain
RT which code for large proteins in vitro.";
RC DNA Res. 7:143-150(2000).
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB040913; BA936004.1; -.
DR HSSP; P21836; 1MAA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR000379; Ser_estra_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLOGIN.
KW Hypothetical protein; Hydrolase.
FT NON_TER
SQ SEQUENCE 682 AA; 75592 MW; 9E6E6DBF44F5DC31 CRC64;

Query Match 52.0%; Score 2344; DB 4; Length 682;
Best Local Similarity 65.7%; Pred. No. 1e-164;
Matches 452; Conservative 82; Mismatches 104; Indels 50; Gaps 12;

QY 168 DTDTRDGGKVPMLFLHGGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSTGDO 227
Db 25 DEDIRDSGAKPVMYIHHGGSYMEGTGMNIDGSLASYGNVIVITLNYRVGVLFSTGDO 84
QY 228 AAKNGYLLDQIQALRWLSNIAHFGDPRITIFSGAGASCWNLLILSHSEGLFQKA 287
Db 85 AAKNGYLLDQIQALRWLSNIAHFGDPRITIFSGAGASCWNLLILSHSEGLFQKA 144
QY 288 IAQSGTAISSWSVNYQPLKYLRLAAVCGDREDSAEAECLRRKPSRELVDQVQARY 347
Db 145 IIQSGSALSWAVNYQPVKYSLLADVGVNLDVDMVDCLRQKSAKEIVQDIQARY 204
QY 348 HIAGRPVVDGVDPDDPEILMQOGEFLNYDMLGVNQEGKLVESASESDGVSASF 407
Db 205 HVAFGPVVDGVDPDDPEILMQOGEFLNYDMLGVNQEGKLVESASESDGVSASF 264
QY 408 FTVSNFVDNLYGYPEGKXDLRETIKFMVTDWDRDNGEMERKTLALFTDHWVAPAV 467
Db 265 YSVSNFVDNLYGYPEGKXDLRETIKFMVTDWDRDNGEMERKTLALFTDHWVAPAV 324
QY 468 AKLHADYQSPVYFTFYHHCQAEGRPEWADAAGDELPHYVGVPMVGATDLFPNFSK 527
Db 325 ADLHARYGSPTYFYAFYHHCQSLMKPAWSADAAGDEVYVGVPMVGATDLFPNFSK 384

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QY 528 VMLSAAVMTYTNFAKTGDPNQVPODTKFIHTKPNRPEEVVWSKFNSEKQYLIHGLKP 587
Db 385 VMLSAAVMTYTNFAKTGDPNQVPODTKFIHTKANRPEEVVWSKFNSEKQYLIHGLKP 444
QY 588 RVDNRYANKAFVLELYPHLNLHTELF---TTITRLPP---YATRWPPRPAGAGT 640
Db 445 RVRDHYRATKAFVLELYPHLNLHTELF---DMFHYTSTTTKRVPPDPTTHSSHITRRPNKWTST 503
QY 641 RRPPTATLPP-----PEPEGPRAVDYRFPDGRSDYSTELSVTVAVGASLLFLNIIA 693
Db 504 KRPALSPAYSNAQGSWNGQDAGPLVE---NPRDYSTELSVTVAVGASLLFLNIIA 559
QY 694 FAALYKCDRRQELRCRLSPGGSGGVPGGPIILPAAGRELPEEELVSLQKRGGV 753
Db 560 FAALYKCDRRQELRCRLSPGGSGGVPGGPIILPAAGRELPEEELVSLQKRGGV 605
QY 754 -----GADPAEALRACPPDYITLALRAPDDVLLAPGALTLLPSGLP PPPPPPSLHP 808
Db 606 HHECEAGPHDTLRLTALPDYITLARSDDIPFMTPTNITWIPNLSL-----VGLQTLHP 660
QY 809 FGFPFPPPTATSHNNVLPHPHSTTRV 835
Db 661 YNTF-----AAGFNSTGLPHSHSTTRV 682

RESULT 15
Q9Y2F8 PRELIMINARY; PRT; 648 AA.
AC Q9Y2F8;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein KIAA0951.
GN KIAA0951.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB023168; BAA76795.1; -.
DR HSSP; P21836; 1MAA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR000379; Ser_estra_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLOGIN.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 648 AA; 72885 MW; 1A2E6727A709BFBC CRC64;

Query Match 50.7%; Score 2287; DB 4; Length 648;
Best Local Similarity 64.8%; Pred. No. 1.5e-160;
Matches 437; Conservative 80; Mismatches 113; Indels 44; Gaps 10;

QY 180 MLFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSTGDOAAKNGYLLDQI 239
Db 1 MVYIHGGSYMEGTGMNIDGSLASYGNVIVITLNYRLGVLFSTGDOAAKNGYLLDQI 60
QY 240 QALRWLSNIAHFGDPRITIFSGAGASCWNLLILSHSEGLFQKAIQSGTAISSWS 299
Db 61 QALRWLSNIAHFGDPRITIFSGAGASCWNLLILSHSEGLFQKAIQSGTAISSWS 120
QY 300 VNYQPLKYLRLAAVCGDREDSAEAECLRRKPSRELVDQVQARYHIAFGVVDGV 359

```

121	Db	VNYQPAKYTRILADKVGONMLDTHVMECLKNKYNKELIQOTITPATYHIAFGPVIDGV	180
360	Qy	VPDDPEILMQGEBFLNYDMLIGNVQGBGLKFVEDSAESDGSYASAFDFTVSNFVDNLVG	419
181	Db	IPDDPQILMEQGBFLNYDMLIGNVQGBGLKFVDGIVDNEGDTVPDDFSFSNFDNLVG	240
420	Qy	YPEGKDVLRETIKMYITWDADRNGEMRKTLLALFTDQWVAPAVATAKLHADYQSPVY	479
241	Db	YPEGKDTLRETIKMYITWDACKENPETERKTLVALFTDQWVAPAVATADLHAQYGSPTY	300
480	Qy	FYTFYHHCQABRPEWADAAGHDELPLYFCVPMVAGTDLFPNCFSKNDVMLSAVVMTYWT	539
301	Db	PYAFYHHCQSEMKFSWADSAGDEVVPVFGIPMIGTELFSCNFSKNDVMLSAVVMTYWT	360
540	Qy	NFATGTGDPNPVPODTKFIHTKPNRFEVVVWSKFNKQYHLHGLKPRVRDNYRANKVA	599
361	Db	NFATGTGDPNPVPODTKFIHTKPNRFEVAVSKYNPKDQLYHLHGLKPRVRDHYRATKVA	420
600	Qy	FWLELVPHLNLHITELF---TTTITRIP-----PYATRWPRPPAGA--PGTTRRPPPPAT	648
421	Db	FWLELVPHLNLNLN--EIQYVSTTITTKVPPDMDTSPYGTW---RSPAKIWPTTKRAITPA	476
649	Qy	LPPEPEPEP---GPRAYDRPFGDSRDYSTELSVTVAVGASLLFLNLFAALYYKRRDRQ	705
477	Db	NNPKHSDPHKTGTEDTIVLIETKRDYSTELSVTVIAGSLLFLNLFAALYYKDKRR	536
706	Qy	ELRCRLRSLPPGGSGSVFGGGLPLPAAGRELPEEBELVSLQKR-----GGGVGADPAEAL	761
537	Db	HETTRHPSQRNTNDTITH-----IQNEEIMSLQKLEHDECESLQAHDTL	584
762	Qy	RPACPPDYTLALRAPPDDVPLAPGALTLPSGLGPPPPPPPSLHPFPFPFPFPPTATS	821
585	Db	RLTCPPDYTLTLRSPDDIPFMTPTNTIMTIPNLMGQP-----LHTFTFP-----SGGQ	634
822	Qy	HNNTLPHPHSTTRY	835
635	Db	NSTNLPHGHSTTRY	648

Search completed: February 13, 2004, 13:13:38
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 13, 2004, 13:11:12 ; Search time 22 Seconds
(without alignments)
1605.889 Million cell updates/sec

Title: US-09-934-323-2
Perfect score: 4508
Sequence: 1 MWLLALCLVLAGAQRGGGG.....PPTATSHNLTLPHPKSTTRV 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata1/iaa/6A COMB.pep:*
4: /cgn2_6/prodata1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata1/iaa/6C COMB.pep:*
6: /cgn2_6/prodata1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4415.5	97.9	836	4	US-09-491-356C-21
2	2771.6	61.5	843	4	US-09-491-356C-20
3	2746.6	60.9	848	4	US-09-491-356C-22
4	2741.6	60.8	823	4	US-09-491-356C-23
5	1996.4	44.3	553	4	US-09-491-356C-24
6	872.1	19.3	723	6	5200183-4
7	855.1	19.0	602	3	US-08-446-100-1
8	855.1	19.0	602	3	US-08-446-100-3
9	855.1	19.0	602	3	US-08-446-100-4
10	855.1	19.0	602	3	US-08-446-100-6
11	855.1	19.0	602	3	US-08-446-100-24
12	855.1	19.0	602	3	US-09-334-489-3
13	855.1	19.0	602	3	US-09-334-489-4
14	855.1	19.0	602	6	5215903-11
15	854.1	18.9	602	3	US-08-446-100-2
16	854.1	18.9	602	3	US-08-446-100-7
17	853.1	18.9	602	3	US-08-446-100-13
18	852.1	18.9	602	3	US-08-446-100-8
19	852.1	18.9	602	3	US-08-446-100-17
20	852.1	18.9	602	3	US-08-446-100-18
21	851.1	18.9	602	3	US-08-446-100-5
22	849.1	18.8	602	3	US-08-446-100-10
23	849.1	18.8	602	3	US-08-446-100-14
24	848.1	18.8	602	3	US-08-446-100-15
25	848.1	18.8	602	3	US-08-446-100-16
26	846.1	18.8	602	3	US-08-446-100-9
27	844.1	18.7	602	3	US-08-446-100-12

28	843.5	18.7	602	3	US-08-446-100-11	Sequence 11, Appl
29	836.5	18.6	617	2	US-08-370-156-6	Sequence 6, Appl
30	836.5	18.6	617	3	US-08-814-095-6	Sequence 6, Appl
31	831.1	18.4	600	2	US-08-370-156-4	Sequence 4, Appl
32	831.1	18.4	600	3	US-08-814-095-4	Sequence 4, Appl
33	831.1	18.4	600	3	US-08-975-084-1	Sequence 1, Appl
34	829.5	18.4	722	1	US-08-445-050-7	Sequence 7, Appl
35	829.5	18.4	722	2	US-08-204-691-7	Sequence 7, Appl
36	828.5	18.4	722	1	US-08-347-718B-1	Sequence 3, Appl
37	828.5	18.4	722	1	US-08-445-050-3	Sequence 1, Appl
38	828.5	18.4	722	2	US-08-482-262-1	Sequence 3, Appl
39	828.5	18.4	722	2	US-08-204-691-3	Sequence 3, Appl
40	828.5	18.4	722	4	US-09-355-295B-4	Sequence 4, Appl
41	828.5	18.4	722	6	5200183-3	Patent No. 5200183
42	828.5	18.4	742	1	US-08-347-718B-2	Sequence 2, Appl
43	828.5	18.4	742	2	US-08-482-262-2	Sequence 2, Appl
44	828.5	18.4	742	6	5200183-2	Patent No. 5200183
45	828.5	18.4	745	1	US-08-445-050-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-491-356C-21

Sequence 21, Application US/09491356C

Patent No. 5566061

GENERAL INFORMATION:

APPLICANT: Philibert, Robert A.

APPLICANT: Ginns, Edward I.

APPLICANT: Delisi, Lynn

TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13

FILE REFERENCE: 9465-6US11

CURRENT APPLICATION NUMBER: US/09/491,356C

CURRENT FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: PCT/US99/09365

PRIOR FILING DATE: 1999-04-29

PRIOR APPLICATION NUMBER: 60/083,465

PRIOR FILING DATE: 1998-04-29

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 836

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-491-356C-21

Query Match 97.9%; Score 4415.5; DB 4; Length 836;

Best Local Similarity 98.3%; Pred. No. 0;

Matches 822; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

Qy	1	MWLLALCLVLAGAQRGGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVRELNN	60
Db	1	MWLLALCLVLAGAQRGGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVRELNN	60
Qy	61	EILGPVQFLGVPYATPPLGARFPQPEAPASPGVGRNATLPPACFQNLHGALPAIMLP	120
Db	61	EILGPVQFLGVPYATPPLGARFPQPEAPASPGVGRNATLPPACFQNLHGALPAIMLP	120
Qy	121	VWFTDNLEAATYVQNSDECLYINLYVPTDGLTKRDEATLNPDTPDIRPKKPYM	180
Db	121	VWFTDNLEAATYVQNSDECLYINLYVPTDGLTKRDEATLNPDTPDIRSGKKPYM	180
Qy	181	LFLHGGSYMEGTGNMFDGSLAAYGNIVATLNYRLGVLFGLSTGDOAAKNGYGLDQIQ	240
Db	181	LFLHGGSYMEGTGNMFDGSLAAYGNIVATLNYRLGVLFGLSTGDOAAKNGYGLDQIQ	240
Qy	241	ALRWLSNIAHFQGDPERITIFGSGAGASCNNLLIILSHSEGLFQKAIAGSGTAISSWSV	300
Db	241	ALRWLSNIAHFQGDPERITIFGSGAGASCNNLLIILSHSEGLFQKAIAGSGTAISSWSV	300
Qy	301	NYQPLKYTELLAAKVGCDRDSABAVECLRKPSRELAVDQVQPARVHIAFGPVWDGVV	360

Db 301 NYQPLKYTRLLAAKVGCDREDS TEAVECLRRKSRRLVDQDQVARYHIAFGVVDGVV 360
QY 361 PDDPEILMOQGEFLNVDMLIGNVQSGELKXVEDSAESDGVSAFDFTVSNFVNLXYG 420
Db 361 PDDPEILMOQGEFLNVDMLIGNVQSGELKXVEDSAESDGVSAFDFTVSNFVNLXYG 420
QY 421 PEGKDVLRITIKMYTDMADRDNGEMRRKTLTLLALFTDQWVAPAVATAKLHADYQSPVYF 480
Db 421 PEGKDVLRITIKMYTDMADRDNGEMRRKTLTLLALFTDQWVAPAVATAKLHADYQSPVYF 480
QY 481 YTFYHHCQAEGRPEWADAAGDELPTVFGVMYGATDLFFCNFSKNDVMSAVVMYTYTN 540
Db 481 YTFYHHCQAEGRPEWADAAGDELPTVFGVMYGATDLFFCNFSKNDVMSAVVMYTYTN 540
QY 541 FAKTGPNOVPQDTEFIHTKPNRPEVWVSKFNSKEKYLHIGLKPRVDRNRYANKVAF 600
Db 541 FAKTGPNOVPQDTEFIHTKPNRPEVWVSKFNSKEKYLHIGLKPRVDRNRYANKVAF 600
QY 601 WLELVPHLNLHTELETTTTRLPYATRWPPPPA-GAPGTRRPPPPATLPPEPEPECP 659
Db 601 WLELVPHLNLHTELETTTTRLPYATRWPPPPA-GAPGTRRPPPPATLPPEPEPECP 659
QY 660 RAYDRPFGSRDYSSTLSVTAVGASLLFNILAFALYKRDQRQELRCRLSPGGSG 719
Db 661 RAYDRPFGSRDYSSTLSVTAVGASLLFNILAFALYKRDQRQELRCRLSPGGSG 720
QY 720 SGVPGGGLPAPAGRELPPPEELVSLQKRGSGVADPAELRPACPDYTLALRRAPDD 779
Db 721 SGVPGGGLPAPAGRELPPPEELVSLQKRGSGVADPAELRPACPDYTLALRRAPDD 780
QY 780 VPLLAGALTLPSGLGPPPPPPPSLHPFPFPPPPPTATSHNNTLPHPHSTTRV 835
Db 781 VPLLAGALTLPSGLGPPPPPPPSLHPFPFPPPPPTATSHNNTLPHPHSTTRV 836

RESULT 2

US-09-491-356C-20
; Sequence 20, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-491-356C-20

Query Match 61.5%; Score 2771; DB 4; Length 843;
Best Local Similarity 61.1%; Pred. No. 1.4e-202;
Matches 546; Conservative 100; Mismatches 133; Indels 114; Gaps 21;
QY 1 MW-----LLALCLVLAGAQRGGGGGAGFGGGLGSLG-----LTLCLLGLCLQTFHVLQSKLDVDD 52
Db 7 MNPVYVWAMACV-----HRGSGAP-----LTLCLLGLCLQTFHVLQSKLDVDD 52
QY 42 PVVNTAYGVRGVRRLNNEILGVVQVGLGVYATPPGARRFQPEAPASHPGVRNATT 101
Db 53 PLVTNFGKIRGKKELNNEILGVVQVGLGVYATPPGARRFQPEAPASHPGVRNATT 112
QY 102 LPPACQON-LHGALPAIMLVNFTNLEAAATVQNSDCLYLNLYVPTDGLTKKRD 160

Db 113 FAPVCPQNIIDGRLEPVMPLPWFTNNLDVSVSVQDSBEDCLYINIVVPTD---VKRIS 169
QY 161 EATLNPPDT-----DIRDP-GKKPVMFLFHGGSYMEGTGNMFDGSLAAYGNIVATLN 213
Db 170 KECARKPKKXIKRGGDIRDSGGPKPMVYIHGGSYMEGTGNLYDGSVLASYGNVIVITVN 229
QY 214 YRLGVLFSTGDOAAKNGNYGLDIOALRWLSENTAHFGGDDPERITIFSGGAGASCNL 273
Db 230 YRLGVLFSTGDOAAKNGNYGLDIOALRWLSENTAHFGGDDPERITIFSGGAGASCNL 289
QY 274 LILSHHSE-----GLFQKAIAGSGTAISSWSVNYQPLKYTRLIAAKVGGCDREDSAE 324
Db 290 LTLSHVSEGNRWSNSTKGLFQRAIAQSGTALSNAVSPQAKYARILATVGCNVSTVE 349
QY 325 AVECLRKPRRELVDQVQPARYHIAFGPVVDGVDVDDPEILMOQGEFLNYDMLGVNQ 384
Db 350 LVECLQKPKYELVDQVQPARYHIAFGPVVDGVDVDDPEILMOQGEFLNYDMLGVNQ 409
QY 385 GEGLKPFVEDSAESDGVSAFDFTVSNFVDNLYGYPEGKDVLRITIKMYTDMADRDNG 444
Db 410 GEGLKPFVENIVDSDGVSASDFDFAVSNFVDNLYGYPEGKDVLRITIKMYTDMADRDNG 469
QY 445 EMRRKTLALFTDQWVAPAVATAKLHADYQSPVYTYTFYHHCQAEGRPEWADAAGDEL 504
Db 470 ETRRKTLLALFTDQWVAPAVATAKLHADYQSPVYTYTFYHHCQAEGRPEWADAAGDEL 529
QY 505 PYVFGVMVGATDLFCNFSKNDVMSAVVMYTYTNFAKTGDPNQVPODTKEIHTKPNR 564
Db 530 PYVFGVMVGATDLFCNFSKNDVMSAVVMYTYTNFAKTGDPNQVPODTKEIHTKPNR 589
QY 565 FEEVWWSKFNKSKQVLIHIGLKPRVDRNRYANKVAFWLELVPHLNLH---TELFTTTTTL 622
Db 590 FEEVWWSKFNKSKQVLIHIGLKPRVDRNRYANKVAFWLELVPHLNLHNDISQVTSITTKV 649
QY 623 PPVATRWPPPPAGACGCTRRPPPPAT-----LPPPEPEPEGRPRAYDRPFGDGRDYSTEL 676
Db 650 P--STDITLTP-----TRKNSTFVTSAPPTAKQDDPKQSPS-----FSDVQDYSTEL 696
QY 677 SVTVAVGASLLFNILAFALYKRDQRQELRCRLSPGGSGSGVPGGGLPAPAGREL 736
Db 697 SVTVAVGASLLFNILAFALYKRDQRQELRCRLSPGGSGSGVPGGGLPAPAGREL 745
QY 737 PPEELVSLQKRGSGVAD-----PAE-ALRPACPDYTLALRRAPDDVPLLAGAL 788
Db 746 -PEEIMSLQMKH---TDLDECESTHPHEVLRITACPDYTLAMRRSPDDVPLMTNTI 801
QY 789 TLPSGLGPPPPPPPSLHPFPFPPPPPTATSHNNTLPHP-----HSTTRV 835
Db 802 TMIPNTI-----PGIQLPHTFTF-----TGGQNNTLPHPHPHSHSTTRV 843

RESULT 3

US-09-491-356C-22
; Sequence 22, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 22
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Rattus norvegicus

US-09-491-356C-22

Query Match 60.9%; Score 2746; DB 4; Length 848;
Best Local Similarity 61.1%; Pred. No. 1.2e-200;
Matches 538; Conservative 101; Mismatches 138; Indels 104; Gaps 18;

QY 1 MWLLALCLVGLAGAQGGGPGGAPGGLGSLGSEERFPVNTAYGRVGRVRELN 60
DB 26 LWFSLVL--RASQ-----APA-----PTVTHFGKLGARVPLPS 60

QY 61 EILGPVQFLGVYATPPLGARRFPPEAPASWPGVRNATLPPACPNLHGALPALMLP 120
DB 61 EILGPVQFLGVYATPPLGARRFPPEAPASWPGVRNATLPPACPNLHGALPALMLP 120

QY 121 VWFNTDLAAATYVQNSQEDCLYLNLYPTEDPLTKRDEATLN--PPTDTRDPCK 177
DB 121 VWFNTDLAAATYVQNSQEDCLYLNLYPTEDPLTKRDEATLN--PPTDTRDPCK 177

QY 178 PWMLFHGGSYMEGTGMNFDGSLAAYGNVIVATLNLVGLFSLSTGDAAGNLYGLD 237
DB 178 PWMLFHGGSYMEGTGMNFDGSLAAYGNVIVATLNLVGLFSLSTGDAAGNLYGLD 237

QY 238 QIQALRWLSENIAHFGDPERITIFGSGAGACVNLILSHSEGLFQKATAQSTAISS 297
DB 238 QIQALRWLSENIAHFGDPERITIFGSGAGACVNLILSHSEGLFQKATAQSTAISS 297

QY 298 WSNVQPLUKYTRLLAAKVGCDREDSAEAECLRRKPSRELVDQVQPARYHAFGPVVDG 357
DB 298 WSNVQPLUKYTRLLAAKVGCDREDSAEAECLRRKPSRELVDQVQPARYHAFGPVVDG 357

QY 358 DVPPDDPILMQGFEFLNYDMLIGNQEGELKFVEDSAESEDGVSASAFDTVGNFYDNL 417
DB 358 DVPPDDPILMQGFEFLNYDMLIGNQEGELKFVEDSAESEDGVSASAFDTVGNFYDNL 417

QY 418 YGYPEGKDLRETIFKMYTDMWDRDNGEMRRKTLALFTDHWVAPAVATAKLHADYQSP 477
DB 418 YGYPEGKDLRETIFKMYTDMWDRDNGEMRRKTLALFTDHWVAPAVATAKLHADYQSP 477

QY 478 VYFTFVHHQCAQGRPEWADAAGHDELPHYVGVPMVGATDLPCNFKNDVMLSAVMTY 537
DB 478 VYFTFVHHQCAQGRPEWADAAGHDELPHYVGVPMVGATDLPCNFKNDVMLSAVMTY 537

QY 538 WTNFAKTGDPNQPQDTKFIHTKPNRFEFVWMSKFNKQVHLHGLKPRVRDNYRANK 597
DB 538 WTNFAKTGDPNQPQDTKFIHTKPNRFEFVWMSKFNKQVHLHGLKPRVRDNYRANK 597

QY 598 VAFWLELVPHLNLHTELF---TTTTLPP-----YATRWPPPPAGAPGTRRRPPPTLP 650
DB 598 VAFWLELVPHLNLHTELF---TTTTLPP-----YATRWPPPPAGAPGTRRRPPPTLP 650

QY 651 PE-----PEPEGPRAAYDRFPQDSRDYSTELSVTVVAGASLLFLNLFAALYKRD 703
DB 651 PE-----PEPEGPRAAYDRFPQDSRDYSTELSVTVVAGASLLFLNLFAALYKRD 703

QY 704 ROELRCRLSPGGSGVPGGGPLLPAGRELPEBELVSLQKRGGV-----GADPA 758
DB 704 ROELRCRLSPGGSGVPGGGPLLPAGRELPEBELVSLQKRGGV-----GADPA 758

QY 758 VAFWLELVPHLNLHTELF---TTTTLPP-----YATRWPPPPAGAPGTRRRPPPTLP 650
DB 758 VAFWLELVPHLNLHTELF---TTTTLPP-----YATRWPPPPAGAPGTRRRPPPTLP 650

RESULT 4

US-09-491-356C-23
; Sequence 23, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.

QY 759 EALRPACPDYTLARRADDVPLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPT 818
 Db 762 DTLRLTALFDYTLRLSRSPDDIPMTENTITIPNSL-----VGLQTLHPYNTF----- 810
 QY 819 ATSHNNT-LPHPH 830
 Db 811 AAGFNSTGLPHSH 823

RESULT 5
 US-09-491-356C-24
 ; Sequence 24, Application US/09491356C
 ; Patent No. 6566061
 ; GENERAL INFORMATION:
 ; APPLICANT: Philibert, Robert A.
 ; APPLICANT: Ginns, Edward I.
 ; APPLICANT: Delisi, Lynn
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
 ; FILE REFERENCE: 9465.6US11
 ; CURRENT APPLICATION NUMBER: US/09/491,356C
 ; CURRENT FILING DATE: 2000-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US99/09365
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 60/083,465
 ; PRIOR FILING DATE: 1998-04-29
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 24
 ; LENGTH: 553
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-491-356C-24

Query Match 44.3%; Score 1996; DB 4; Length 553;
 Best Local Similarity 67.1%; Pred. No. 8.2e-144;
 Matches 371; Conservative 58; Mismatches 76; Indels 48; Gaps 5;

QY 1 MWLLALCLVLAGAQRGGGPGGPGGLGSLGEERFPVNTAYGRVGRVRELN 60
 Db 26 LWFSLAL--RSTQ-----APA-----PTVTHGKLGARVPLPS 60
 QY 61 EILGPVQFLGVPYATPPGARRFPPEAPAPSWPGVNRATLLPACPNLHGALPAILMP 120
 Db 61 EILGPVQFLGVPYAAPPGKRFLLPPEPPPSWSGIRNATHFPVPCQNIHTAVDEVMLP 120
 QY 121 VMTDNLAAATVQVQNSDCLYLYPTD-----GPI TKRD 160
 Db 121 VMTANLDIVATYIQEPNEDCLYLYVYPTEDVVKRISKCAKPNKKICRGGGAKKQ 180
 QY 161 EATLN---PPDTRDPGKKPVMLFHGGSYMEGTGNMFDGSLAAYGNVIVATLNYRLG 217
 Db 181 EDLADNGDEDEDIRDSGAKPVWVYTHGGSYMEGTGNMIDGSLASYGNVIVITLNVAVG 240
 QY 218 VLGLSTGQAAKNGVLLDQIALRWLSNIAHFGGDPERITIFGSGAGASCYNLLIS 277
 Db 241 VLGLSTGQAAKNGVLLDQIALRWLSNIAHFGGDPERITIFGSGAGASCYNLLIS 300
 QY 278 HSEGLFQKAIQAQSGTAISSWSVNYQPLKYTLRLAAKVCDCREDSAAVECLRRKPSREL 337
 Db 301 HSEGLFQKAIQAQSGTALSSWSVNYQPLKYTLRLAAKVCDCREDSAAVECLRRKPSREL 360
 QY 338 VQDVQPARHYHAFGVPVGVDDVDPDDPEILMQQGEFLNYDMLIGNQOEGKLFVEDSAES 397
 Db 361 VQDVQPARHYHAFGVPVGVDDVDPDDPEILMQQGEFLNYDMLIGNQOEGKLFVEDSAES 420
 QY 398 EDGVSASAFDFTVSNFVDNLYGYPGKQVLRRTIKFMTDWRONGEMRKTLLALPTD 457
 Db 421 EDGVSCTDFDYSVNFVDNLYGYPGKQVLRRTIKFMTDWRONGEMRKTLLALPTD 480
 QY 458 HQWAPAVATAKLHADYQSPVYTFYHHCQAGPEWADAAGDELVPFGVPMVGATD 517
 Db 481 HQWVPSVVTADLHARYGSPYTFYAFYHHCQNLKMPAWSAAHGDVEVPFGVPMVGATD 540

QY 518 LFPCNFSKNDVML 530
 Db 541 LFPCNFSKNDVML 553

RESULT 6
 5200183-4
 ; Patent No. 5200183
 ; APPLICANT: TANG, JORDAN J.N.;WANG, CHI-SUN
 ; TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
 ; NUMBER OF SEQUENCES: 22
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/537,426
 ; FILING DATE: 12-JUN-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 504,635
 ; FILING DATE: 04-APR-1990
 ; APPLICATION NUMBER: 122,410
 ; FILING DATE: 19-NOV-1987
 ; SEQ ID NO:4:
 ; LENGTH: 723
 5200183-4

Query Match 19.3%; Score 872; DB 6; Length 723;
 Best Local Similarity 30.9%; Pred. No. 4.6e-58;
 Matches 255; Conservative 103; Mismatches 280; Indels 186; Gaps 32;

QY 46 TAYGRVGRVRELNNEILG--PVVQFLGVPYATPPGARRFPPEAPAPSWPGVNRATLLP 103
 Db 8 TEGGFVEGVNKKLS--LLGDSVDIFKGPFFAT---ATKLENPQRHPQWQGLKATDFK 62
 QY 104 PACQNLHGALPALMPVMTDNLAAATVQVQNS---EDCLYLYLYVPTDGLTKRD 160
 Db 63 KRCLQ-----ATITQDSTYQSDCLYLYNIVWP---QGRKQVHRD 98
 QY 161 EATLNPPDTRDPGKKPVMLFHGGSYMEGTGN-----MFDGSLAAYGNVIVATL 212
 Db 99 -----LPVWVYIGGAFMGSGQGANFLKNLYLDGEEIATRGVIVWTF 142
 QY 213 NYRLGVGLSTGQAAKNGVLLDQIALRWLSNIAHFGGDPERITIFGSGAGASCYN 272
 Db 143 NYRVGLGLSTGDANLPGNFGLDQDMAWKRNIIAAFGDPDNITIFGSGAGAIYS 202
 QY 273 LLILSHHSEGLFQKAIQAQSGTAISSWSVNYQPLKYTLRLAAKVCDCREDSAAVECLRRK 332
 Db 203 LQTLSPYKGLIRRAISQSGVALSPWAIQENPLFWAKTIKKVGCPTEDTAKWAGCLKIT 262
 QY 333 PSREL-----VDQDVQPARHYHAFGVPVGVDDVDPDDPEILMQQGEFLNYDMLIGNO 385
 Db 263 DPEALTLAVRLPLKSOEYPIVHYLAFIPVVDGDFIPDDPINLYDNAADIDY--LAGINDM 320
 QY 386 EGLKFVEDSAESDGVSAFADFTVSNFVDNLYGYPGKQVLRRTIKF--MYTD--WADRON 443
 Db 321 DGHLFATVDMVAIDKAKQ---DVTEEDFYRLVSGHTVAKGLGKGTQATFYIHESWAQDPS 377
 QY 444 GEMRKTLLALFTDHWQVAP---AVATAKLHADYQSPVYTFYHHCQAGPEWADAHAH 500
 Db 378 QENMKKTWVAFETDILFLIPTEMALAQHRAHAK-SAKTYSYLFSSHPSRPIYPKWMGADH 436
 QY 501 GDELPVVEGVPVGVATDLPFCNFSKNDVMLSAVWMTYNTNFAKTGDP---NOPVPQDTKF 557
 Db 437 ADDLQVFGKPP--AT---PLGYRAQDRTVSKAMTAYNTNFAKSGDPNMGNSFPVPTH--- 488
 QY 558 IHTKPNRFEVWVNSKFSKEQYLIHGLK---PRVRDNYRANKVAFW---LELVPHLHL 611
 Db 489 -----WYPTWENGNYLDINKKITSTSMKEHLREKLFKFWAVTFEMLP----- 531
 QY 612 HTLFTTTTTLPEYATRWPRPPAGATRRPPPPATLPPPEPEPGPAYDRFFGDSRD 671
 Db 532 -----TVWGDATHYPPEDDSEA-----APVPTDDSQGGP-----VPPTDSD 569
 QY 672 YSTELSVTVAVGASLILFLNILAFAALYKRRDRQRRLCRSLRSLSPGGSGSGVPGGGLLPA 731

Db 570 QTTPVPTDNSQAGV-----PPTGD-SGAP---PVPT 599
QY 732 AGRELPEELSVLQKGGVGADPAELRACPPDYTLALRAPDDVPLIAPGALTLL 791
Db 600 GDGSGAPP-----VPPTGDSGAPPV-----PPTGDSG---APPVPTGDSGAPPVP 641
QY 792 PSG-LGPPPPPP-----PPSLHPFGFPFPPPPPTATSHNNVTLPHP 829
Db 642 PTGDAGPPVPPTGDSGAPPVPPTGDSGAPPVPTPTGDSGAPPVP 685

RESULT 7
US-08-446-100-1
; Sequence 1, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-1

Query Match 19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.le-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY 2 LLALCLVLGAGAQGGGGGPGGAPGGLGLGSLGEERFPVVNTAYGRVGRVRELNNE 61
Db 15 WFLLCML-----IKSHTEDDIIATKXKVRG-----WMLT 47
QY 62 IL-GPVVQFVGVYATPPLGARFPQPEAPASWPGVYRNATLPPACFQNLHGALPAILMP 120
Db 48 VFGTVAFLGIPYACPLGRFLRFXKPSLTKNSDIWNATKVANSQQNIDQSFPGFHGS 107
QY 121 VWTDNLEAAATVQVQSEDCLYNLVYPTDGLTKRDEATLNPDPDIDRPGKPYW 180

Db 108 EWMNPNTDL-----SEDCLYNLVWIPAP-----KPKNATVL 138
QY 181 LFLGGGSWEGTGM--FDGSLVLAAYGNVIATNLNRYLGLVGLFELS-TGDQAAGNYGLLD 237
Db 139 IWIYGGGQTSLSLHVDGKFLARVERVIVSWNYRGALGFLALPQNPAPGNGLFD 198
QY 238 QIOALRWLSENIAHFPGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSTAISS 297
Db 199 QOLALQWQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSVN--YQPLKYTRLAAKVCDDREDSAEAVECLRRKESRELVDQDVPARY-----HIAF 351
Db 259 WAVTSLYEARNRITLAKLTGCSRENETEIKLRNKDPOBILNEAFVVPVYGTPLSVNF 318
QY 352 GPVVVDGVPDPBILMQQGEFLNYDMLIGVNOGEGKLFVEDSAE--SEDCVSASAFDFT 409
Db 319 GPTVDGFLTDMPDILLELQFKTKQILVGNKDEGTAFLVYGAPGFSKONNSI---IT 374
QY 410 VSNFVDNL-YGYPEGKDVLRITIKFMTDADNRONGEMRRKTLALLTDDHOWVAPAVATA 468
Db 375 RKEFQEGKLIFFPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYVNFICPALEFT 434
QY 469 KLHAYOSPVVYFYTHHCOAEGRPENADAAHGDDELFPVFGVPMVGATDLPPCNFSKNDV 528
Db 435 KKFSEWGNNAFFYFEHRSSKLPHPEWGMVHGVEIEFVGLPLERRD-----NYTKAE 489
QY 529 MLSAVMYTNTNFAKTGDPNQFVQDPTKFIHTKPNRFEVVVWSKFNSEKQYHLIGLK-P 587
Db 490 ILSRIVKRWANFAKYNPNETQNNST-----WPVFKSTEOKYLLTNTST 536
QY 588 RVRDNYRANKVAFWLELVP 606
Db 537 RIMTKLRAQCRFTWTSFP 555

RESULT 8
US-08-446-100-3
; Sequence 3, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-3

Query Match      19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY 2 WLLALCLVGLAGAQGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVRELNNE 61
Db 15 WFLLCML-----IGKSHTEDDIIATKNGKVRG---MNLIT 47

QY 62 IL-GPVVQFLGVFYATPPLGARRFPQPEAPASWPGVGRNATLPPACPNLHGALPAIMLP 120
Db 48 VFGGTVAFGLGIPYAQPLGLRLFRKPKQSLTKWSDIWNATKYANSCCNIDQSPFGHGS 107

QY 121 VMTDNLAAATVQNSQEDCLINLYVPTDGLTKKDEATLNPDPDIRDPGKKPYM 180
Db 108 EMNPNITDL-----SEDCLYLNWIAP-----KPKNATVL 138

QY 181 LFLHGSYMEGTGNM--FDGSVLAAYGNVIVATNLNRLGLVGLFLS--TGDOAAKNGYGLLD 237
Db 139 IMIYGGGFTGTSSLHVYDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFD 198

QY 238 QIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIQAQSTAIS 297
Db 199 QQLALQWQKNIAAFGNPKSVTLFGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAP 258

QY 298 WSVN--YQPLKYTRLLAAKVGCDREDSAEAVCLRKPSRELVDQDVPARY----HIAF 351
Db 259 WAVTSLYEARNTLNLAUATGCSRENETEIIKLRNKDQPEILLNEAFVVPYGTPHSVNF 318

QY 352 GPVVDGDDVDDPEILMQQGEFLNYDMLIGVNGEGELKFVEDSAE--SEDCGVASAFDFT 409
Db 319 GPTVDGDFLTDMPDILLEGQFKTKQILYGVNKNDEGTAFLVYGAPGFSKDNNSI----IT 374

QY 410 VSNFVDNL--YGYPEGKDVRETIKFWYTDWDRDNGEMERKTLTLLFTDHWVAPAVATA 468
Db 375 RKEFQGLKIFPFGVSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFICPALETF 434

QY 469 KIHADYQSPVYFYTFVHHCOAEGRPDWAHAAGDELPLYVFGVPMVGATDLPCNFKNDV 528
Db 435 KKFSEGNNAFFYFPHRSKLPWPEWGMVGHYIEFVFGLPLEERD-----NYTKAEE 489

QY 529 MLSAVVMTYNTNFAKTGDPNPQDPTKFIHTKPNRFEVWWSKFNSEKQYLHIGLK-P 587
Db 490 ILRSRIVKRWANPAKYGNPNETQNNSTS-----WPFVKSTEQKYLTLNTEST 536

QY 588 RYRDNRANKVAFWLELVP 606
Db 537 RIMTKURAOCCRFWTSFFP 555

```

RESULT 9

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US-08-446-100-4
; Sequence 4, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; City: Fairfax
; STATE: VA

```

```

; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/446,100
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-4

```

Query Match 19.0%; Score 855; DB 3; Length 602;

Best Local Similarity 32.5%; Pred. No. 7.1e-57; Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

```

QY 2 WLLALCLVGLAGAQGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVRELNNE 61
Db 15 WFLLCML-----IGKSHTEDDIIATKNGKVRG---MNLIT 47

QY 62 IL-GPVVQFLGVFYATPPLGARRFPQPEAPASWPGVGRNATLPPACPNLHGALPAIMLP 120
Db 48 VFGGTVAFGLGIPYAQPLGLRLFRKPKQSLTKWSDIWNATKYANSCCNIDQSPFGHGS 107

QY 121 VMTDNLAAATVQNSQEDCLINLYVPTDGLTKKDEATLNPDPDIRDPGKKPYM 180
Db 108 EMNPNITDL-----SEDCLYLNWIAP-----KPKNATVL 138

QY 181 LFLHGSYMEGTGNM--FDGSVLAAYGNVIVATNLNRLGLVGLFLS--TGDOAAKNGYGLLD 237
Db 139 IMIYGGGFTGTSSLHVYDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFD 198

QY 238 QIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIQAQSTAIS 297
Db 199 QQLALQWQKNIAAFGNPKSVTLFGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAP 258

QY 298 WSVN--YQPLKYTRLLAAKVGCDREDSAEAVCLRKPSRELVDQDVPARY----HIAF 351
Db 259 WAVTSLYEARNTLNLAUATGCSRENETEIIKLRNKDQPEILLNEAFVVPYGTPHSVNF 318

QY 352 GPVVDGDDVDDPEILMQQGEFLNYDMLIGVNGEGELKFVEDSAE--SEDCGVASAFDFT 409
Db 319 GPTVDGDFLTDMPDILLEGQFKTKQILYGVNKNDEGTAFLVYGAPGFSKDNNSI----IT 374

QY 410 VSNFVDNL--YGYPEGKDVRETIKFWYTDWDRDNGEMERKTLTLLFTDHWVAPAVATA 468
Db 375 RKEFQGLKIFPFGVSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFICPALETF 434

QY 469 KIHADYQSPVYFYTFVHHCOAEGRPDWAHAAGDELPLYVFGVPMVGATDLPCNFKNDV 528
Db 435 KKFSEGNNAFFYFPHRSKLPWPEWGMVGHYIEFVFGLPLEERD-----NYTKAEE 489

QY 529 MLSAVVMTYNTNFAKTGDPNPQDPTKFIHTKPNRFEVWWSKFNSEKQYLHIGLK-P 587
Db 490 ILRSRIVKRWANPAKYGNPNETQNNSTS-----WPFVKSTEQKYLTLNTEST 536

QY 588 RYRDNRANKVAFWLELVP 606
Db 537 RIMTKURAOCCRFWTSFFP 555

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139 IWIYGGKQTGTSSLHVYDVGKFLARVERVIVVMNRYVGALGFLALPGNPEAFGNMGLFD 199
238 QIQLRWLSENIAHFGGDPERITIFGSGAGASCVMNLLILSHHSEGLFQKAIAGSGTAISS 297
199 QQLALQWQKNIAAFGGNPKSVTLFGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
298 WSVN--YQFLKYTRLLAAKVGCDREDSABAVECLRRKXPSRELVDDQVQARY-----HIAF 351
259 MAWTSGLYFARNTLNLAKLTCSSRENETEIKCLRKNDPOEIIILNEAFVVPYGTPLSVNF 318
352 GPWVDGDDVVPDDPEILMOQGEFLVNDMLIGVNOQEGCLKFVEDSAE--SEDGVSASAFDFT 409
319 GTVUGDGLTDMPDILLLELGGFKTKTLVGNKDEGTAFLVYGAPGSKDNNSI-----IT 374
410 VSNFVDNL-YGYPEGKQVLRRTIKFMTYDMADRDNGEMRKTLLALFTDHWVAPAVATA 468
375 RKEFOEGLKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGDVVVDYNFICPALEFT 434
469 KLHADYQSPVVFYTFYHHCQAEGRPEWADAAGDELFPYFVGPMVGATDLFPCNFKSKNDV 528
435 KFSWGNNAFYFYFHRSSKLPPWPMVGNVHGVEIEFVFGLEPDERD-----NYTKAEE 489
529 MLSAVMTYTNFNTAKTGDPNQVPQDTKFHTKPNRFEVVMVSKFNSKEKQYLHLGLK-P 587
490 ILRSIVKRWANFAKYGNEPNETONNSTS-----WPVFKSTEQKYLTLTNEST 536
588 RYRDNYRANKVAFWLELVP 606
537 RIMTKLRAQQCRFWTSFPF 555

RESULT 11
US-08-446-100-24
; Sequence 24, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Okeana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

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; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-24

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```

Query Match      19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

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QY 2 WLLALCLVLAGAQRGGGGPGGAPGGLGSLGSERPVNTAYGRVGRVRELNNE 61
DB 15 WFLLCML-----IGKSHTEDEIIATKNGKVRG-----MNL 47
QY 62 IL-SPVVOFLGVPYATPPLGARFPQPEAPASWPGVNRNATLPPACQNLHGALPAIMLP 120
DB 48 VFGTGTAFGLGIPYAQPPLGRLRFKPKQSLTKWSDIWNATKYANSCCQNDQSPFGHGS 107
QY 121 VMTDNLEAAATYVQNSQEDCLYLNLYVPTDGLTKRDEATLNPDPDIDRDPGKPYM 180
DB 108 EMNPNIDL-----SEDCLYLNWIPAP-----KPKNATVL 138
QY 181 LFLHGGSYMEGTGNN--FDGSVLAAYGNVIVATLNYRLVGLGFLS--TGDQAAKGNVGLLD 237
DB 139 IWIYGGGFQGTSSLHYVDGKFLARVERVIVVSMYRVGALGFLALPGNPEAPGNWGLFD 198
QY 238 QIQALRWLSNIAHFQGDPERITIFGSGAGASCWNLLILSHHSEGLFQKAIAGSGTAISS 297
DB 199 QQLALQWQKNIAAFQGNPKSVTLFGESAGAAVSJHLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSVN--YQPLKYTRLAALKVGCDDREDSAAVECLRRKPSRELVDQDVQARY---HIAF 351
DB 259 WATSLYEARNRTLNLAUKLTGCSRENETEIIKLRNKDQOEILLNEAFVVPYGTPLSVNF 318
QY 352 GPVVDGVDVDDPEILMQOGEFLNYDMLIGVNOGEGKLFVEDSAE--SEDGVSASAFDFT 409
DB 319 GPTVDGDFLTDMPDILLELQGFKKTQILVGVNKGDEGTAFLVYGAPGFSKONNSI---IT 374
QY 410 VSNFVDNL-YGYPEGKDVLETKFMYTWDADRDNGEMRKTLALLFTDHWVAPAVATA 468
DB 375 RKEFQGLKIFFGVSEFGKESILFHYTDWVDQRPENTREALGDVVGVDYNFICPALEFT 434
QY 469 KLHADYQSPVYFTFYHHCOAEGRPWADAAGHDELPPYVFGVPMVGATDLFPCNFSKNDV 528
DB 435 KKFSEWGNNAFFYYFEHRSKLPWPENWGMVHGVEIEFVGLPLERD-----NYTKAE 489
QY 529 MLSAVMTWTWNTAKTGDNPQVPQDTKFIHTKPNRFEVVMWKSFKNSKEKQYHLGLK-P 587
DB 490 ILRSIVKRWANFAKYGNPNETQNNSTS-----WPFVKSTEQKYLTLNTEST 536
QY 588 RVRDNYRANKVAFWLELVP 606
DB 537 RIMTKLRAQOCRWTSFPP 555

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RESULT 12
US-09-334-489-3

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; Sequence 3, Application US/09334489
; Patent No. 6291175

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```

; GENERAL INFORMATION:

```

```

; APPLICANT: Pierre Sevigny

```

```

; APPLICANT: Keith Schappert

```

```

; APPLICANT: Heiko Wiesbusch

```

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; TITLE OF INVENTION: METHODS FOR TREATING A NEUROLOGICAL

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; FILE REFERENCE: 08523/013002

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; CURRENT APPLICATION NUMBER: US/09/334,489

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; PRIOR FILING DATE: 1999-06-16

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; PRIOR FILING DATE: 1998-06-18

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; NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3

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; LENGTH: 602

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; TYPE: PRT

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-334-489-3

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```

Query Match      19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

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QY 2 WLLALCLVLAGAQRGGGGPGGAPGGLGSLGSERPVNTAYGRVGRVRELNNE 61
DB 15 WFLLCML-----IGKSHTEDEIIATKNGKVRG-----MNL 47
QY 62 IL-SPVVOFLGVPYATPPLGARFPQPEAPASWPGVNRNATLPPACQNLHGALPAIMLP 120
DB 48 VFGTGTAFGLGIPYAQPPLGRLRFKPKQSLTKWSDIWNATKYANSCCQNDQSPFGHGS 107
QY 121 VMTDNLEAAATYVQNSQEDCLYLNLYVPTDGLTKRDEATLNPDPDIDRDPGKPYM 180
DB 108 EMNPNIDL-----SEDCLYLNWIPAP-----KPKNATVL 138
QY 181 LFLHGGSYMEGTGNN--FDGSVLAAYGNVIVATLNYRLVGLGFLS--TGDQAAKGNVGLLD 237
DB 139 IWIYGGGFQGTSSLHYVDGKFLARVERVIVVSMYRVGALGFLALPGNPEAPGNWGLFD 198
QY 238 QIQALRWLSNIAHFQGDPERITIFGSGAGASCWNLLILSHHSEGLFQKAIAGSGTAISS 297
DB 199 QQLALQWQKNIAAFQGNPKSVTLFGESAGAAVSJHLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSVN--YQPLKYTRLAALKVGCDDREDSAAVECLRRKPSRELVDQDVQARY---HIAF 351
DB 259 WATSLYEARNRTLNLAUKLTGCSRENETEIIKLRNKDQOEILLNEAFVVPYGTPLSVNF 318
QY 352 GPVVDGVDVDDPEILMQOGEFLNYDMLIGVNOGEGKLFVEDSAE--SEDGVSASAFDFT 409
DB 319 GPTVDGDFLTDMPDILLELQGFKKTQILVGVNKGDEGTAFLVYGAPGFSKONNSI---IT 374
QY 410 VSNFVDNL-YGYPEGKDVLETKFMYTWDADRDNGEMRKTLALLFTDHWVAPAVATA 468
DB 375 RKEFQGLKIFFGVSEFGKESILFHYTDWVDQRPENTREALGDVVGVDYNFICPALEFT 434
QY 469 KLHADYQSPVYFTFYHHCOAEGRPWADAAGHDELPPYVFGVPMVGATDLFPCNFSKNDV 528
DB 435 KKFSEWGNNAFFYYFEHRSKLPWPENWGMVHGVEIEFVGLPLERD-----NYTKAE 489
QY 529 MLSAVMTWTWNTAKTGDNPQVPQDTKFIHTKPNRFEVVMWKSFKNSKEKQYHLGLK-P 587
DB 490 ILRSIVKRWANFAKYGNPNETQNNSTS-----WPFVKSTEQKYLTLNTEST 536
QY 588 RVRDNYRANKVAFWLELVP 606
DB 537 RIMTKLRAQOCRWTSFPP 555

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RESULT 13

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US-09-334-489-4

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; Sequence 4, Application US/09334489

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; Patent No. 6291175

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; GENERAL INFORMATION:

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; APPLICANT: Pierre Sevigny

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; APPLICANT: Keith Schappert

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; APPLICANT: Heiko Wiesbusch

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; TITLE OF INVENTION: METHODS FOR TREATING A NEUROLOGICAL

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; FILE REFERENCE: 08523/013002

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; CURRENT APPLICATION NUMBER: US/09/334,489

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; PRIOR FILING DATE: 1999-06-16

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; PRIOR FILING DATE: 1998-06-18

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; NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 4

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; LENGTH: 602

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; TYPE: PRT

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ORGANISM: Homo sapiens
US-09-334-489-4

Query Match 19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY 2 WLIALCLVLAGAQRGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVRELNNE 61
DB 15 WFLLLCML-----IGKSHTEDDIIATKXGKVRG-----NNLT 47
QY 62 IL-GPVVQFLGVPYATPPLGARRFOPPEAPAPGWGNATTLPPACQNLHGALPAILMP 120
DB 48 VFGSTVTAFLGIPYAPPLGRFKKQSLTKWSDIWNATKYANSCCNIDQSPFGFHGS 107
QY 121 VNFDTNLEAAATYVQNSQEDCLYLNLYVPTDGLTKKREDEATLNPPTDIRDPGKPPVM 180
DB 108 EWMNPNTDL-----SEDCLYLNWVPAP-----KPKNATVL 138
QY 181 LFLHGSYMEGTGNM--PDGSLVLAAYGNVIVATLNYRLGVLGFLS--TGDQAAGNYGLLD 237
DB 139 IWIYGGGFGTQSSHLVYDGFARVERVIVVMYRVGALGFALPGENPEAPGNMGLFD 198
QY 238 QIOLRWLSENIAHFGDPERITIFSGAGASCYNLLILSHHSEGLFQKAIQSGTAISS 297
DB 199 QQLALQWQKNIAAFQGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSNV--YQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVOPARY-----HIAF 351
DB 259 WAVTSLYEARNRTNLAKLTGCSRENETEIIKLRNKDQOEILLNEAFVVPYGTPLSVNF 318
QY 352 GPVVDGVDVDDPEILMQOGBFLYDMLIGNVQEGELKFVEDSAE--SEDGVASAFDFT 409
DB 319 GPTVDGDLTMDPILLELQGFKTQILVGNKDEGTAFLVYGAPGSKNNSI-----IT 374
QY 410 VSNFVDNL--YGYPEGKDVLRITKFMYTDWADRDNGEMRRKTLALFTDHWVAPAVATA 468
DB 375 RKEFOEGLKIFPPGVSEFGKSIILFHYTDWDDQBPENYREALGDVVDYNYFCPALEFT 434
QY 469 KLHAYQSPVYFTFYHHCQAEGRPEWADAAGDELPHYVGVPMVGATDLFPNPKNDV 528
DB 435 KKFSEWGNNAFFYFHRSSKLPWPMWGVHGEIEFVGLPLERRD-----NYTKAE 489
QY 529 MLSAVMTYNTNFAKTDGPNQVPODTKFIHKPNRFEVWVSKNSKEQYHLGLK-P 587
DB 490 ILRSIVKRWANFAKYNPNETQNNST-----WPFKSTEQKYLTLNTEST 536
QY 588 RVRDNYRANKVAFWLELVP 606
DB 537 RIMTKLRAQQRFTWTSFPF 555

RESULT 14
5215909-11
; Patent No. 5215909
; APPLICANT: SOREO, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:11:
; LENGTH: 602
5215909-11

Query Match 19.0%; Score 855; DB 6; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY 2 WLIALCLVLAGAQRGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVRELNNE 61
DB 15 WFLLLCML-----IGKSHTEDDIIATKXGKVRG-----NNLT 47
QY 62 IL-GPVVQFLGVPYATPPLGARRFOPPEAPAPGWGNATTLPPACQNLHGALPAILMP 120
DB 48 VFGSTVTAFLGIPYAPPLGRFKKQSLTKWSDIWNATKYANSCCNIDQSPFGFHGS 107
QY 121 VNFDTNLEAAATYVQNSQEDCLYLNLYVPTDGLTKKREDEATLNPPTDIRDPGKPPVM 180
DB 108 EWMNPNTDL-----SEDCLYLNWVPAP-----KPKNATVL 138
QY 181 LFLHGSYMEGTGNM--PDGSLVLAAYGNVIVATLNYRLGVLGFLS--TGDQAAGNYGLLD 237
DB 139 IWIYGGGFGTQSSHLVYDGFARVERVIVVMYRVGALGFALPGENPEAPGNMGLFD 198
QY 238 QIOLRWLSENIAHFGDPERITIFSGAGASCYNLLILSHHSEGLFQKAIQSGTAISS 297
DB 199 QQLALQWQKNIAAFQGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSNV--YQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVOPARY-----HIAF 351
DB 259 WAVTSLYEARNRTNLAKLTGCSRENETEIIKLRNKDQOEILLNEAFVVPYGTPLSVNF 318
QY 352 GPVVDGVDVDDPEILMQOGBFLYDMLIGNVQEGELKFVEDSAE--SEDGVASAFDFT 409
DB 319 GPTVDGDLTMDPILLELQGFKTQILVGNKDEGTAFLVYGAPGSKNNSI-----IT 374
QY 410 VSNFVDNL--YGYPEGKDVLRITKFMYTDWADRDNGEMRRKTLALFTDHWVAPAVATA 468
DB 375 RKEFOEGLKIFPPGVSEFGKSIILFHYTDWDDQBPENYREALGDVVDYNYFCPALEFT 434
QY 469 KLHAYQSPVYFTFYHHCQAEGRPEWADAAGDELPHYVGVPMVGATDLFPNPKNDV 528
DB 435 KKFSEWGNNAFFYFHRSSKLPWPMWGVHGEIEFVGLPLERRD-----NYTKAE 489
QY 529 MLSAVMTYNTNFAKTDGPNQVPODTKFIHKPNRFEVWVSKNSKEQYHLGLK-P 587
DB 490 ILRSIVKRWANFAKYNPNETQNNST-----WPFKSTEQKYLTLNTEST 536
QY 588 RVRDNYRANKVAFWLELVP 606
DB 537 RIMTKLRAQQRFTWTSFPF 555

RESULT 15
US-08-446-100-2
; Sequence 2, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-2

Query Match      18.9%; Score 854; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 8.4e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY      2 WLLALCLVLAGAQRGGGPGGAPGGPGLGSLGEERPPVNTAYGRVGRVRELNNE 61
Db      15 WFLLCML-----IGKSHTEDDIIATKNGKVRG---MNL 47

QY      62 IL-GPVVQFLGVPYATPPLGARBPQPEAPASWPGVGNATLTPPACPNLHGALPAIMLP 120
Db      48 VFGGTVTAFLGIPYAPQPLGLRPFKPSLTKWSDIWNATKYANSCCNIDQSPFGFHGS 107

QY      121 WFTDNLEAAATVYQNOSEDCLYNLYVPTDQGLTKKDEATLNPPDTRDPGKKPYM 180
Db      108 EMNPNTDL-----SEDCLYNVWIPAP-----KPKNATVL 138

QY      181 LFLHGSSYMEGTGWM--FDGSLAAAYGNVIVATLNYLVLGVLGLS-TGDAQAKNGYGLLD 237
Db      139 IWYGGHFQGTSLHVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFD 198

QY      238 QIQALRWLSNIAHFGDPERITIFGSGAGASCVNLLIILSHSEGLFQKAIQSGTATSS 297
Db      199 QQLALQWQVQNIAAFGGNPKSVILFGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAP 258

QY      298 WSVN--YQPLKYTRLLAAKVGCDREDSAAZAEVCLRRKPSRELVDQVQPARY-----HIAP 351
Db      259 WAVTSLYEARNRTLNLAQLTGCSRENETETIKLRNKPQEIILLNEAFVVPYCTPLSVNF 318

QY      352 GPVVGDGVDPDDPEILMQOGEFLNYDMLGVNQGELKFVEDSAE--SEDGVSASAFDFT 409
Db      319 GPVVDGDFLTDMPDILLELGQFKQTQILGVNKGDEGTAFLVYGAPGFSKNNNSI----IT 374

QY      410 VSNFVNL-YGYPEGKDVLRRTIKFMYTDWDRDNGEMERKTLLALFTDHWVAPAVATA 468
Db      375 RKEFQGLKIFFGVSEFGKESILFHYTDWDDQRPENYREALGDVVGDFNYFCPALFT 434

QY      469 KLHADYQSPVYFVYVHCOAGRPEDWADAAGDELPPYVGVPMVGATDLFCNFSKNDV 528
Db      435 KFSSEGNNAFFYFHRSSKLPWPMWGMVHGHEIEFVFGFLERRD-----NYTKAE 489

QY      529 MLSAVVMYTNFAKTGDPNQVPQDTKFIHTKPNRFEVWMSKFNSEKQYLIHLK-P 587
Db      490 ILSRSIVKRWANFAKYNFNETQNNST-----WPFVKSTEQKYLTLNTEST 536

QY      588 RVRDNYRANKVAFWLELVP 606
Db      537 RIMTKLRAQQCRFTSFFP 555
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Search completed: February 13, 2004, 13:14:50
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2004, 13:06:01, Search time 47 Seconds
(without alignments)
2819.930 Million cell updates/sec

Title: US-09-934-323-2
Perfect score: 4508
Sequence: 1 MWLLALCLVGLAGRGGGG.....PPATSHNHTLPHPHSTTRV 835

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4508	100.0	835	23 AAE25020	Human drug metabol
2	4508	100.0	835	23 ABB97215	Novel human protei
3	4508	100.0	835	23 ABB07675	Human carboxyleste
4	4422	98.1	837	22 ABB62400	Human MBS4 polype
5	4075.5	50.4	801	23 ABB07524	Human drug metabol
6	2770	61.4	828	23 ABB43803	3 isoform protein.
7	2731	60.6	816	20 AAY41740	Human PRO701 prote
8	2731	60.6	816	21 AAB44296	Human PRO701 (UN03
9	2731	60.6	816	21 AAB33427	Human PRO701 prote

10	2731	60.6	816	24 ABU61126	Human PRO701 polyp
11	2713.5	60.2	817	24 ABB82852	CES2 related polyp
12	2678.5	59.4	816	23 AAM48908	Human neurotrophin
13	2361	52.4	1434	22 ABG10270	Novel human diagno
14	1747	38.8	726	22 ABG10264	Novel human diagno
15	1745.5	38.7	509	22 AAM93205	Human polypeptide,
16	1685	37.4	308	21 AAB40734	Human ORFX ORF498
17	1681	37.3	509	22 AAB94127	Human protein sequ
18	1681	37.3	509	24 ABB82853	CES2 related polyp
19	1381	30.6	396	22 AAU87273	Novel central nerv
20	1359	30.1	271	22 ABG10266	Novel human diagno
21	993	22.0	229	21 ABA44913	Human secreted pro
22	954	21.2	335	22 AAM93345	Human polypeptide,
23	906	20.1	229	21 AAB44314	Human secreted pro
24	863	19.1	165	22 ABG10269	Novel human diagno
25	859	19.1	574	23 AAO18905	Rat butyrylcholine
26	858.5	19.0	614	24 ABP59222	Human drug metabol
27	855	19.0	602	14 AAR37442	Full-length human
28	855	19.0	602	21 AAY44573	Human wild type Bu
29	855	19.0	602	21 AAY44574	Human Butyrylcholi
30	855	19.0	602	21 AAY49471	Human wild-type bu
31	855	19.0	602	21 AAY49473	Human butyryl chol
32	855	19.0	602	21 AAY49474	Human butyryl chol
33	855	19.0	602	21 AAY49476	Human butyryl chol
34	855	19.0	602	21 AAY59235	Human butyryl chol
35	854	18.9	602	21 AAY49472	Human butyryl chol
36	854	18.9	602	21 AAY49477	Human butyryl chol
37	853	18.9	602	21 AAY49483	Human butyryl chol
38	853	18.9	602	23 AAO18897	Human butyrylcholi
39	852	18.9	602	21 AAY49478	Human butyryl chol
40	852	18.9	602	21 AAY49487	Human butyryl chol
41	852	18.9	602	21 AAY49488	Human butyryl chol
42	851	18.9	602	21 AAY49475	Human butyryl chol
43	849	18.8	602	21 AAY49480	Human butyryl chol
44	849	18.8	602	21 AAY49484	Human butyryl chol
45	848	18.8	602	21 AAY49485	Human butyryl chol

ALIGNMENTS

RESULT 1
AAE25020
ID AAE25020 standard; Protein; 835 AA.
XX
AAE25020;
AC
XX
DT 30-OCT-2002 (first entry)
XX
DE Human drug metabolising enzyme (DME-5).
XX
KW Human; drug metabolising enzyme; autoimmune; inflammatory disorder;
KW acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;
KW proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;
KW asthma; neurological disorder; Alzheimer's disease; Huntington's disease;
KW dementia; Parkinson's disease; developmental disorder; anaemia; adenoma;
KW drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;
KW renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;
KW anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;
KW goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant;
KW anticonvulsant; nootropic; enzyme; DME-5.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..14
FT /label= Signal_peptide
FT Protein 15..835
FT /note= "Mature human DME-5"
FT Peptide 1..16
FT /label= Signal_peptide
FT Protein 17..835
FT /note= "Mature human DME-5"

Db	121	VFTNTNLRAAATYYQNQEDCLYLNLVPTEDGSLTKKRDEATLNPDDTDIRDPGKKPV	180
Qy	181	LFLHGSSYMEGTGNMFDGSLVLAAYGNVIVATNLRYLGLVGLSTGQAAKNGYGLLDQIQ	240
Db	181	LFLHGSSYMEGTGNMFDGSLVLAAYGNVIVATNLRYLGLVGLSTGQAAKNGYGLLDQIQ	240
Qy	241	ALRWLSENTAHFGDGPERRITTFSGAGASCWNLLILSHHSEGLFQKAIAGSGTAISWSV	300
Db	241	ALRWLSENTAHFGDGPERRITTFSGAGASCWNLLILSHHSEGLFQKAIAGSGTAISWSV	300
Qy	301	NYQPLKYTRLAAKVGCDREDSAAVECLRKRSRELVDQDVOPARYHIAFGVWDGVV	360
Db	301	NYQPLKYTRLAAKVGCDREDSAAVECLRKRSRELVDQDVOPARYHIAFGVWDGVV	360
Qy	361	PDDPILMQQGEFLNYDMLIGVNGEGELKFVEDSASESDGVSSAFDFTVSNFVMDLNYG	420
Db	361	PDDPILMQQGEFLNYDMLIGVNGEGELKFVEDSASESDGVSSAFDFTVSNFVMDLNYG	420
Qy	421	PEGKQVLRETIKFMYTDMWDRDNGEMRRKTLALFTDQHWVAVATAKLHADYQSPVTF	480
Db	421	PEGKQVLRETIKFMYTDMWDRDNGEMRRKTLALFTDQHWVAVATAKLHADYQSPVTF	480
Qy	481	YTFYHHCQAEGRPEWADAAGDELPLYVFGVPMVGATDLFFCNFSKNDVMLSAVVMTYTN	540
Db	481	YTFYHHCQAEGRPEWADAAGDELPLYVFGVPMVGATDLFFCNFSKNDVMLSAVVMTYTN	540
Qy	541	FAKTDGPNQVPQDTKFLHTKPNRFEEVWSKNSKEQVLIHGLKPRVDRDNYRANKVAF	600
Db	541	FAKTDGPNQVPQDTKFLHTKPNRFEEVWSKNSKEQVLIHGLKPRVDRDNYRANKVAF	600
Qy	601	WLELVPHLNLHLELFTTTTLRPPYATRWPPRPAGAGTRRPPEPPATLPPPEPEEPPGR	660
Db	601	WLELVPHLNLHLELFTTTTLRPPYATRWPPRPAGAGTRRPPEPPATLPPPEPEEPPGR	660
Qy	661	AYDRPFGSDRDIYSTELSVTVAVAGSLFLPILAFALYYKDRRQBLRCRLSPPGGSGS	720
Db	661	AYDRPFGSDRDIYSTELSVTVAVAGSLFLPILAFALYYKDRRQBLRCRLSPPGGSGS	720
Qy	721	GVPGGGPPLLPAAGRELPEEELVSLQKRGCGVGADPAEALRPACPPDYTLALRRAPDDV	780
Db	721	GVPGGGPPLLPAAGRELPEEELVSLQKRGCGVGADPAEALRPACPPDYTLALRRAPDDV	780
Qy	781	PLLAFGALTLLPSGLGPPPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV	835
Db	781	PLLAFGALTLLPSGLGPPPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV	835
RESULT 2			
ABB97215			
ID	ABB97215 standard; Protein; 835 AA.		
XX	AC		
XX	ABB97215;		
DT	27-JUN-2002 (first entry)		
DE	Novel human protein SEQ ID NO: 483.		
XX	Human; antianaemic; vulnerable; antiinflammatory; immunomodulator;		
KW	antifertility; cerebroprotective; cycostatic; rheumatic; gene therapy;		
KW	neuroprotective; antiparkinsonian; protein therapy; EST;		
KW	expressed sequence tag.		
OS	Homo sapiens		
XX	NO200222660-A2.		
XX	21-MAR-2002.		
XX	10-SEP-2001; 2001WO-US26015.		
XX	11-SEP-2000; 2000US-0659671.		
XX	(HYSE-) HYSEQ INC.		

Qy	661	AYDRFPGSDSDYSTEISVTVAVGASLLFLNLIFAALYYKDRRQELRCRLSPGGSGS	720
Db	661	AYDRFPGSDSDYSTEISVTVAVGASLLFLNLIFAALYYKDRRQELRCRLSPGGSGS	720
Qy	721	GVPGGGPLLPAAGRELPPEELVSLQKRGGGVGADPAELRACPDYTLARRAPDDV	780
Db	721	GVPGGGPLLPAAGRELPPEELVSLQKRGGGVGADPAELRACPDYTLARRAPDDV	780
Qy	781	PLIAPGALTLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHPHSTTRV	835
Db	781	PLIAPGALTLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHPHSTTRV	835
RESULT 3			
ABB07675			
XX	ID	ABB07675 standard; Protein; 835 AA.	
XX	AC	ABB07675;	
XX	XX		
DT	10-JUN-2002	(first entry)	
XX	XX		
DE	Human carboxylesterase family member, 33410 polypeptide.		
XX	XX		
KW	Carboxylesterase; 33410; cytostatic; cardiant; dermatological; human;		
KW	antidiabetic; antirheumatic; antiarthritic; antiarrhythmic; vasotropic;		
KW	vulnerable; neuroprotective; antiinflammatory; antiulcer; antiasthmatic;		
KW	antiallergic; antiviral; hepatotropic; nephrotropic; anti-HIV; enzyme;		
KW	antiparkinsonian; tuberculostatic; hypotensive; antithrombotic;		
KW	nootropic; antisense therapy; angiogenesis; gene therapy.		
XX	XX		
OS	homo sapiens.		
XX	XX		
XX	WC200216616-A2.		
XX	28-FEB-2002.		
PD			
XX	21-AUG-2001; 2001WO-US26091.		
PF			
XX			
XX	21-AUG-2000; 2000US-226774P.		
PR			
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Curtis RAJ;		
XX			
XX	WPI; 2002-257916/30.		
DR			
XX	N-PSDB; ABA95199, ABA95200.		
DR			
PT	New carboxylesterase nucleic acid 33410, useful for the treatment and		
PT	diagnosis of immune, cardiovascular, reproductive and cancerous		
PT	disorders -		
XX			
PS	Claim 1; Page 110; 123pp; English.		
XX			
CC	The invention provides a novel carboxylesterase family member, designated		
CC	33410. Compounds that binds to or modulate the activity or expression of		
CC	33410, are useful for treating or preventing a disorder such as cellular		
CC	proliferative or differentiative, neural, cardiovascular, prostatic, skin		
CC	brain and skeletal muscular disorders, protein-protein interaction		
CC	disorders, signal transduction disorders, immune (e.g. diabetes and		
CC	rheumatoid arthritis), reproductive, cardiovascular (e.g. hypertension,		
CC	atherosclerosis, coronary artery disease, arrhythmia, ischaemic heart		
CC	disease and angina pectoris), vascular disorders (e.g. varicose veins,		
CC	Wegener's granulomatosis and wound healing) or cancerous disorders,		
CC	multiple sclerosis, Crohn's disease, ulcers, asthma, allergy, infection,		
CC	kidney disease (glomerulonephritis), idiopathic thrombocytopenic purpura,		
CC	hepatitis, tuberculosis, human immunodeficiency virus, Alzheimer's and		
CC	Parkinson's. The 33410 polynucleotide and polypeptide are useful for		
CC	diagnosis of a predisposition to a disorder, for evaluating the efficacy		
CC	of a therapeutic or prophylactic disorder, for chromosome mapping, as		
CC	immunogens, for drug screening, for the detection of mutations in the		
CC	gene and for tissue typing. The present sequence represents the human		
CC	carboxylesterase family member, 33410.		
XX			

SQ Sequence 835 AA;
 Query Match 100.0%; Score 4508; DB 23; Length 835;
 Best Local Similarity 100.0%; Pred. No. 4.3e-316;
 Matches 835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVREINN 60
 DB 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVREINN 60
 QY 61 ELIGPVVQFLGVYATPLGARRFQPPAPASWFGVNRNATLPPACQNLHGALPALMLP 120
 DB 61 ELIGPVVQFLGVYATPLGARRFQPPAPASWFGVNRNATLPPACQNLHGALPALMLP 120
 QY 121 VWFDTNLEAAATYVQNSQEDCLYNLYPTEDGGLTKRDEATLNPEDTIRDPGKPFV 180
 DB 121 VWFDTNLEAAATYVQNSQEDCLYNLYPTEDGGLTKRDEATLNPEDTIRDPGKPFV 180
 QY 181 LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATLNLRLGVLGFLSTGDOAAKNGYLLDQIQ 240
 DB 181 LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATLNLRLGVLGFLSTGDOAAKNGYLLDQIQ 240
 QY 241 ALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISSWSV 300
 DB 241 ALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISSWSV 300
 QY 301 NYQPLKYTRLIAAKVGCDDREDSABAECLRRKPSRELVDQDVQPARVHIAFGPVWDGDDV 360
 DB 301 NYQPLKYTRLIAAKVGCDDREDSABAECLRRKPSRELVDQDVQPARVHIAFGPVWDGDDV 360
 QY 361 PDDPEILMQGGEFLNYDMLIGNVQGEGLKFVEDSAESDGVSAFDTVSFVNDLYGY 420
 DB 361 PDDPEILMQGGEFLNYDMLIGNVQGEGLKFVEDSAESDGVSAFDTVSFVNDLYGY 420
 QY 421 PEGKDVLRRTIKMYTWDADNGEMERKTLALFTDQHWAPAVATAKLHADYQSFVYF 480
 DB 421 PEGKDVLRRTIKMYTWDADNGEMERKTLALFTDQHWAPAVATAKLHADYQSFVYF 480
 QY 481 YTFYHHCQAEGRPEWADAAGDELPIYFVGVPMVGATDLFFCNFSKNDVWLSAVVMYWTN 540
 DB 481 YTFYHHCQAEGRPEWADAAGDELPIYFVGVPMVGATDLFFCNFSKNDVWLSAVVMYWTN 540
 QY 541 FAKTGDNDQNPQDTKIHTKPNRFEVWVSKNSKEQYLHGLKPRVRDNRANKVAF 600
 DB 541 FAKTGDNDQNPQDTKIHTKPNRFEVWVSKNSKEQYLHGLKPRVRDNRANKVAF 600
 QY 601 WLELVPHLHNLHTELFITTLRLPPYATRWPPRPAGAPGTRPPPPATLPEPEPEPGPR 660
 DB 601 WLELVPHLHNLHTELFITTLRLPPYATRWPPRPAGAPGTRPPPPATLPEPEPEPGPR 660
 QY 661 AYDRFGDSRDYSTELSVTVAVGASLLFLNILAPALYYKRRRQELRCRLSPGSGSGS 720
 DB 661 AYDRFGDSRDYSTELSVTVAVGASLLFLNILAPALYYKRRRQELRCRLSPGSGSGS 720
 QY 721 GVPGGGFLLPAGRELPEELVSLQKRGGVGADPAEALRACPPDYTLALRRAPDDV 780
 DB 721 GVPGGGFLLPAGRELPEELVSLQKRGGVGADPAEALRACPPDYTLALRRAPDDV 780
 QY 781 PLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPPPTATSHNLTLPHPHSTTRV 835
 DB 781 PLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPPPTATSHNLTLPHPHSTTRV 835

RESULT 4
 AAB62400

ID AAB62400 standard; Protein; 837 AA.

XX AC AAB62400;

XX AC AAB62400;

DT 29-JUN-2001 (first entry)

DE Human MBSP4 polypeptide (clone 21417374.0.9).

KW MBSPX; cancer; preclampsia; immune system; neurological; cytostatic;
 KW gynecological; antiinflammatory; neuroprotective; inotropic; relaxant;
 KW cardiac; dermatological; gene therapy; human; MBSP4.
 OS Homo sapiens.
 XX
 XX WO200127277-A2.
 XX PD 19-APR-2001.
 XX PF 13-OCT-2000; 2000WO-US28480.
 XX PR 13-OCT-1999; 99US-0159231.
 PR 12-JAN-2000; 2000US-0175670.
 PR 12-OCT-2000; 2000US-0159231.
 XX
 XX (CURA-) CURAGEN CORP.
 XX Shinkets RA, Lichenstein H, Boldog FL;
 XX WPI; 2001-282030/29.
 DR N-PSDB; AAF82996.
 XX
 PT Novel human polynucleotide sequences and the membrane bound or secreted
 PT polypeptides encoded by these sequences, designated MBSPX -
 XX
 PS Claim 1; Page 26-29; 157pp; English.
 XX
 CC The invention relates to novel polypeptides, termed MBSPX and
 CC polynucleotides encoding the MBSPX polypeptides. The MBSPX polypeptide,
 CC nucleic acid and an MBSPX antibody are useful for treating or preventing
 CC a pathology associated with the protein especially in humans. The MBSPX
 CC nucleic acid can be used to express MBSPX protein (e.g. via a recombinant
 CC expression vector in a host cell in gene therapy applications), an to
 CC detect MBSPX mRNA in a biological sample or a genetic lesion in a MBSPX
 CC gene. Disorders associated with insufficient or excessive production of
 CC MBSPX protein include cancer, preclampsia, immune system disorders and
 CC inflammation, neurological disorders, cardiovascular disorders; and skin
 CC and muscle abnormalities. The anti-MBSPX antibodies can be used to detect
 CC and isolate MBSPX proteins and modulate MBSPX activity. The present
 CC sequence represents the amino acid sequence of MBSP4, a human neurologin
 CC 2 homologue.
 XX
 SQ Sequence 837 AA;
 Query Match 98.1%; Score 4422; DB 22; Length 837;
 Best Local Similarity 98.6%; Pred. No. 6.9e-310;
 Matches 825; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVREINN 60
 DB 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVREINN 60
 QY 61 ELIGPVVQFLGVYATPLGARRFQPPAPASWFGVNRNATLPPACQNLHGALPALMLP 120
 DB 61 ELIGPVVQFLGVYATPLGARRFQPPAPASWFGVNRNATLPPACQNLHGALPALMLP 120
 QY 121 VWFDTNLEAAATYVQNSQEDCLYNLYPTEDGGLTKRDEATLNPEDTIRDPGKPFV 180
 DB 121 VWFDTNLEAAATYVQNSQEDCLYNLYPTEDGGLTKRDEATLNPEDTIRDPGKPFV 180
 QY 181 LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATLNLRLGVLGFLSTGDOAAKNGYLLDQIQ 240
 DB 181 LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATLNLRLGVLGFLSTGDOAAKNGYLLDQIQ 240
 QY 241 ALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISSWSV 300
 DB 241 ALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISSWSV 300
 QY 301 NYQPLKYTRLIAAKVGCDDREDSABAECLRRKPSRELVDQDVQPARVHIAFGPVWDGDDV 360
 DB 301 NYQPLKYTRLIAAKVGCDDREDSABAECLRRKPSRELVDQDVQPARVHIAFGPVWDGDDV 360

QY 361 PDDPEILMOQGEFLNYDMLIGNQEGGLKFVEDSASESDGVSASAFDFTVSNFVNDLYGY 420
 Db 361 PDDPEILMOQGEFLNYDMLIGNQEGGLKFVEDSASESDGVSASAFDFTVSNFVNDLYGY 420
 QY 421 PEGKDVLRITIKFMYTWDADRNGEMRRKTLTLLAFTDQWVAPAVATAKLHADYQSPVYF 480
 Db 421 PEGKDVLRITIKFMYTWDADRNGEMRRKTLTLLAFTDQWVAPAVATAKLHADYQSPVYF 480
 QY 481 YTFYHHCQAEGRPEWADAAGDELPIYFGVPMVGATDLFPCNFKNDVMSAVVMTWTN 540
 Db 481 YTFYHHCQAEGRPEWADAAGDELPIYFGVPMVGATDLFPCNFKNDVMSAVVMTWTN 540
 QY 541 FAKTGDNPQVQDQKFTHTKPNRPEEYVWVKFSKEKQYLIHGLKPRVRDNYRANKVAF 600
 Db 541 FAKTGDNPQVQDQKFTHTKPNRPEEYVWVKFSKEKQYLIHGLKPRVRDNYRANKVAF 600
 QY 601 WLELVPHLHNLHTELTFTTTTLPPVATWPPRP-AGAGTRRPPPPATLPPPEPEPPG 659
 Db 601 WLELVPHLHNLHTELTFTTTTLPPVATWPPRP-AGAGTRRPPPPATLPPPEPEPPG 660
 QY 660 RAYDRFPDSDYSELVTVAVASLLFLNILAFAALYKRRRQELRCRRLSPPGSG 719
 Db 661 RAYDRFPDSDYSELVTVAVASLLFLNILAFAALYKRRRQELRCRRLSPPGSG 720
 QY 720 SGVPGGGLLPAAGRELPEELVSLQKRGGVGADPAEALRPACPPDYTLALRRAPDD 779
 Db 721 SGVPGGGLLPAAGRELPEELVSLQKRGGVGADPAEALRPACPPDYTLALRRAPDD 780
 QY 780 VLLAPGALTLLPSGLPDPDPDPDP-LLHPPGPPPPPPPTATSHNNTLPHPHSTTRV 835
 Db 781 VLLAPGALTLLPSGLPDPDPDPDP-LLHPPGPPPPPPPTATSHNNTLPHPHSTTRV 837

RESULT 5

ABB07524
 ID ABB07524 standard; Protein; 801 AA.

AC ABB07524;

DT 23-APR-2002 (first entry)

DE Human drug metabolizing enzyme (DME) (ID: 7473875CD1).

XX Drug metabolizing enzyme; DME; antiallergic; antianemic; antiasthmatic;
 KW osteopathic; antirheumatic; antiarthritic; dermatological; nephrotropic;
 KW antiinflammatory; vulnery; antibacterial; virucide; antiparasitic;
 KW protozoacide; fungicide; antihelminthic; cytostatic; ophthalmological;
 KW antiarteriosclerotic; hepatotropic; antidiabetic; anorectic; human;
 KW thrombolytic; metabolic; anticoagulant; antithyroid; gynecological;
 KW angiogenic; antitumor; antidiarrhoeic; laxative; enzyme.

OS Homo sapiens.

XX WO200204612-A2.

XX 17-JAN-2002.

XX 05-JUL-2001; 2001WO-US21324.

XX 07-JUL-2000; 2000US-216804P.

XX 14-JUL-2000; 2000US-218948P.

XX 21-JUL-2000; 2000US-220037P.

XX 28-JUL-2000; 2000US-221837P.

XX (INCY-) INCYTE GENOMICS INC.

XX Baughn MR, Bruns CM, Das D, Ding L, Elliott VS, Gandhi AR;

PI Hafalia AJA, Kearney L, Khan P, Lal P, Lee EA, Lu DM, Lu Y;

PI Nguyen DB, Patterson C, Ramkumar J, Ring HZ, Sanjanwala MS; Xu Y;

PI Tang Y, Thangavue K, Thornton M, Tribouley CM, Walla NK, Xu Y;

PI Yang JT, Yao MG, Yue H;

XX WPI; 2002-164641/21.

DR N-PSDB; ABA94727.

XX Novel drug metabolizing enzymes and polynucleotides encoding the
 PT enzymes, useful for treating, diagnosing or preventing
 PT autoimmune/inflammatory, cell proliferative, developmental and
 PT endocrine disorders -
 XX

PS Claim 1; Page 148-149; 167pp; English.

XX The invention provides human drug metabolizing enzyme (DME) polypeptides
 CC and polynucleotides. DMEs can be expressed by standard recombinant
 CC methodology. The DME polypeptides, polynucleotides, modulators and
 CC antibodies are useful from diagnosing, treating and preventing autoimmune
 CC /inflammatory (e.g. allergies, anemia, osteoporosis, rheumatoid
 CC arthritis, atopic dermatitis, glomerulonephritis and irritable bowel
 CC syndrome, trauma, and bacterial, viral, parasitic, protozoal, fungal or
 CC helminthic infections), cell proliferative (e.g. cancer, atherosclerosis,
 CC and hepatitis), developmental (e.g. cerebral palsy and cataract),
 CC endocrine (e.g. thrombosis, goiter, hyperplasia, amenorrhea and
 CC gynecomastia), eye (e.g. iritis and glaucoma, metabolic (e.g. Addison's
 CC disease, diabetes and obesity), and gastrointestinal disorders (e.g.
 CC anorexia, nausea, abdominal angina, ulcerative colitis, diarrhoea and
 CC constipation). The DME polypeptides are useful in drug screening
 CC techniques, and to analyse the proteome of a tissue or cell type. The DME
 CC polynucleotides are useful for creating knock-in humanized animals or
 CC transgenic animals to model human diseases, and in somatic or germline
 CC gene therapy. The present sequence represents a human DME polypeptide
 CC sequence.

XX Sequence 801 AA;

SQ Query Match 90.4%; Score 4075.5; DB 23; Length 801;

Best Local Similarity 95.1%; Pred No. 6.1e-285;

Matches 770; Conservative 3; Mismatches 18; Indels 19; Gaps 3;

QY 1 MWLLALCLVLGAGAQGGGPGGAPGGGLGSLGSEERFPVNTAYGRVGRRELNN 60

Db 1 MWLLALCLVLGAGAQGGGPGGAPGGGLGSLGSEERFPVNTAYGRVGRRELNN 60

QY 61 ETLGPVQVFLGVPYATPLGAREFPPEAPAPSWPGRNATLPPACPNLHGALPAIMLP 120

Db 61 ETLGPVQVFLGVPYATPLGAREFPPEAPAPSWPGRNATLPPACPNLHGALPAIMLP 120

QY 121 WFTDNLEAAATYVQNSDCLYLNLYVPTDGLTKRDEATLNPPTDTRDPPGKPPVM 180

Db 121 WFTDNLEAAATYVQNSDCLYLNLYVPTDGLTKRDEATLNPPTDTRDPPGKPPVM 180

QY 181 LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATINVLGVGLSTGDAQAKNYGLLDQIQ 240

Db 181 LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATINVLGVGLSTGDAQAKNYGLLDQIQ 240

QY 241 ALRWLSENIAHFGGDPERITIFGSGAGASCYNLLILSHHSEGLFQKALQSGTAISSWSV 300

Db 241 ALRWLSENIAHFGGDPERITIFGSGAGASCYNLLILSHHSEGLFQKALQSGTAISSWSV 300

QY 301 NYQPLKYTRLLAAKVGCDREDSAEVCELRKPSRELVDQVQPARYHIAFGPVVDGVW 360

Db 301 NYQPLKYTRLLAAKVGCDREDSAEVCELRKPSRELVDQVQPARYHIAFGPVVDGVW 360

QY 361 PDDPEILMOQGEFLNYDMLIGNQEGGLKFVEDSASESDGVSASAFDFTVSNFVNDLYGY 420

Db 361 PDDPEILMOQGEFLNYDMLIGNQEGGLKFVEDSASESDGVSASAFDFTVSNFVNDLYGY 420

QY 421 PEGKDVLRITIKFMYTWDADRNGEMRRKTLTLLAFTDQWVAPAVATAKLHADYQSPVYF 480

Db 421 PEGKDVLRITIKFMYTWDADRNGEMRRKTLTLLAFTDQWVAPAVATAKLHADYQSPVYF 480

QY 481 YTFYHHCQAEGRPEWADAAGDELPIYFGVPMVGATDLFPCNFKNDVMSAVVMTWTN 540

Db 481 YTFYHHCQAEGRPEWADAAGDELPIYFGVPMVGATDLFPCNFKNDVMSAVVMTWTN 540

QY 541 FAKTGDNPQVQDQKFTHTKPNRPEEYVWVKFSKEKQYLIHGLKPRVRDNYRANKVAF 600

Db	541	FAKTGDPNPV	QDQTKFIHTKPNRE	EEVWSKFN	SKQYLIH	GLKRPVRDNT	RAKVAF	600
Qy	601	WLELVPHLHNL	HTLFTTTITRL	PPVATRW	PPRPAGAPG	TRPPPPATL	PEPEPEPGPR	660
Db	601	WLELVPHLHNL	HTLFTTTITRL	PPVATRW	PPRPAGAPG	TRPPPPATL	PEPEPEPGPR	660
Qy	661	AYDRPFGDSRD	YSTLSVTVA	VGASLLFIN	LAFALYYK	DRRQELRC	RLSRPPGSGS	720
Db	661	AYDRPFGDSRD	YSTLSVTVA	VGASLLFIN	LAFALYYK	DRRQELRC	RLSRPPGSGS	720
Qy	721	GVPGGGPPLL	PAAGRELPEE	ELVSLQKRG	GVGADPAE	ALRPACPD	DYTLALRRAPDV	780
Db	721	GVPGGGPPLL	PAAGRELPEE	ELVSLQKRG	GVGADPAE	ALRPACPD	DYTLALRRAPDV	780
Qy	781	PLLAGALTL	PLSGLPGPP	PPPPPSL	HPFG	810		
Db	776	-----	LSSLSGPD	QRP	-----	HPWG	791	

RESULT 6
ABP43803

ID ABP43803 standard; Protein; 828 AA.

AC ABP43803;

DT 26-FEB-2003 (first entry)

DE 3 isoform protein.

Neuroprotective; immunomodulator; cancer; chromosome Xq13.1;
cytostatic; anti-inflammatory; gene therapy; nutritional supplement;
wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
vulnerability.

XX Homo sapiens.

XX PN WO200231111-A2.

XX
PD 18-APR-2002.XX
PF
11-OCT-2001; 2001WO-US27760.

XX
PR 12-OCT-2000; 2000US-0687527.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

DR WPI; 2002-426278/45.

DR N-PSDB; ABQ61047.

New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or inflammation -

PS Claim 20; SEQ ID # 706; 357pp + sequence listing; English.

The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnary, neuroprotective, immunomodulator, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records AB943544-AB943989 represent polypeptides encoded by polynucleotides of the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

[illegible]

XX AC AAY41740;
 XX DT 07-DEC-1999 (first entry)
 XX DE Human PRO701 protein sequence.
 XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX OS Homo sapiens.
 XX EN WO9946281-A2.
 XX PD 16-SEP-1999.
 XX PF 08-MAR-1999; 99WO-US05028.
 XX PR 10-MAR-1998; 98US-0077450.
 XX PR 11-MAR-1998; 98US-0077632.
 XX PR 11-MAR-1998; 98US-0077641.
 XX PR 11-MAR-1998; 98US-0077649.
 XX PR 12-MAR-1998; 98US-0077791.
 XX PR 13-MAR-1998; 98US-0078004.
 XX PR 17-MAR-1998; 98US-0040220.
 XX PR 20-MAR-1998; 98US-0078888.
 XX PR 20-MAR-1998; 98US-0078910.
 XX PR 20-MAR-1998; 98US-0078936.
 XX PR 20-MAR-1998; 98US-0078939.
 XX PR 25-MAR-1998; 98US-0079294.
 XX PR 26-MAR-1998; 98US-0079656.
 XX PR 27-MAR-1998; 98US-0079663.
 XX PR 27-MAR-1998; 98US-0078664.
 XX PR 27-MAR-1998; 98US-0079689.
 XX PR 27-MAR-1998; 98US-0079728.
 XX PR 27-MAR-1998; 98US-0079786.
 XX PR 30-MAR-1998; 98US-0079920.
 XX PR 30-MAR-1998; 98US-0079923.
 XX PR 31-MAR-1998; 98US-0080105.
 XX PR 31-MAR-1998; 98US-0080107.
 XX PR 31-MAR-1998; 98US-0080165.
 XX PR 31-MAR-1998; 98US-0080194.
 XX PR 01-APR-1998; 98US-0080327.
 XX PR 01-APR-1998; 98US-0080328.
 XX PR 01-APR-1998; 98US-0080333.
 XX PR 01-APR-1998; 98US-0080334.
 XX PR 08-APR-1998; 98US-0081049.
 XX PR 08-APR-1998; 98US-0081070.
 XX PR 08-APR-1998; 98US-0081071.
 XX PR 09-APR-1998; 98US-0081195.
 XX PR 09-APR-1998; 98US-0081203.
 XX PR 09-APR-1998; 98US-0081229.
 XX PR 15-APR-1998; 98US-0081817.
 XX PR 15-APR-1998; 98US-0081838.
 XX PR 15-APR-1998; 98US-0081952.
 XX PR 15-APR-1998; 98US-0081955.
 XX PR 21-APR-1998; 98US-0082568.
 XX PR 21-APR-1998; 98US-0082569.
 XX PR 22-APR-1998; 98US-0082700.
 XX PR 22-APR-1998; 98US-0082704.
 XX PR 22-APR-1998; 98US-0082804.
 XX PR 23-APR-1998; 98US-0082767.
 XX PR 23-APR-1998; 98US-0082796.
 XX PR 27-APR-1998; 98US-0083336.
 XX PR 28-APR-1998; 98US-0083322.
 XX PR 29-APR-1998; 98US-0083392.
 XX PR 29-APR-1998; 98US-0083435.
 XX PR 29-APR-1998; 98US-0083456.
 XX PR 29-APR-1998; 98US-0083499.
 XX PR 29-APR-1998; 98US-0083500.
 XX PR 29-APR-1998; 98US-0083545.
 XX PR 29-APR-1998; 98US-0083554.

PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.

(GETH) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

N-PSDB; AAZ34209.

New secreted and transmembrane polypeptides and their polynucleotides,
 useful for treating blood coagulation disorders, cancers and cellular
 adhesion disorders -

Claim 12; Fig 151; 530pp; English.

The present invention describes secreted and transmembrane polypeptides
 and their polynucleotides. The nucleotide sequences are useful as
 sources of probes, primers, for chromosome mapping, and for generation
 of antisense sequences. They can also be used to create transgenic
 animals. The proteins can be used to treat a variety of diseases and
 disorders, depending on their function. Diseases that may be treated
 include blood coagulation disorders, cancers and cellular adhesion
 disorders. They may also be used to raise antibodies. AAZ3891 to
 AAZ34338, and AA41685 to AA41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 invention.

SQ Sequence 816 AA;

Query Match 60.6%; Score 2731; DB 20; Length 816;

Best Local Similarity 64.2%; Pred. No. 4.9e-188;

Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;

QY 38 EERFPVNTAYGRVGRVREINNEILGVVQFLGVPTATPPLGARRFOPPPAPASWPOVR 97

Db 23 QAQYEVNTNYGKINGLRTPLNEILGEVQYLGVPYASPTGRRFOPPPPSWTGIR 82

QY 98 NATTLPPACPNL-HGALPAIMLPWFMTDNLAAATYVQNOSEDCGLNLYVPTEDGFLT 156

Db 83 NTTQFAAVCPQHLDERSLLHDMLEPIWFTANLDTLMTYVQDQNECLNLYVPTEDGANT 142

QY	157	KKR-DEATLP--PDTDIRDP-GKKFVMLFLHGGSYMEGTGNMDFGSLAAYGNVIVATL	212
DB	143	KNADDTITSNDREGDSIHQNSKKFVMVYHGGSYMEGTGNMIDGSLAAYGNVIVIT	202
QY	213	NYRLGVLGFLSTGDQAAGNYGLLQIQIALRWLSNIAHFGGDPERTITFGSGAGASCVN	272
DB	203	NYRLGILGFLSTGDQAAGNYGLLQIQIALRWIEENVGAFGDPKRVITIFGSGAGASCVS	262
QY	273	LLILSHSSEGLFOKAIQAQSGTAISWSVNYQPLKVTLLAAKVGCDREDSAAEVECLRRK	332
DB	263	LLTLSHYSSEGLFOKAIQSGTALSWSAVNYQPAKVTIRLADKVCNMCLDITDMVECLRNK	322
QY	333	PSRELVDQVQPARYHIAFGPVYDGVDPDDPEILMQQGEFLNDMLIGNVQCEGLKFVE	392
DB	323	NYKELTQQITPATYHIAFGPIDGVDPDDPQILMEQGEFLNDMLIGNVQCEGLKFVD	382
QY	393	DSAESDGSVASAFDPTVSNFVNDNLGYSGEKQVNLRETIKFMYTDWADRDNGEMRRKTL	452
DB	383	GIVDNEDGVTPNDFDPSVSNFVNDNLGYSGEKQVNLRETIKFMYTDWADKENPETRRKTLV	442
QY	453	ALFTDQHWAPAVATAKLHADVCSPVYFVTFVHHCOAGREPEWADAAGDELPAVVGPM	512
DB	443	ALFTDQHWAPAVA-ADLHAQGSPTYFYAFHHQCEMKFESWADSAGHDEVPIVFGPM	501
QY	513	VGATDLFPCNFSKNDVMLSAVMTYTNFNAKTGDPNPQVQDTKFHTKPNRFEFVWMSK	572
DB	502	IGTPELFCNFSKNDVMLSAVMTYTNFNAKTGDPNPQVQDTKFHTKPNRFEFVWMSK	561
QY	573	FNSKEQYLHIGKPRVRDNYEANKVAFWLELVPHLNLHTELF---TTTTRLP-----	623
DB	562	YNPKQQLYLHIGKPRVRDHYEATKVAFWLELVPHLNLN-EIFQYVSTTKVPPPDMTS	620
QY	624	-PYATWPPRPAPAGA-PGTRRRPPPPATLPPPEPEP---GPRAYDRPGDSRDYSTELSV	678
DB	621	FPVGYR---RSPAKIWPITKRPALTPANNPKSKDPKHTGPDVTVLIEIKRDYSTELSV	677
QY	679	TVANGASLLFLNLAFAALYYKDRDRQELRCRLSPGGSGSGVPGGGLLPAAGRELPP	738
DB	678	TVANGASLLFLNLAFAALYYKKDKRRHETHRRPSPQRNTNDIAH-----IQ	725
QY	739	EEELVSLQIKR---GGGVGADPAALRAPCPDDYTLALRAAPDDVPLAPGALTLLPSG	794
DB	726	NEEIMSLQKQLEHDEHCESLQAHDTLKLTCPPDYTTLARSPPDIPMTPTITMIPMT	785
QY	795	LGPPPPPPPSLHRGFPFPPPPPTATSHNNTLPHPHSTTRV	835
DB	786	LTMQSP-----LHTNTE-----SGGQNSLNLPHGHSTTRV	816
RESULT 8			
AA	44296	AAB44296 standard; Protein; 816 AA.	
XX	AC	AAB44296;	
XX	DT	08-FEB-2001 (first entry)	
XX	DE	Human PRO701 (UNQ365) protein sequence SEQ ID NO:375.	
XX	KW	Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;	
XX	KW	expressed sequence tag; detection; cancer.	
XX	OS	Homo sapiens.	
XX	PN	WO200053756-A2.	
XX	PD	14-SEP-2000.	
XX	XX	18-FEB-2000; 2000WO-US04341.	
XX	PF	08-MAR-1999; 99WO-US05028.	
FR	12-MAR-1999;	99US-0123957.	

Query Match		60.6%; Score 2731; DB 21; Length 816;
Best Local Similarity		64.2%; Pred. No. 4.9e-188;
Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;		
QY	38	BERPVTNAYGRVGRRELNNELGVVQVFLGVYATPLGARRFPQPEAPASWPGVR 97
DB	23	QAQPVVNTNYGKIRGLRPLNEILGVQYLGVPVYASPTGERFPQPEPSSWTGIR 82
QY	98	NATLTPACPNL-HGALPATMLVWFTDNLEAAATVQNSQEDCLYLNLYVTEGGLT 156
DB	83	NTTQFAVCPQHLDERSLHLDMLPWFANLDTLMTYVQDQNECLYLNLYVTEGANT 142
QY	157	KKR-DEATLNP--PDTIRDP-GKKPVMLFHGSGYMEGTGNMDFGSLAAAYGNVATL 212
DB	143	KKNADDITSDRGDEDEIDHQNSKKPVWYHGGSYMEGTGNMDSILLASYGNVITL 202
QY	213	NYRLGVGLSTGQAAKNGYLLDQIQALRWLSENIAHFGDPERITIFSGAGASCVN 272
DB	203	NYRLGILGLSTGQAAKNGYLLDQIQALRWLSENIAHFGDPERITIFSGAGASCVS 262
QY	273	LLILSHHSEGLFOKAIQAQSGTAISSWVNYQPLKYTELLAAKVGCDREDSABAVECLRK 332
DB	263	LLTSHYSEGLFOKAIQSGTALSSWVNYQPAKYTRILADKVGCMWLTDDVCELRNK 322
QY	333	PSRELVDQVOPARYHIAFGVVDGVDDPBLMQQGEFLNYDMLIGNVQGEGLKFYE 392
DB	323	NYKELIQOTTTPATYHIAFGVIDGVIPDDPQILMQQGEFLNYDMLIGNVQGEGLKFVD 382
QY	393	DSAESEGVASAFDETVSNFVNLGYPRGKVLRETIKFMYTDNRDNGEMRKILL 452
DB	383	GIVDNEGVTPNDFSVFVNLGYPRGKVLRETIKFMYTDNRDNGEMRKILL 442
QY	453	ALFTDQHWAPAVATAKLHADYQSPVYFTFYHHCQAEGRPEWADAAGDELPPVFGVPM 512
DB	443	ALFTDQHWAPAVA-ADLHAQYGSPTVYAFYHHCQSEMKPSWADSAHGDVYVFGIEM 501
QY	513	VGATDLPCNFKNDMLSAVWYTNFPAKTGDPQVPODTPKTHTPKNRFEVVMWSK 572
DB	502	IGPTLFCNFKNDVMSAVWYTNFPAKTGDPQVPODTPKTHTPKNRFEVVMWSK 561
QY	573	FNSKEQYHLGKPRVRDNYRANKVAFWLELPHLNLHTELF-----TTTTRLP----- 623
DB	562	YNPKDQYHLGKPRVRDHYRATKVAFWLELPHLNLN-EIFQVSVTITTKVPDPDMS 620
QY	624	-PVATRWPPPPAGA-PGTRPPPPATLPPPEPPEP---GPRAYRFPDSDYDSTELSV 678
DB	621	FPYGTG---RSPAKINPTTKRPAITPANPKHSDPKHTGPDITVLITKEDYSTELSV 677
QY	679	TVAVGASLLFLNLAALYKDRQELRCRLSPGGSGVPGGGPILLPAAGRELPP 738
DB	678	TVAVGASLLFLNLAALYKDRQELRCRLSPGGSGVPGGGPILLPAAGRELPP 725
QY	739	EEELVSLQKLR-----GGVGADPAELRACPPDYTLALRRAPDDVPLAPGALLPSG 794
DB	726	NEBIMSLQKLEHDEHESLQADHLRLTCCPDYTLTLRRSPDDIPLMTPTNTIWIPT 785
QY	795	LGPPPPPPPSLHPGPPPPPTATSHNNTIHPHSTTRV 835
DB	786	LTGQMP-----LHTFNTF-----SGGQNSTNLPHGHSTTRV 816
RESULT 10		
ABU61126		
ID	ABU61126	standard; Protein; 816 AA.
XX	AC	ABU61126;
XX	DT	08-MAY-2003 (first entry)
XX	DE	Human PRO701 polypeptide.
XX	DE	Human; PRO polypeptide; secreted and transmembrane protein;
XX	KW	immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW		

KW	cardiac insufficiency; nervous system disorder; kidney disorder;
KW	bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW	genetic disorder; cytosolic; antidiabetic; antiinflammatory;
KW	antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
XX	cardiant.
OS	Homo sapiens.
XX	US2002169284-A1.
XX	14-NOV-2002.
XX	16-OCT-2001; 2001US-0978697.
XX	07-OCT-1998; 98WO-US21141.
PR	20-NOV-1998; 98WO-US24855.
PR	05-JAN-1999; 99WO-US00106.
PR	08-MAR-1999; 99WO-US05028.
PR	10-MAR-1999; 99WO-US05190.
PR	14-MAY-1999; 99WO-US10733.
PR	02-JUN-1999; 99WO-US12252.
PR	30-NOV-1999; 99WO-US28313.
PR	02-DEC-1999; 99WO-US28551.
PR	16-DEC-1999; 99WO-US28565.
PR	30-DEC-1999; 99WO-US30095.
PR	30-DEC-1999; 99WO-US31243.
PR	30-DEC-1999; 99WO-US31274.
PR	05-JAN-2000; 2000WO-US00219.
PR	06-JAN-2000; 2000WO-US00277.
PR	06-JAN-2000; 2000WO-US00376.
PR	11-FEB-2000; 2000WO-US03565.
PR	18-FEB-2000; 2000WO-US04341.
PR	24-FEB-2000; 2000WO-US05004.
PR	02-MAR-2000; 2000WO-US05841.
PR	10-MAR-2000; 2000WO-US06319.
PR	21-MAR-2000; 2000WO-US07532.
PR	30-MAR-2000; 2000WO-US08439.
PR	17-MAY-2000; 2000WO-US13705.
PR	22-MAY-2000; 2000WO-US14042.
PR	30-MAY-2000; 2000WO-US14941.
PR	02-JUN-2000; 2000WO-US15264.
PR	28-JUL-2000; 2000WO-US20710.
PR	24-AUG-2000; 2000WO-US23328.
PR	01-DEC-2000; 2000WO-US23678.
PR	28-FEB-2001; 2001WO-US06520.
PR	22-MAR-2001; 2001WO-US09552.
PR	25-MAY-2001; 2001WO-US17032.
PR	01-JUN-2001; 2001WO-US17800.
PR	20-JUN-2001; 2001WO-US19692.
PR	29-JUN-2001; 2001WO-US21066.
PR	17-OCT-1997; 97US-062250P.
PR	03-NOV-1997; 97US-064249P.
PR	13-NOV-1997; 97US-065311P.
PR	21-NOV-1997; 97US-066364P.
PR	10-MAR-1998; 98US-077450P.
PR	11-MAR-1998; 98US-077632P.
PR	11-MAR-1998; 98US-077641P.
PR	12-MAR-1998; 98US-077649P.
PR	13-MAR-1998; 98US-077791P.
PR	20-MAR-1998; 98US-078866P.
PR	20-MAR-1998; 98US-078910P.
PR	20-MAR-1998; 98US-078936P.
PR	25-MAR-1998; 98US-079294P.
PR	26-MAR-1998; 98US-079566P.
PR	27-MAR-1998; 98US-079663P.
PR	27-MAR-1998; 98US-079664P.
PR	27-MAR-1998; 98US-079689P.
PR	27-MAR-1998; 98US-079728P.
PR	27-MAR-1998; 98US-079786P.

RESULT 13	
ABG10270	
ID	ABG10270 standard; Protein; 1434 AA.
XX	
XX	
AC	ABG10270;
XX	
DT	13-FEB-2002 (first entry)
XX	
XX	
DE	Novel human diagnostic protein #10261.

Db 122 GDVDDPEILMQGEEFLNDMLGVNQGEGLKFEVDSAESEDSVSAFDTFVSNFDN 181
 QY 417 LYGYPEGKDLVRETIFKMYTWDADRDNGEMRRKTLTALFTDHWAPAVATAKLHADYQS 476
 Db 182 LYGYPEGKD-----DWADRDNGEMRRKTLTALFTDHWAPAVATAKLHADYQS 230
 QY 477 PVYFTYFHHCOAGREPWADAAGHDELPLVFGVPMVGATDLFPFCNFKNDVMSAVVMT 536
 Db 231 PVYFTYFHHCOAGREPWADAAGHDELPLVFGVPM-----NDVMSAVVMT 277
 QY 537 YWTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNSKEKOYLHGLKPRVDNYRAN 596
 Db 278 YWTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNSKEKOYLHGLKPRVDNYRAN 337
 QY 597 KVAFWLELVPHLNLHTELTFTTTRLPDYATRWPPRPPAGAPTRPPPPATLPPPEPE 656
 Db 338 KVAFWLELVPHLNLHTELTFTTTRLPDYATRWPPRPPAGAPCTTPPPATLPPPEPE 397
 QY 657 PGPRAYDRFPDGRDYSTELSVTVAVGASLLFLNLAFAALYVYKRRORLECRRLSPG 716
 Db 398 PSFRAYDRFPDGRDYSTELSVTVAVGASLLFLNLAFAALYVYKRRORLECRRLSPG 457
 QY 717 GSGGVGPG-----GGPFLPAAGRELPPPEELVS--LQKRGGGVGADPAE-----ALRPAC 765
 Db 458 GSGGVGPGRIYDARDMRRRLRELTREVEALSGCYPLAGSGSTABETSXNWWVRSITGR 517
 QY 766 PPDYTLALRAP---DDVPLALPAGALTLLPSGL 795
 Db 518 CNOY-----QSPHDAEDILLLLGLLVLVNI 546

RESULT 14

ABG10264
 ID ABG10264 standard; Protein; 726 AA.
 XX AC ABG10264;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #10255.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO2001.75067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 XX DR N-PSDB; AAS74451.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 XX PT diagnostics, forensics, gene mapping, identification of mutations
 XX PT responsible for genetic disorders or other traits and to assess
 XX PT biodiversity -
 XX PS Claim 20; SEQ ID No 40623; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 726 AA;

Query Match 38.8%; Score 1747; DB 22; Length 726;
 Best Local Similarity 57.4%; Pred. No. 3.5e-117;
 Matches 377; Conservative 27; Mismatches 105; Indels 148; Gaps 13;
 QY 171 IRDGGKXPVMLFLGGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSTGDOAAK 230
 Db 1 IRDGGKXPVMLFLGGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSTGDOAAK 60
 QY 231 GNYGLLDQIQALRWLSNIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQ 290
 Db 61 GNYGLLDQIQALRWLSNIAHFGGDPERITIFG-----QPGLSYHI 93
 QY 291 SGTAISSWVNYQLKYTRLLAAKVGCDDSDSABAVECLRRKPSRELVDQVQPA-RYHI 349
 Db 94 -----RYS-----QPGLSYHI 104
 QY 350 AFGPVVDGDDVVDPEILMQGEEFLNDMLGVNQGEGLKFEVDSAESEDSVSAFDT 409
 Db 105 AFGPVVDGDDVVDPEILMQGEEFLNDMLGVNQGEGLKFEVDSAESEDSG-----ADFT 160
 QY 410 VSNFVDNLYGYPEGKVLRETIFKMYTWDADRDNGEMRRKTLTALFTDHWAPAVATAK 469
 Db 161 VSNFVDNLYGYPEGKVLRETIFKMYTWDADRDNGEMRRKTLTALFTDHWAPAVATAK 220
 QY 470 LHADYQSPVYFTYFHHCOAGREPWADAAGHDELPLVFGVPMVGATDLFPFCNFKNDV 529
 Db 221 LHADYQSPVYFTYFHHCOAGREPWADAAGHDELPLVFGVPMVGATDLFPFCNFKNDV 280
 QY 530 LSAVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNSKEKOYLHGLKPRV 589
 Db 281 LSAVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNSKEKOYLHGLKPR 340
 QY 590 RDNVANKVAFWLELVPHLNLHTELTFTTTRLPDYATRWPPRPPAGAPTRPPPPATL 649
 Db 341 WSRFRG-----VLYQVFHDTICEKAPKSLRKQTQPPKQSSPAVHLRCTMDPVM 393
 QY 650 PPEPEPEPRAYDRFPDGRDYSTELSVTVAVGASLLFLNLAFAALYVYKRRORLECR 709
 Db 394 TVSPPP-----AHHRRRGSGPTRC 412
 QY 710 RR--LSPFGSGSGVGGPGLLPAAARELPPEELVSLQKRGGGVGADPAEALRPACPP 767
 Db 413 AHCFAWAPADTDDEKPHQYPAICSYHWDVP--EDWEGFQHTQGTWV---PWSQAPESPP 467
 QY 768 DYTLLARRAPDDVPELLAPGALTLLPSGLGPPPPPPPPPSLHPFGPPPPPPPTATSHN 824
 Db 468 Q-TIRQPTVEERPL-----KTGINSLEG-----LRAYVFPNP-PFPPSPASHKN 512

RESULT 15
 AAM93205
 ID AAM93205 standard; Protein; 509 AA.

QY	43	VVNATYGRVGRVRELNNEILG	VQVFLGVPVATPPLGARR	FOPPPAPASWPGVRATTL	102
		:: :: :: :: :: :: :: :: ::			
Db	12	IITTKNGRGINLVPFG---	GTVATFLGIPTAQPLGR	LRFKFKPOSFLKWSDIWATKY	68
QY	103	PAPCPONLHGALPAIMLP	VWFTDNLBAATYVQNS	EDCLYLMNYPTDGLTKRDEA	162
		:: :: :: :: :: :: :: :: ::			
Db	69	ANSCCNIDQSFPGFHGSEMM	NPNTDL-----	SEDCLYLNVWPIPTP-----	109
QY	163	TLNPPDTRD	PGKPKVMPLFHGGSYMEGT	TGNM--FDGSVLAAYAGNVI	VATLNYRLGVLG 220
		:: :: :: :: :: :: :: :: ::			
Db	110	-----	KPKNATVM	IWYGGFGTQSSLOVY	DGKFLTEVERVIVVMRYRGALG 159
QY	221	FLS--TGDQAAGNYGLLD	QIALRWLSENIAHFGD	PERITTFPGSGAGASCVN	LLILSHH 279
		:: :: :: :: :: :: :: :: ::			
Db	160	FLALPNPEAPNGMLFD	QDLALQWYKQNI	AAFGNGPKSVTTFG	ESAGASVSHLLSPR 219
QY	280	SEGLFOKA	LAQSGTALSSWSVN--	YOPLKYTLLAAKVGCD	REDSAEAVECLRRKPSREL 337


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Db 220 SHPLFTRALOGSSNAPWMSLHEARNRTLTAKFVGCSSTENETETIICLRNKAQEI 279
Qy 338 VDQDVQPARY-----HIAFGPVVDGVDVPPDEILMQOGEFLNYDMILGVNQSGGLKAFVED 393
Db 280 LLNEVFVVPFDSLLSNVFGPTVDGDFLTDMPDTLLQLGQLKTKQILGVNKGSTAFVLY 339
Qy 394 SAE--SEDGVSASAFDFTVSNFVNL-YGYPEGKDVLRITKPMYTDWADRNGEWRKT 450
Db 340 GAPGSKDNTSI-----ITRKEFQGLKIFFPGVSEFGKESILFHYTDWDEQRPENYREA 395
Qy 451 LLALFTDHWAVAPATAKLHADYQSPVYFYTFVHHQCAEGRPWADAAGHDELPPVFGV 510
Db 396 LDDVGVGYNFICPALETTKFESEGNNAFFYYEHRSSKLPWEMWGMVHGIEIEFVGL 455
Qy 511 PMVGATDLFCNFSKNDVMSAVVMTWTNPAKTGDPNQVPQDTKPIHTKPNRFEVVW 570
Db 456 PLERRV-----NYTKAEILRSIMKRWANFAKYNPNGTQNNSTR-----W 497
Qy 571 SKFNSKEQYHLGLK-PRVRDNYRANKVAFW-----LELVPHLNLHTELFTTTTL 622
Db 498 PVFKSTQKYLTLNTESPRYTKLRAQCQRFWTLFPFKVLEMTGNIDEAEQWAGFHRW 557
Qy 623 PPVATRW 629
Db 558 NNYMMAW 564

RESULT 2
ACHU
cholinesterase (EC 3.1.1.8) precursor [validated] - human
N/Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence revision 23-Feb-1996 #text_change 08-Dec-2000
C/Accession: A33769; A26613; A33887; A34668; A00772
R/Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
Biochemistry 29, 124-131, 1990
A/Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single co
A/Reference number: A33769; MUID:90212557; PMID:2322535
A/Accession: A33769
A/Molecule type: DNA
A/Residues: 'MSVQSNLQAGAAASCTSPKYMIFTPCKLCHCCRESEIN',1-602 <ARP>
A/Cross-references: GB:M32391; GB:J02879
R/Note: two ARG codons found upstream of Met-1 do not lie in a favorable context for tra
R/Prody, C.A.; Zevin-Sonkin, D.; Gnat, A.; Goldberg, O.; Soreg, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987
A/Title: Isolation and characterization of full-length cDNA clones coding for cholineste
A/Reference number: A26613; MUID:87231856; PMID:3035536
A/Accession: A26613
A/Molecule type: mRNA
A/Residues: 1-133,'D',135-602 <PRO>
R/McTiernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A/Title: Brain cDNA clone for human cholinesterase.
A/Reference number: A33887; MUID:88016155; PMID:3477799
A/Accession: A33887
A/Molecule type: mRNA
A/Residues: 'MSVQSNLQAGAAASCTSPKYMIFTPCKLYHCCRESEIN',1-602 <MCT>
R/Note: two ARG codons found upstream of Met-1 do not lie in a favorable context for tra
R/Nogueira, C.P.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,
Am. J. Hum. Genet. 46, 934-942, 1990
A/Title: Identification of a frameshift mutation responsible for the silent phenotype of
A/Reference number: A34668; MUID:90252779; PMID:2339692
A/Accession: A34668
A/Molecule type: DNA
A/Residues: 143-145,'VSNWNIIFTCL' <NOG>
R/Note: frameshift mutant in codon for residue 145 (Gly)
R/Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.
J. Biol. Chem. 262, 549-557, 1987
A/Title: Complete amino acid sequence of human serum cholinesterase.
A/Reference number: A00772; MUID:18710944; PMID:3542989
A/Accession: A00772
A/Molecule type: protein

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A/Residues: 29-602 <LOC>
A/Experimental source: plasma
C/Comment: Cholinesterase is present in most cells (except erythrocytes).
C/Genetics:
A/Gens: GDB:BCH; CHE1
A/Cross-references: GDB:120558; OMIM:177400
A/Map position: 3q26.1-3q26.2
A/Introns: 506/2; 562/1
C/Function:
A/Description: hydrolyzes acylcholines to choline and a carboxylic acid
A/Note: this cholinesterase is highly reactive with organophosphate esters
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F/1-28/Domain: signal sequence #status predicted <SIG>
F/29-602/Product: cholinesterase #status experimental <MAT>
F/56-556/Domain: cholinesterase homology <CH>
F/45-85/134,269,284,369,483,509,514/Binding site: carbohydrate (Asn) (covalent) #status
F/226/Active site: Ser #status experimental

Query Match 19.0%; Score 855; DB 1; Length 602;
Best Local Similarity 32.5%; Pred. No. 4e-45;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

Qy 2 WLLALCLVLGAGAQKGGGPGGAPGGLGLSLGSERPVVTATYGRVGRRELNNE 61
Db 15 WFLLLCML-----IGKSHTEDDIIITATKXKVRG-----WNL 47

Qy 62 IL-GPVVQFLGVPYATPPLGARRPQPPEAPASWPGVGNATTLPPACQNTLHGALPAIMLP 120
Db 48 VFGTVAFLGIPYAQPFLGRFLRPKQSLTKMSDIWNATKYANSCQNTDQSPGPHGS 107

Qy 121 VVETDNLAAATYVQNSQSECLVNLVPTEDGTLTKRDEATLNPDDTDIRPGKPKVM 180
Db 108 EMMNPNDL-----SEDCLLYNWIPAP-----KPKNATVL 138

Qy 181 LFLHGGSYMEGTGMN--FDGSLVLAAYGNVIVATLNYRLVGLVGLS-TGDOAAKXNGYLLD 237
Db 139 IWIYGGGFQRTSSLHVYDCKFLARVERVIVSMYRVGALGFLLALPGNPEAPGNMGLFD 198

Qy 238 QIQALRWLSENIAHFGDPERITIFGSGACASCNLLILSHHSEGLPQKAIAGSGTAISS 297
Db 199 QQLALQWQKNIAAFGNGNPKSVTLFGESAGAAVSLLHLSPGSHSLFTRAILQSGSFNAP 258

Qy 298 WSVN--YQPLKYRLLAALKVGCDDRESAEVCLRRKPSRELVDQVQPARY----HIAF 351
Db 259 WAVTSLYEARNLTNLAKLTGCSRENETHIICLRNKDQEIILNEAFVVPYCTPLSVNF 318

Qy 352 GPVVDGVDVDDPEILMQOGEFLNYDMILGVNQSGGLKAFVEDSAE--SEDGVSASAFDFT 409
Db 319 GPTVDGDFLTDMPDILLELQGFKTKQILGVNKGDEGTAFLVYGAPGFSKDNNSI----IT 374

Qy 410 VSNFVDNL-YGYPEGKDVLRITKPMYTDWADRNGEMRRKTLALLFTDHWAVAPATA 468
Db 375 RKEFQGLKIFFPGVSEFGKESILFHYTDWDDORPENREALGDVVGYNFICPALEFT 434

Qy 469 KLHADYQSPVYFYTFVHHQCAEGRPWADAAGHDELPPVFGVPMVGATDLFCNFSKNDV 528
Db 435 KKFSEGNNAFFYYEHRSSKLPWEMWGMVHGIEIEFVGLPLERRD-----NYTKASE 489

Qy 529 MLSAVVMTWTNPAKTGDPNQVPQDTKPIHTKPNRFEVWWSKNSKEQYHLGLK-P 587
Db 490 ILRSIVKRWANFAKYNPNETQNNST-----WPFVKSTQKYLTLNTEST 536

Qy 588 RVRDNYRANKVAFWLELVP 606
Db 537 RIMTKLRAQCQRFWTSFEP 555

RESULT 3
JH0314
acetylcholinesterase (EC 3.1.1.7) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999

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C:Accession: JH0811
J:Legacy, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulié, J.
J. Neurochem. 60, 337-346, 1993
A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of multi-
A:Reference number: JH0811; MUID:93107932; PMID:8417155
A:Accession: JH0811
A:Molecule type: mRNA
A:Residues: 1-614 <LEG>
A:Cross-references: GB:S50879; NID:g262092; PIDN:AAB24586.1; PID:g262093
A:Experimental source: striatum
C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic synapses.
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; neuromuscular junction; synaptic transmission
E:1-31/Domain: signal sequence #status predicted <SIG>
F:63-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>
F:63-569/Domain: cholinesterase homology <CHE>
F:100-127,288-303,440-560/Disulfide bonds: #status predicted
F:234,365,478/Active site: Ser, Glu, His #status predicted
F:296,381,495/Binding site: carbohydra (Asn) (covalent) #status predicted

Query Match 18.8%; Score 846.5; DB 2; Length 614;
Best Local Similarity 33.0%; Pred. No. 1.4e-44;
Matches 205; Conservative 98; Mismatches 235; Indels 83; Gaps 17;

Qy	31	LGGLGLEERPP---VNTAYGRVGRVARELNEILGPVQVFLGVPYATPPPLGARFQPP	87
Db	25	LGGAAREGREDDPQLLVRRVGGQLRGISLKAPG---GPVSAFLGIPFAEPVPSRRFMPP	81
Qy	88	EAPASWPGVNRATLLPPACPNQLHGALPAIMLPVWFTDNLEAAATVYQNSDCLYNLY	147
Db	82	EPRKPGSILDATTFQNVCIQVDTLYPGFEGTEWMNPNREL-----SEDCLYNVV	133
Qy	148	VPTEDGLTKRDEATLNPPTDIRDPKPKVMLFLHGSGYMEGTGNM--FDGSVLAAAY	205
Db	134	TPYP-----RPTSPFLVIWYGGGFGYSGASSLDVYDGRFLAQVE	173
Qy	206	NVIVATNLYRGLVGLFELS--TGDQAAGNYGLDDIQALRWLSENIAHFQGGDPERITFGS	264
Db	174	GTVLVSNMYRVGTGTFGLPALGSRRAPGNVGLLDQRLALQWQENIAAFGGDPMVSLTFGE	233
Qy	265	GAGACVNNLILSHHSEGLFOKAIAQSGTAISSWSV--NYQPLKTYTRLIAAKVYGC	318
Db	234	SAGAASVGMHILSPRSLSLPHRAVLQSTPGNPWATVSAGEARRRATLLARLVGCPGGA	293
Qy	319	REDSAAVECLRRKPSRELNDQD----VOPARYHTAFGPVVDGDVVPDPEILMQQGEFL	374
Db	294	GGNDTELISLURTPAQDLVDHEWHVLPQESIFRFSPVVDGDFLSDTPDALINTGDFQ	353
Qy	375	NYDMLIGVNGQEGLKVF-----EDSAESEDGVSASAFDTVSNFVDNLYGYPEGKDWLRE	429
Db	354	DLQVLGVWDXDEGSFYLVYGVPGFSKDNESLISRAQFLAGVR-----IGVPAQASDLAAE	407
Qy	430	TIKEMYTDWADRONGEMRRKTLIALFTDQHWAPAVATAKLHADYQSPYVFTFYHHQCA	489
Db	408	AVLVHYTDMLHPEDFAHLRDAMSAVVGDNHNVCPVAQLAGRLAACARVYATIFEHRAST	467
Qy	490	EGRPWADAAGDELPPYVFGVPMVGATDLFFCNFSKNDVMSAVVYTYWTFNFAKTGDPNQ	549
Db	468	LTPWLMGVPHGYEIEFIFGLPLDPS-----LNVTVBERIPAOQLMQYWTNFARTGDPND	522
Qy	550	VPQDRTKFIHTKNRFEVVVWSKNSKEKOVYHLGILKP--RYRDNYRANKVAFWLELVPHL	608
Db	523	--PRDSK-----WPPYTTAAQQVSLNLKPELVRRGLRAQTCAPWNRFLP--	568
Qy	609	HNLHTELFITTTTRLLPPPYATRW	629
Db	569	-----KLLSATDITLDEAEROW	584

RESULT 5
S70849
cholinesterase (EC 3.1.1.8) - mouse
NAlternate names: butyrylcholine esterase

Db 490 EIFSRSIMKWNAPKAYGHEN-----GTQGN---STMVPVFTSTEQKYLTLNTEK 536

Qy 587 PVRVDNVRANKVAFWLELVPHLNLHTELFPTTTTLRPPVATRW 629

Db 537 SKYSKLRAQCQFWRLLFPFKVLEMTGDDIDETEQEWKAGFHRW 579

RESULT 6

S19307

carboxylesterase (EC 3.1.1.1) precursor - pig

N:Alternate names: proline-beta-naphthylamidase

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999

C:Accession: S19307; S23607

R:Matsumura, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Takahashi; FEBS Lett. 293, 37-41, 1991

A:Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-carboxylesterase

A:Reference number: S19307; MUID:92070571; PMID:1959668

A:Accession: S19307

A:Molecule type: mRNA

A:Residues: 1-566 <MAT1>

A:Cross-references: EMBL:X63323; NID:G1930; PIDN:CAA44929.1; PID:G1931

A:Accession: S23607

A:Molecule type: protein

A:Residues: 19-40 <MAT2>

A:Note: 28-Lys and 33-Leu were also found

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-566/Product: carboxylesterase #status experimental <MAT>

F:51-552/Domain: cholinesterase homology <CHE>

F:80/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:222,467/Active site: Ser, His #status predicted

Query Match 18.6%; Score 836.5; DB 2; Length 566;

Best Local Similarity 32.7%; Pred. No. 5.1e-44;

Matches 206; Conservative 100; Mismatches 219; Indels 105; Gaps 18;

Qy 1 MWLLALCLVGLAGQGGGPGGAPGGGLGSLGERFPVNTAYGRVGRVRELNN 60

Db 1 MWLLPLVLTSLSS-----ATWAGQPASP-----PVDTAQGRVLGKYVLEG 43

Qy 61 EILGPVVQFLGVPYATPPGARRFQPEAPASWPVGRNATLPPACPNLHGLPALI-M 118

Db 44 -LAQPVAVELGVFPFAPKPLGLSLRFAPPQPAEPWFSVKNTSYPPMCCQD-----PVVEQM 97

Qy 119 LPWFVFTDNLAAATYYQNSECLYINLVPTEDGPLTKKRDEATLNPDTDIRPGKKP 178

Db 98 TSDLFTNGKERLT-----EPSECLYINIVTPAD-----LTKR-----GRUP 135

Qy 179 VMLFLHGGSYMEGTGMFPGSVLAAYGNIVATNLNRYLVGLFSTGDOAAKNGYGLLDQ 238

Db 136 VMVVIHGGGLVGLGAPMYDGVVLAAHNVVVVAIQYRLGINGFFSTGDEHSRGNWGLDQ 195

Qy 239 IQALRWLSENIAHFQGDPRITIFSGGAGASCWNLLIISHSEGLFQKAIAGSTAISSW 298

Db 196 VAALHWQENIAFNGDGPQSVITIFGSEGGESVSLVLSPLAKNLFHRAISSGVALTVA 255

Qy 299 SVNYPQLKYLTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVQ-----PARY 347

Db 256 LVKDKMAAKAQIADVLAGCKTTTSVAVFVHCLRKSEDELLDLTKMKFLTLDPHGDQRES 315

Qy 348 HIAFGVVDGVVDPPDPEILMQCGEFLNVDMLIGVNGQE-----GLKPFVDSASSE 398

Db 316 HPFLPTVVDGVLLPKMPEILAEKDFTVPTVYGVINKQEFQWLLPTMMGFPLSEGLDQK 375

Qy 399 DGVSAASAFDFTVSNFDVNLGYPEGKQVLRETIKMYTDMADRDNGEMERKTLALFTDH 458

Db 376 TATSLLWKSYPINPEEL--TPVATD-----KYL-----GGTDDPVKKQLFLDMGDV 423

Qy 459 QWVAPAVATAKLHADYQSPVYFTFYHH--COAEGRPWEADAAGDELFPYVFGVPMVGTAT 516

Db 424 VFGVSVTVARQHRDAGAPTYWYFYQRPFSFSSDKKPKTVIGDHGDEIFSVFEGFLKKG- 482

RESULT 8

S13586

triacylglycerol lipase (EC 3.1.1.3) precursor, bile salt-activated - human

N:Alternate names: bile salt-stimulated lipase; carboxyl ester lipase; lipoamidase; panc

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 18-Jun-1999

C:Accession: S13586; S34490; S12983; S34489; A37916; A42864; S13917; A31520; S32

R:Nilsson, J.; Blackberg, L.; Carlsson, P.; Enerbaeck, S.; Hernell, O.; Bjursell, G.

Eur. J. Biochem. 192, 543-550, 1990

A:Title: cDNA cloning of human-milk bile-salt-stimulated lipase and evidence for its id

A:Reference number: S13586; MUID:91006144; PMID:1698625

A:Accession: S13586

A:Molecule type: mRNA

A:Residues: 1-745 <NII>

A:Cross-references: EMBL:X54457; NID:g29500; PIDN:CAA38325.1; PID:g29501

A:Accession: S34490

A:Molecule type: protein

A:Residues: 55-63;361-378;387-403;436-446 <NI2>

R:Hui, D.Y.; Kissel, J.A.

FEBS Lett. 276, 131-134, 1990

A:Title: Sequence identity between human pancreatic cholesterol esterase and bile salt

A:Reference number: S12983; MUID:91092399; PMID:2265692

A:Accession: S12983

A:Molecule type: mRNA

A:Residues: 1-745 <HUI>

A:Cross-references: EMBL:M85201

R:Hui, D.Y.; Kissel, J.A.

submitted to the EMBL Data Library, February 1992

A:Description: Molecular cloning and tentative identification of the catalytic triad of l

A:Reference number: S34489

A:Accession: S34489

A:Molecule type: mRNA

A:Residues: 1-715; 'CAPRVTLRLCPQMPTRKRLCQIGFSPV' <HU2>

A:Cross-references: EMBL:M85201; NID:g180481; PIDN:AAA52014.1; PID:g180482

R:Baba, T.; Downs, D.; Jackson, K.W.; Tang, J.; Wang, C.S.

Biochemistry 30, 500-510, 1991

A:Title: Structure of human milk bile salt activated lipase.

A:Reference number: A37916; MUID:91105134; PMID:1998041

A:Accession: A37916

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 4-745 <BAB>

A:Cross-references: GB:M54994; GB:J05301; NID:g187149; PIDN:AAA63211.1; PID:g187150

A:Note: it is uncertain whether Met-1 or Met-4 is the initiator

R:Lidberg, U.; Nilsson, J.; Stromberg, K.; Stenman, G.; Sahlin, P.; Enerback, S.; Bjurse

Genomics 13, 630-640, 1992

A:Title: Genomic organization, sequence analysis, and chromosomal localization of the hu

A:Reference number: A42824; MUID:92347858; PMID:1639390

A:Accession: A42824

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 433-498 <LID>

A:Cross-references: GB:M34579

A:Note: the authors translated the codon TAC for residue 7 as Thr

R:Kumar, B.V.; Aleman-Gomez, J.A.; Colwell, N.; Lopez-Candales, A.; Bosner, M.S.; Spilbu

Biochemistry 31, 6077-6081, 1992

A:Title: Structure of the human pancreatic cholesterol esterase gene.

A:Reference number: A42864; MUID:92329425; PMID:1627550

A:Accession: A42864

A:Molecule type: DNA

A:Residues: 458-485 <KUM>

A:Cross-references: GB:S40178; NID:g251572; PIDN:AAB22537.1; PID:g251573

A:Experimental source: pWE 15, PTCF

A:Note: sequence extracted from NCBI backbone (NCBIN:109184, NCBIp:109185)

R:Christie, D.L.; Cleverly, D.R.; O'Connor, C.J.

FEBS Lett. 278, 190-194, 1991

A:Title: Human milk bile-salt stimulated lipase. Sequence similarity with rat lysophosph

A:Reference number: S13917; MUID:91122282; PMID:1991511

A:Accession: S13917

A>Status: preliminary

A:Molecule type: protein

A;Residues: 24-40,135-170;278-286,'V',288-294,'L',296;305-340;534-543 <CHR>
 R;Wang, C.S.
 Biochem. Biophys. Res. Commun. 155, 950-955, 1988
 A;Title: Purification of carboxyl ester lipase from human pancreas and the amino acid se
 A;Reference number: A31520; MUID:88339990; PMID:3421974
 A;Accession: A31520
 A;Molecule type: protein
 A;Residues: 24-33 <WAN>
 R;Hui, D.Y.; Hayakawa, K.; Oizumi, J.
 Biochem. J. 291, 65-69, 1993
 A;Title: Lipomerase activity in normal and mutagenized pancreatic cholesterol esterase
 A;Reference number: S32318; MUID:93228634; PMID:8471055
 A;Accession: S32318
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 54,'X',56-75;77-79;359-377 <HUS>
 R;Roudani, S.; Miralles, F.; Margotat, A.; Escoribano, M.J.; Lombardo, D.
 Biochim. Biophys. Acta 1264, 141-150, 1995
 A;Title: Bile salt-dependent lipase transcripts in human fetal tissues.
 A;Reference number: S59907; MUID:96038831; PMID:7578248
 A;Accession: S59907
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 26-729 <ROU>
 R;Loomes, K.M.
 Eur. J. Biochem. 230, 607-613, 1995
 A;Title: Structural organisation of human bile-salt-activated lipase probed by limited F
 A;Reference number: S65641; MUID:95331299; PMID:7607235
 A;Accession: S65641
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 24-30;31-32;109-110;456-459;545-552 <LOO>
 C;Genetics:
 A;Gene: GDB:CEL
 A;Cross-references: GDB:127527; OMIM:114840
 A;Map position: 9q34.3-9q34.3
 C;Superfamily: cholinesterase, cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; glycoprotein
 F;1-23/Domain: (or 4-23) signal sequence #status predicted <SIG>
 F;24-745/Product: triacylglycerol lipase, bile salt-activated #status predicted <MAT>
 F;53-536/Domain: cholinesterase homology <CHE>
 F;210/Binding site: carbohydrate (Aen) (covalent) #status predicted
 F;217,456/Active site: Ser, His #status predicted

Query Match 18.4%; Score 828.5; DB 2; Length 745;
 Best Local Similarity 30.6%; Pred. No. 2.3e-43;
 Matches 253; Conservative 98; Mismatches 288; Indels 187; Gaps 34;

QY 44 VNTAYGRVGRVRELNNILGPVQV-FUGVYATPPLGARRFQPEAPASWPGVNRATTL 102
 DB 29 VYTEGGFVEGVNKKLG--LLGDSVDIFKGIFFAAP---TKALENPQHPGQGTAKRNF 83
 QY 103 PPACQNLHGLPATMLPFWFTDNLAAATVQNS---EDCLYINLYVPTDGLTKKR 159
 DB 84 KRCLQ-----ATITQDSTYGDDECLYNIWVP--QGRKQVSR 119
 QY 160 DEATLNPPDITDRPGKPMFLHGGSYMEGTN-----MFDGSVLAAGNVIVAT 211
 DB 120 D-----LPFWIYGGAFLLHGGSGHGANFNLLNYDGEETATGNVIWT 163
 QY 212 LNYRLGLGFTSTGDAQAKNGYLLDQTQALRWLSENIAHFGDPERTITFGSAGASCV 271
 DB 164 FNYRVGLGFLSTGDANLPNGYLRDQHMALAWKRNIAAFGDPNNITLFGSAGASV 223
 QY 272 NLLTILSHSEGLFQKATAQSTALSSVSNVQPKYTRLLAAKVGCDREDSABECLRR 331
 DB 224 SLQTLSPNKGILIRALSSQSVALSPVIOKNPLFWAKKVAEKVCGCPVGDAARMAQCLKV 283
 QY 332 KPSREL-----VDQVQVARYHIAFGPVVDGWDVDDPEILMQCGEFLNYDMLIGVQ 384
 DB 284 TDPRALTAYKVPAGLEYPMLHYGVFPVIDGDFIADPILNYANADIDY--IAGTNN 341
 QY 385 GEGLEK--VEDSAESEDGVSASADF--TVSNF--VDNLYGPEGKDVLRETIKFYTDW 438

Db 342 MDGHIFASIDWPAINKGNKKVTEEDFYKLVSSEFTITKGLGAKTTFDVTYES-----W 394
 QY 439 ADRDNGEMRKTLLALFTDQWAPA-VATAKLHAYQS-PVYFYFHHQAGREPEWA 496
 Db 395 AQDPSQNKKTIVVDFDLVFLVPTTEIALAQHRNAKSAKTYAYLFSHPSRMPVYPKW 454
 QY 497 DAAGDELPIYVFGVPMVGATDLFPFCNFKNDVMSAVVMTYTNFAKTGDN---QVVPQ 553
 Db 455 GADHADDIQVFGKPF--AI---PTGVRPODRIVSKAMIAWTNFAKTGDPNMGDSAVPT 509
 QY 554 DTKEIHTKPNRFVWVSKNSKEKYLHIGLK---PRVDNVRANKVAFWELVPHLHN 610
 Db 510 H-----WEPYTTENSGYLEITKMGSSMKRSLRTNFLRYW--TLTYL-A 551
 QY 611 LHTELEFTTTRLPPYA-TRWPPRPAGAGQTRRRPPPPATLPPPEPEPGPRAVDRPGDS 669
 Db 552 LPTVTQEAFTVPTGDSATVPVPTGDSATVPVPTGSGAPVPP-----TGDS 602
 QY 670 RDISTELSVTVAGASLLFLNLAFAALYYKRRDRQELRCRLSPGSGSGVPGGGLL 729
 Db 603 -----GAPPV-----PPTGD-SGAP---PVP 619
 QY 730 PAAARELPPBEELVSLQKKGAGVADPAELARPACPDYTLALRRAPDDVLLARQALT 789
 Db 620 PTGDSGAPP-----VPTGDSGAPPV-----PPTGDSG---APVVPPTGDSGAPP 661
 QY 790 LLPSG-LGPPPPPP-----PPSLHPFGPPPPPPPTATSHNNTLPHP. 829
 Db 662 VPPTGDAGPPVPVPTGDSGAPPVPTGDSGAPPVPTGDSATVP 707

RESULT 9
 A39256
 acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
 C;Species: Homo sapiens (man)
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1999
 C;Accession: A39256; S03959
 R;Soreg, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Ghatt, A.; Neville, L.; Lieman-Hurw
 Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
 A;Title: Molecular cloning and construction of the coding region for human acetylcholine
 A;Reference number: A39256; MUID:91088577; PMID:2263619
 A;Accession: A39256
 A;Molecule type: mRNA; DNA
 A;Residues: 1-614 <SOR>
 A;Cross-references: GB:M55040; NID:g177974; PIDN:AAA68151.1; PID:g177975
 A;Note: this sequence represents composite of clones including clone ABGACHE from adult
 ice should represent an authentic brain splice form
 R;Chhajlani, V.; Derr, D.; Earles, B.; Schwell, E.; August, T.
 FEBS Lett. 247, 279-282, 1989
 A;Title: Purification and partial amino acid sequence analysis of human erythrocyte acet
 A;Reference number: S03959; MUID:89232136; PMID:2714437
 A;Accession: S03959
 A;Molecule type: protein
 A;Residues: 256-266,'Y',268-273;306-308,'X',310-313,'X',315-316,'D',318-323,'D',325-326;
 Y,532-551 <CH>
 A;Experimental source: erythrocytes
 A;Note: this form was a disulfide-linked homodimer
 C;Genetics:
 A;Gene: GDB:ACHE; YT
 A;Cross-references: GDB:118746; OMIM:100740
 A;Map position: 7q22-7q22
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphatidy
 F;63-569/Domain: cholinesterase homology <CHE>

Query Match 18.4%; Score 827.5; DB 2; Length 614;
 Best Local Similarity 32.2%; Pred. No. 2.1e-43;
 Matches 201; Conservative 96; Mismatches 238; Indels 89; Gaps 16;

QY 30 GLGLSGLEERFPVNTAY-GRVGRRELNNILGPVQVFLGVYATPPLGARRFOPPE 88
 Db 26 GGVGAEGREDAELLIVRGRLGRLKTPG---GPVSAFLGIPFAEPMPRRFLPPE 82

QY 89 APASWPGVNRATLPPACPNLHGAFAIMLPVWFTDNLEAAATVYQVQSEDCLYLNLYV 148
 Db 83 PKQPSGVVADATTFQSCYQVDTLYPQFEGTEMNENREL-----SEDCLYLNWVT 134
 QY 149 PTEGSLTKKDEATLPPDTRDPCKPVMFLHGGSGWEGTGM--PDGSLVLAAYGN 206
 Db 135 PYP-----RPTSPFVLMYGGFGYSGASSLDVYDGRFLVQAER 174
 QY 207 VIVATLNYRLGVGLFS--TGDAAGNKGGLDQALRWLSNIAHFGGDPERITIFGSG 265
 Db 175 TVLVSMYRVGAFGLALPGSREAPGNVGLDQRLALQWCVNVAAGDPTSVTLFGES 234
 QY 266 AGASCYNLLILSHSEGLFOKATAQSTALSSSV--NYQPLKYTRLAAKVC-----DR 319
 Db 235 AGAASVGNHLLSPSRGLFRAVLQSGAPNGPWTVMGGEARRATQLAHLVCGPFGGTG 294
 QY 320 EDSAEAVECLRRKPSRELVPDQ-----VQPARYHIAFGPVVDGVDVDDPEILMQQGEFLN 375
 Db 295 GNDPFLVACLTTRPAQVLVNHWHVLPQESVFRFSFVVDGDFLSDTTEALINAGDFHG 354
 QY 376 YDMLIGNVQEGGLKVFEDSA-----ESEDGVSASAFDFTVSNFVNDLYGYPEGKQVLR 430
 Db 355 LQVLGVGVKDEGSYFLYAGPFGSKNESLISRAEFLAGVR-----VGVPQVSDLAEEA 408
 QY 431 IKFMYTDWADRDNGEMERKTLALFTDQWVAPAVATAKLHADYQSPVYFYTFYHHQAE 490
 Db 409 VVLYHTDNLHPEDPARLEALSDVGDHNVVCPVAQLAGLAAQARVYAYVEHRASTL 468
 QY 491 GRPEWADAAGDELPPYVGVPMVGTDLFPNCFSKNDVMSAVVMTYTNFAKTGDPNQP 550
 Db 469 SWPLMGMVPHGYEIEFIFGIPDPSP-----NVTAEKIFAQRLMYANFARTGDPNEP 523
 QY 551 ----VPQDTXFIHTKPNRFEVVMVSKFENKEXYLIHGLKPRVRYNRYANKVAFWLELV 605
 Db 524 RDKAPQ-----WPFYTAGAQYVSLDLEPLEVRRLGLRAQAQAFWNRFL 567
 QY 606 PHLNLHTELTFTTTLRPPVATRW 629
 Db 568 P-----KLSATDNLDEAERQM 584

RESULT 10
 A55281
 N;Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 18-Jun-1999
 C;Accession: A55281
 R;Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.;
 Genomics 11, 956-967, 1991
 A;Title: Characterization and functional expression of a cDNA encoding egasyn (esterase-
 A;Reference number: A55281; MUID:92147141; PMID:1783403
 A;Accession: A55281
 A;Status: preliminary
 A;Molecule type: mRNA; protein
 A;Residues: 1-562 <OVN>
 A;Cross-references: GB:S80191; NID:9244727; PIDN:AAB21335.1; PID:9244728
 A;Note: sequence extracted from NCBI backbone (NCBI:80191, NCBIP:80194)
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum
 F;51-552/Domain: cholinesterase homology <CHE>
 F;222,467/Active site: Ser, His #status predicted

Query Match 18.3%; Score 823.5; DB 2; Length 562;
 Best Local Similarity 33.8%; Pred. No. 3,2e-43;
 Matches 220; Conservative 102; Mismatches 204; Indels 125; Gaps 25;

QY 1 MWLLALCLVGLAQRGGGPGGAPGGLGLSLGIBERRFPVNTAYGRVGRVRELNN 60
 Db 1 MCLSALILVSLAFTAGAGHP--SSP-----PMWDTQGVKGLKYSISLEG 43
 QY 61 EILGPVQVGLGVYATPPLGARRFPPEAPASWPGVNRATLPPACPN-LHGALPAIML 119

Db 44 -PTQPVAVFLGVPPAKPIGLSLRFAPPQPAEPWSSVKATSPYPCFQDPTVQIWNLL 102
 QY 120 -----PWFTDNLEAAATVYQVQSEDCLYLNLYVPTEDGSLTKKDEATLPPDTR 172
 Db 103 TWRKSKILQF-----SEDCLYNIYTPAD-----LTKS----- 131
 QY 173 DPGKPFVLMFLHGGSGWEGTGMFDSGLAAYGNVIVATLNYRLGVGLFSLTGDAAGN 232
 Db 132 ----DRLPVMVWHGGGLVGLGASTYDGLVLSHENVVVVIOYRLGIWGFSTGDSHSGN 189
 QY 233 YGLLDIQALRWLSNIAHFGGDPERITIFGSGAGASCYNLLILSHSEGLFOKATAQSG 292
 Db 190 MHLDOVAALHWHVQDNIAKFGDPSVTIFGESAGGESVSLVLSPLAKNLFQRAISSG 249
 QY 293 TAISGSVNYQPLKYTRLAAKV-----CCDREDSAEAVECLRRKPSRELVPDQVQ----- 343
 Db 250 VALTAGLVK-----XNTRPLAEKIAVISCKNTTGAAMVHCLQRKTEBELTGTTLKINLFK 305
 QY 344 -----PARYHIAFGP-VVDGVDVDDPEILMQQGEFLNLYGVNQGE-----GLKXFV 391
 Db 306 LDHLGDSRSQHPFVPTVLDGVLLPKMPEEILAEKNFTVPVIVGINKQEGFWILPTMNY 365
 QY 392 EDSASEDGVGSASAFDFTVSNFVNDLYGYPEGKQVLRITI-KFMYTDWADRDNGEMRRKT 450
 Db 366 PPSVDKLDQMTAMSL-LKSSFLNL-----PS--DAIAVAIEKYL-----RDKDYTGRNKDQ 415
 QY 451 LLALFTDQWVAPAVATAKLHADYQSPVYFYTFYH--HCOAEGRPWADAAGHDELPPVF 508
 Db 416 LLELIGDVVGVPSVIVSRGHRDAGATYMYEFQYSPFSSEMKPDTVVGDPHGBEIVSVF 475
 QY 509 GVPVY-GATDLFPNCFKNDVMSAVVMTYTNFAKTGDPN-QVPQDTXFIHTKPNRFE 566
 Db 476 GAPILRGST-----SEETINLSKMMKFWANFARNGNPNQGLPH----- 515
 QY 567 EVMWAKNSKEKQYLIHGLKPRVDRDNYRANKVAFWLELV--PHLNLHTEL 615
 Db 516 ---WPEYDQKE-GYLOIGATTQQAQKLEKEVAFWTELLAKQLPTEHTEL 562

RESULT 11
 JC2447
 carboxylesterase (EC 3.1.1.1) ES-3 precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
 C;Accession: JC2447; S23462
 R;Robbi, M.; Beaufay, H.
 Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994
 A;Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (EGASYN).
 A;Reference number: JC2447; MUID:95032008; PMID:7945287
 A;Accession: JC2447
 A;Molecule type: mRNA
 A;Residues: 1-561 <ROB>
 A;Cross-references: GB:X81395; NID:G550146; PIDN:CAA57158.1; PID:G550147
 A;Experimental source: liver
 R;Medda, S.; Proia, R.L.
 Eur. J. Biochem. 206, 801-806, 1992
 A;Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting ti
 A;Reference number: S23460; MUID:92299008; PMID:1606962
 A;Accession: S23462
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 503-554, 'R', 556-561 <MED>
 A;Cross-references: EMBL:X65295; NID:G57557; PIDN:CAA46390.1; PID:G57558
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; glycoprotein
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-561/Product: carboxylesterase ES-3 #status predicted <NAT>
 F;50-551/Domain: cholinesterase homology <CHE>
 F;79,107,489/Binding site: carbonyl site: Ser, His #status predicted
 F;221,466/Active site: Ser, His #status predicted

Query Match 18.2%; Score 819; DB 2; Length 561;

QY 241 ALRWLSNIAHFGDDBRITIFSGAGASCNVNLLSHSEGLFQKAIQSGTAISSWSV 300
 Db 197 ALRWQDNIAHFGDDBRITIFSGAGASCNVNLLSHSEGLFQKAIQSGTAISSWSV 256
 QY 301 NYQPLK-YRLLAAKVCDDREDAEVECLRRKPSRELVDQ-----DVG--PARVH 348
 Db 257 KGDVRFPLAQIAITAGCKTTTSAVHVHCLQRKTEELLETUMLKFLSLDQDDPRESQ 316
 QY 349 IAPGPVVDGVDVPPDEILMQOGEFLNYDMLGVNQEGELKFVEDSAESDGVSAFDF 408
 Db 317 PLLGTWIDGMLLTKTEELQAERNFHTVPVWVGINQOE-----FGW 357
 QY 409 TVSNFVDNLYGYP--SG-----KDVLR-TIKMYTDWDRDNG 444
 Db 358 LIPM---QLMSYPLSGQLDQKTMALLKWSYPLVCIKELIPEATEKYL-----GTDDET 410
 QY 445 EMRKLTLLALFTDHWQVAPAVATAKLHADYQSVYFYTFYHH--COAGRPWADAAGHD 502
 Db 411 VKKKDLFLDLIADVGVGPSVIVARNHRDAGAFYMYEFQYRPSFSSDKPKTVIGDGD 470
 QY 503 ELPVYGVPMV--GATDLFPCNKSNDVMSAVVMTYTNPAKTGDPN--QPVQDTKFTH 559
 Db 471 ELPSVFGAPFLKEGA-----SEEEILSKMKWKFANFARNGNPNNGEGLPH----- 516
 QY 560 TKEPREEVWVSKFNSEKQYHLHGLKPRVDRNYRANKVAFWLEL 604
 Db 517 -----WPEYNQKE-GYLIQIGANTQAQKLDKEVAFWNL 550

RESULT 13

A34967
 N;Alternate names: bile salt-stimulated lipase; carboxyl ester lipase; cholesterol ester
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Mar-1991 #sequence, revision 22-Apr-1995 #text_change 13-Aug-1999
 C;Accession: A34967; A26603; A39595; S33476
 R;Kissel, J.A.; Fontaine, R.N.; Turk, C.W.; Brockman, H.L.; Hui, D.Y.
 Biochim. Biophys. Acta 1006, 227-236, 1989
 A;Title: Molecular cloning and expression of cDNA for rat pancreatic cholesterol esterase
 A;Reference number: A34967; UID:90089378; PMID:2688744
 A;Accession: A34967
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-512, 'T', 514-612 <KIS>
 A;Cross-references: GB:X16054; NID:G55942; PIDN:CAA34189.1; PID:G55943
 R;Han, J.H.; Stratowa, C.; Rutter, W.J.
 Biochemistry 26, 1617-1625, 1987
 A;Title: Isolation of full-length putative rat lysophospholipase cDNA using improved met
 A;Reference number: A26603; UID:87242339; PMID:3593682
 A;Accession: A26603
 A;Molecule type: mRNA
 A;Residues: 1-25, 'L', 27-216, 'G', 218, 'I', 220-612 <HAN>
 A;Experimental source: pancreas
 A;Note: this enzyme was tentatively identified as a lysophospholipase (EC 3.1.1.5)
 R;Fontaine, R.N.; Carter, C.P.; Hui, D.Y.
 Biochemistry 30, 7008-7014, 1991
 A;Title: Structure of the rat pancreatic cholesterol esterase gene.
 A;Reference number: A39595; UID:91299758; PMID:2069957
 A;Accession: A39595
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-418, 'T', 420-575, 'VV', 578-607, 'VA', 610, 'A', 612 <FON>
 A;Cross-references: GB:M69157; NID:G203457; PIDN:AA846376.1; PID:G203458
 R;Chen, X.; Harrison, E.H.; Fisher, E.A.
 submitted to the EMBL Data Library, May 1993
 A;Reference number: S33476
 A;Accession: S33476
 A;Molecule type: mRNA
 A;Residues: 21-120, 'I', 122-388, 'CA', 391-575, 'VV', 578-607, 'VA', 610-612 <CHEN>
 A;Cross-references: EMBL:222803; NID:G311385; PIDN:CAA80460.1; PID:G311386
 C;Genetics:
 A;Introns: 22/3; 73/1; 114/1; 180/1; 223/3; 259/3; 298/3; 362/3; 429/2; 495/2

C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase
 F;51-582/Domain: cholinesterase homology <CH>

Query Match 18.1%; Score 817; DB 2; Length 612;
 Best Local Similarity 32.4%; Pred. No. 9.1e-43;
 Matches 217; Conservative 94; Mismatches 226; Indels 133; Gaps 24;
 QY 44 VNTAYGRVGRVRELLNNEILG--PVVOFLGVVPYATPPLGARRFQPPAPASWPGVRVATT 101
 Db 26 VYTEGGFVGVNKKLS--LLGGDSVDIFKGIPTAT-----AKTLENPQHPQMGQTLKATD 79
 QY 102 LPPACPQNLHCAIPALMLPVWFTDNLEAAATYVQNS---EDCLYLNLYPTEDGPTTKK 158
 Db 80 FKKECLQ-----ATITODDTYQGEDCLYLNWVP----- 108
 QY 159 RDEATLNPPTDIRDPGKK-----PVWFLHGGSYMEGTGN-----MFDGSLVLAAY 204
 Db 109 -----QGRKQVSHDLFVWVLYGAFMGSGQGAFNLKVLNYDGEETATR 153
 QY 205 GNVIVATLNTVLGVFLSTGDAQAKNGYGLLDIOALRWLSNIAHFGDDBRITIFSG 264
 Db 154 GNVIVVTFNRYGVGLSTGDANLPGNFGLRDQEMAIAWAKRNIAAFGGDPDNITIFGE 213
 QY 265 GAGASCYNLLILSHSSEGLFQKAIQSGTAISSWSVYQPKYKTELLAAKVGCDREDAE 324
 Db 214 SAGAAVSLSQLTSYPNKLIRRAISQGVALSFAIOENFLFWAKTIKKVGCPTEDTAK 273
 QY 325 AVECLREKPSREL-----VDQVQVARYHIAFGPVVDGVVDVPPDEILMQOGEFLNYD 377
 Db 274 MAGCKITDPRALTAYRLPLKQSEYPIVHYLAFIPVWDGDFIPDDPINLYDNAADIDY- 332
 QY 378 MLGVNQEGELKFVEDSAESDGVSAFDTVSNFVDNLYGPEKDVRETIKF-MYT 436
 Db 333 -LAGINDMDGHLFATVDVPAIDRAKQ---DVTBEDFRLVSGHTVAKGLGTQATFDIYT 388
 QY 437 D-WADRDNGEMRRKTLALFTDHWVAP---AVATAKLHADYQSVYFYTFYHHQAEGR 492
 Db 389 ESWAQDSQENMKKTVAFTDILFLIPTEMALAQHRAHAK-SAKTYSYLFSHPSRMPIY 447
 QY 493 PEWADAAGDELPIVGVPMVGATDILPCNFSKNDVMSAVVMTYTNPAKTGDP---NQ 549
 Db 448 PKWMGADHADLQYVFGKPF--AT---PLGYRAQDRTVSKAMIAWTNFAKSGDPNMNGNS 502
 QY 550 PVPQDTKFIHTKPNRPEEVWVSKFNSEKQYHLHGLK---PRVDNRYRANKVAFW---LE 603
 Db 503 PVPTH-----WYPTWENGNYLDINKITSTSMKEHLREKFLKFPWATFE 547
 QY 604 LVPHLHNLTELTFTTTLRPPYATRWPPRPAGAGCTRRPPPP-----ATLPPPEPEPEP 657
 Db 548 MLPTVVGDHTP-----PEDDSEAAFPVPTD-DSCGGGVPTDSDQTTPVPPTDNSQA 598
 QY 658 GPRAYDRFRG 667
 Db 599 GDSVEAQMPG 608

RESULT 14

ACRYE
 N;Alternate names: acetylcholinesterase, asymmetric form
 C;Species: Torpedo californica (Pacific electric ray)
 C;Date: 17-Mar-1987 #sequence, revision 08-Nov-1996 #text_change 15-Sep-2000
 C;Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677
 R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F
 Nature 319, 407-409, 1986
 A;Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its c
 A;Reference number: A00773; UID:86118676; PMID:3753747
 A;Accession: A00773
 A;Molecule type: mRNA
 A;Residues: 'NS', 11-596 <SCH>
 A;Cross-references: GB:X03439; NID:G64389
 A;Experimental source: electric organ

F;51-551/Domain: cholinesterase homology <CHE>
F;80,478,554/Binding site: carbonylrate (Asn) (covalent) #status predicted
F;88-115,275-286,423-542/disulfide bonds: #status experimental
F;105/Binding site: substrate (Trp) #status experimental
F;221/Active site: Ser #status experimental
F;348,461/Active site: Glu, His #status predicted
F;437/Binding site: carbonylate (Asn) (covalent) #status experimental
F;593/Disulfide bonds: interchain #status experimental

Query Match 18.0%; Score 813; DB 1; Length 596;
Best Local Similarity 32.5%; Pred.No.1.5e-42;
Matches 198; Conservative 94; Mismatches 238; Indels 80; Gaps 16;

QY 43 VNTAYGRVGRVERELNELILGPVQVGLGVPATPLGARQQPPAPASWPQVRNATIL 102
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
28 LVNTXSGRWGTRPV---LSHISAFIGIPPAEPPVGNNRFRPBPKPQWGVWNASTY 84
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 103 PPACQNHLHALPALMPLVMFTDNLEAAATYYQNQSECLYLNLXYPTEDGTLTKRDEA 162
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:-MSDECLYNLWVSP----- 125
QY 163 TLNPDPDITDRDGKPKVMLFLHGGSWMEG--TGNMPDGSVLAAAGNVIVATLNLYRLGVLG 220
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
126 -----RPKSTVMWIYGGFGYSGSSLDVNGKYLATBEWLVSLSYRVGAFF 175
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 221 FLST-GDOAKNGNYGLLDIOALRWLSENIAHFEGDPERITFGSAGASCYNLLIISHH 279
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
176 FLAHGSGEQAPGNVGLLDQRMALQWHDNIQFFCGDKPTVIIFGESAGASVGMHLSFG 235
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 280 SEGFLQKAIAQSATAISSW-SVNYOPLKYTRL-LAAKYGCDDREDSABAVECLRPPSRBL 337
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
236 SRDLFRRAILOSGSPNCPSWASVAEGRRRAVELGRNLNCLNSDEELIHCRKKPQL 295
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 338 VDQD-VQF---ARYHIAFGPVVDGVDVDPDEILLMQCEFLNDMLIGNQCEGLKFV-- 391
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
296 IDVENVLFPDSIRPFSSFVPVIDGEFFPTSLEMLNSNFKKTQILLGVNKDEGSFFLIY 355
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 392 ---EDSASESGCVGASAFDTFVSNPDVNLGYPEGKVLRETIKPMYTDAWRDNGEMRR 448
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
356 GAPOFSKDSESKI SREDPFMSGVKLSV-----PHANDLGLDAVTILQYTDWMDNNGIKNR 409
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 449 KTLALFTDHQWAPAVATAKLHADYQSVFYTFYHHCAQAGEPRPEWADAAGDELPLYVF 508
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
410 DGLDDIIVGDHNVICPLMHFNKTYKFGNGTYLYFHNHRASNLVWFPMGWVGHYEIEFVP 469
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 509 GVPVWGATDLPPCNFSKNDMVLSAVMTYTNFAKTGDPNQVPQODTKFIHTKPNRFBEV 568
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
470 GLPILVK-----ELNVTAEAEALSRIHYMATFAKTGNPNEPHSQESK----- 512
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 569 VWSKFSNKEOYLHGIKLP-RVRDNYRNANKVAFWLELVPHLNHLTELF-----TTT 619
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
513 -WPLFTTKQKFIDINTEPMKHORLVRQMVCVFWNQFLPKLNA-TETIDAEAROMKTEF 570
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 620 TRLPPPYATR 629
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
571 HRWSSYNMW 580
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

RESULT 15
S48724
Acetylcholinesterase - rabbit
Species: Oryctolagus cuniculus (domestic rabbit)
Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
Accession: S48724
J Biol Chem. 225, 115-124, 1994
Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbits.
Reference number: S48724; PMID:95010096; PMID:7925428

C;Keywords: glycoprotein

F;32-539/Domain: Cholinesterase homology <CHE>

Query Match	18.0%;	Score 811.5;	DB 2;	Length 584;
Best Local Similarity	32.3%;	Pred. No. 1.9e-42;		
Matches 196;	Conservative 91;	Mismatches 239;	Indels 81;	Gaps 15;

QY	43	VNTAYGRVAGRVARELNNEILGEVQVFLGVVPATPPLGARRFPQPEAPASWPGVRNATTL	102
Db	9	LVTVRGRLGLRLKAPG--GPVSAPFLGIPPEPPVGPRRFLPPPKRPWAGVLDATAF	65
QY	103	PPACPNLHGALPAIMLPWFTNTLEAATYVQNSQEDCLYNLYVPTEDGGLTKKRDAA	162
Db	66	QSVCYQVDTLYFGFEGTEMNPNREL-----SEDCLYLNVTTPY-----	106
QY	163	TLNPPDTDIRDPKGVMLFLHGGSYMEGTGNM---FDGSVLAAYGNVIVATLNYRLGVL	219
Db	107	-----RPTSPTPVLVIYGGFVSGASSLDVYGRFLVQAGTFLVAMHNYRVGAF	157
QY	220	GFLS-TGDAQAKNGYGLLDOIQALRWLSENIAHFGDPERITIFSGAGASCVNLLILSH	278
Db	158	GFTCLFSGREAPGNVGLDQRLALQWQENVAFAFGGDPASVTLFGESAGASVGLHLISP	217
QY	279	HSEGLFOKATAQSGTAISSNS-----VNYOPLKYTRLAAKVGCDREDSAEAVECLARK	332
Db	218	PSRGLFHRAVLQSGAPNGPWATVGVGEARRRATLLARLVVCPGAGGNDTELVACLRTR	277
QY	333	PSRELVDQD---VQARYHIAFGPVVDGVDVDPDPEILMQQGEFLNYDMLIGVNQGEGL	388
Db	278	PAQDLVDHEWRVLPQSSIFRFSFVPVVDGDFLSDTPEALINAGDFQGLQVLGVVVKDEGT	337
QY	389	KFVEDSA-----ESEDGVSASAFDFTVSNFVNLYGYPEGKDVLRETIKFMYTDDWADRDN	443
Db	338	YFLVYGAPGFSKNESFISRAQLAGVR-----VGVPOASDLAAEAVVLHYTDLWHPED	391
QY	444	GEMRKTLTALFTDQWVAPAVATAKLHADYQSPVYFTFYHHCOAEGREPWADAAGHDE	503
Db	392	PARLRDALSDVVGDNHNVCPVAQLAGRLAAQAGARVAVYVFEHRASTLSWPLMWGVPHGYE	451
QY	504	LPYVFGVPMVGATDLFFCNFSKNDVMSAVWVTWNTNFAKTGDPNQPVQDTKFIHTKPN	563
Db	452	IEFIFGLPLEPS-----LNYTEERIFAQRLMYANFARTGDPNE--PRDAK---APQ	500
QY	564	RPEEVVWSKFSKGYLHGLKP-RVRDNYRANKVAFWLELVPHLNLHLEFTTTTL	622
Db	501	-----WPPYTAGAQVYSLNLRPLEVRRLRAQACAFWNRFLP-----KLLSATDTL	547
QY	623	PPYATRW	629
Db	548	DEAERQW	554

Search completed: February 13, 2004, 13:14:15
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 13, 2004, 13:13:42 ; Search time 39 Seconds
(without alignments)
4482.928 Million cell updates/sec

Title: US-09-934-323-2

Perfect score: 4508

Sequence: 1 MWLLALCLVGLAGAQGGGG.....PPATSHNTLPHPHSTTRV 835

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	4508	100.0	835	10	US-09-934-323-2
2	4415.5	97.9	836	10	US-09-934-323-5
3	4075.5	90.4	801	12	US-10-274-694-12
4	2986	66.2	550	10	US-09-934-323-6
5	2746	60.9	848	10	US-09-875-353-5
6	2731	60.6	816	10	US-09-978-295A-375
7	2731	60.6	816	10	US-09-978-697-375
8	2731	60.6	816	10	US-09-978-192A-375
9	2731	60.6	816	10	US-09-999-832A-375
10	2731	60.6	816	11	US-09-978-189-375
11	2731	60.6	816	11	US-09-978-608A-375
12	2731	60.6	816	11	US-09-978-585A-375
13	2731	60.6	816	11	US-09-978-191A-375
14	2731	60.6	816	11	US-09-978-403A-375
15	2731	60.6	816	11	US-09-978-564A-375

16	2731	60.6	816	11	US-09-999-833A-375	Sequence 375, App
17	2731	60.6	816	11	US-09-981-915A-375	Sequence 375, App
18	2731	60.6	816	11	US-09-978-824-375	Sequence 375, App
19	2731	60.6	816	11	US-09-918-585A-375	Sequence 375, App
20	2731	60.6	816	11	US-09-978-423A-375	Sequence 375, App
21	2731	60.6	816	11	US-09-978-193A-375	Sequence 375, App
22	2731	60.6	816	11	US-09-999-830A-375	Sequence 375, App
23	2731	60.6	816	11	US-09-978-757A-375	Sequence 375, App
24	2731	60.6	816	11	US-09-978-187B-375	Sequence 375, App
25	2731	60.6	816	11	US-09-978-643A-375	Sequence 375, App
26	2731	60.6	816	12	US-09-978-375A-375	Sequence 375, App
27	2731	60.6	816	12	US-09-978-188A-375	Sequence 375, App
28	2731	60.6	816	12	US-09-978-298A-375	Sequence 375, App
29	2731	60.6	816	12	US-10-143-031A-375	Sequence 375, App
30	2731	60.6	816	12	US-10-002-967A-375	Sequence 375, App
31	2731	60.6	816	12	US-10-017-083A-375	Sequence 375, App
32	2731	60.6	816	12	US-10-143-030A-375	Sequence 375, App
33	2731	60.6	816	12	US-10-145-128A-375	Sequence 375, App
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35	2731	60.6	816	12	US-10-143-028A-375	Sequence 375, App
36	2731	60.6	816	12	US-10-143-029A-375	Sequence 375, App
37	2731	60.6	816	12	US-10-145-089A-375	Sequence 375, App
38	2731	60.6	816	12	US-10-013-926A-375	Sequence 375, App
39	2731	60.6	816	12	US-10-145-017A-375	Sequence 375, App
40	2731	60.6	816	12	US-10-164-728A-375	Sequence 375, App
41	2731	60.6	816	12	US-10-165-067A-375	Sequence 375, App
42	2731	60.6	816	12	US-10-145-124A-375	Sequence 375, App
43	2731	60.6	816	12	US-10-160-502A-375	Sequence 375, App
44	2731	60.6	816	12	US-10-165-247A-375	Sequence 375, App
45	2731	60.6	816	12	US-09-978-194A-375	Sequence 375, App

ALIGNMENTS

RESULT 1
US-09-934-323-2
; Sequence 2, Application US/09934323
; Patent No. US20020150910A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-081001
; CURRENT APPLICATION NUMBER: US/09/934,323
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,774
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 835
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-323-2

Query Match	100.0%	Score 4508;	DB 10;	Length 835;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches	835;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
0;				
QY	1	MWLLALCLVGLAGAQGGGGPGGAPGGPGLGSLGSEPFVNTAYGRVGRVRELN	60	
Db	1	MWLLALCLVGLAGAQGGGGPGGAPGGPGLGSLGSEPFVNTAYGRVGRVRELN	60	
QY	61	ETLGPVQFLGVPYATPPLGARRFQPEAPASWPGVRNATLPPACPNLHGALPAIMLP	120	
Db	61	ETLGPVQFLGVPYATPPLGARRFQPEAPASWPGVRNATLPPACPNLHGALPAIMLP	120	
QY	121	VNFTONLEAAATYVQNSDCILYLNLYPTDGPITKKRDEATLNPPDTDIRDPCKKPM	180	
Db	121	VNFTONLEAAATYVQNSDCILYLNLYPTDGPITKKRDEATLNPPDTDIRDPCKKPM	180	
QY	181	LFHGGSYMEGTGNMGDSVLAAYGNVIVATLNYLGVLFGLSTGDQAAGKNYGLLDQIQ	240	

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181 LFLHGSYMEGTGNMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAGNYGLDQIQ 240
241 ALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQAQSGTAISSWSV 300
241 ALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQAQSGTAISSWSV 300
301 NYOPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDDV 360
301 NYOPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDDV 360
361 PDDPEILMOQGEFLNYDMLIGVNOQEGLEKFEVDSAESEDSGVSASAFDFTVSNFVNDLYGY 420
361 PDDPEILMOQGEFLNYDMLIGVNOQEGLEKFEVDSAESEDSGVSASAFDFTVSNFVNDLYGY 420
421 PEGKOVLRITIKFMTYTDWADRDNGEMRRKTLIALFTDQHWAPAVATAKLHADYQSPVYF 480
421 PEGKOVLRITIKFMTYTDWADRDNGEMRRKTLIALFTDQHWAPAVATAKLHADYQSPVYF 480
481 YTFYHHCQAEGRPEWADAAGDELPLYVGVPMVGATDLPCNFSKNDVMSAVVMTYWTN 540
481 YTFYHHCQAEGRPEWADAAGDELPLYVGVPMVGATDLPCNFSKNDVMSAVVMTYWTN 540
541 FAKTGDNPQVPQDQTKFIHTKPNRFEVVMKFSKSKQYLIHGLKPRVDRNYRANKVAF 600
541 FAKTGDNPQVPQDQTKFIHTKPNRFEVVMKFSKSKQYLIHGLKPRVDRNYRANKVAF 600
601 WLELVPHLNHLTELFITTTTLPPYATRWPPRPPAGAGTTRPPPPATLPPPEPEPGPR 660
601 WLELVPHLNHLTELFITTTTLPPYATRWPPRPPAGAGTTRPPPPATLPPPEPEPGPR 660
661 AYDRFPGDSRDYSTELSVTVAVGASLLFNILAFALYKEDRQELRCRLSPPGSGS 720
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781 PLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPTATSHNNTLPHPHSTTRV 835
781 PLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPTATSHNNTLPHPHSTTRV 835

RESULT 2
US-09-934-323-5
; Sequence 5, Application US/09934323
; Patent No. US20020150910A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
; FILE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-081001
; CURRENT APPLICATION NUMBER: US/09/934,323
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,774
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-934-323-5

Query Match 97.9%; Score 4415.5; DB 10; Length 836;
Best Local Similarity 98.3%; Pred. No. 4.2e-312;
Matches 822; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 1 MWLLALCLVGLAGAQRGCGGPGGAPGGPGGLGSLGEERFPVYNTAYGRVGRRELNN 60
Db 1 MWLLALCLVGLAGAQRGCGGPGGAPGGPGGLGSLGEERFPVYNTAYGRVGRRELNN 60

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RESULT 3

US-10-274-694-12

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; Sequence 12, Application US/10274694
; Publication NO. US20030143589A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BRUNS, Christopher M.
; APPLICANT: DAS, Debopriya
; APPLICANT: DING, Li
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: KHAN, Farrah A.
; APPLICANT: LAL, Preeti G.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: LU, Yan
; APPLICANT: NGUYEN, Damiel B.
; APPLICANT: PATTERSON, Chandra S.

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QY 61 EILGPVVQFLGVYATPPLGARRFQPEAPASWPVGRNATTLPPACFQNLHGALPAIMLP 120
Db 61 EILGPVVQFLGVYATPPLGARRFQPEAPASWPVGRNATTLPPACFQNLHGALPAIMLP 120
QY 121 WFTDNLAAATVQNSSEDCIYLNLYVPTDGLTKKDEATLNPDDTDIDPGKKPYM 180
Db 121 WFTDNLAAATVQNSSEDCIYLNLYVPTDGLTKKDEATLNPDDTDIDPGKKPYM 180
QY 181 LFLHGSYMEGTGNMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAGNYGLDQIQ 240
Db 181 LFLHGSYMEGTGNMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAGNYGLDQIQ 240
QY 241 ALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQAQSGTAISSWSV 300
Db 241 ALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQAQSGTAISSWSV 300
QY 301 NYOPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDDV 360
Db 301 NYOPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDDV 360
QY 361 PDDPEILMOQGEFLNYDMLIGVNOQEGLEKFEVDSAESEDSGVSASAFDFTVSNFVNDLYGY 420
Db 361 PDDPEILMOQGEFLNYDMLIGVNOQEGLEKFEVDSAESEDSGVSASAFDFTVSNFVNDLYGY 420
QY 421 PEGKOVLRITIKFMTYTDWADRDNGEMRRKTLIALFTDQHWAPAVATAKLHADYQSPVYF 480
Db 421 PEGKOVLRITIKFMTYTDWADRDNGEMRRKTLIALFTDQHWAPAVATAKLHADYQSPVYF 480
QY 481 YTFYHHCQAEGRPEWADAAGDELPLYVGVPMVGATDLPCNFSKNDVMSAVVMTYWTN 540
Db 481 YTFYHHCQAEGRPEWADAAGDELPLYVGVPMVGATDLPCNFSKNDVMSAVVMTYWTN 540
QY 541 FAKTGDNPQVPQDQTKFIHTKPNRFEVVMKFSKSKQYLIHGLKPRVDRNYRANKVAF 600
Db 541 FAKTGDNPQVPQDQTKFIHTKPNRFEVVMKFSKSKQYLIHGLKPRVDRNYRANKVAF 600
QY 601 WLELVPHLNHLTELFITTTTLPPYATRWPPRPPA-GAPGTRRRPPPPATLPPPEPEPGPR 659
Db 601 WLELVPHLNHLTELFITTTTLPPYATRWPPRPPGTSRPPPPATLPPESDIDLGP 660
QY 660 RAYDRFPGDSRDYSTELSVTVAVGASLLFNILAFALYKEDRQELRCRLSPPGSGS 719
Db 661 RAYDRFPGDSRDYSTELSVTVAVGASLLFNILAFALYKEDRQELRCRLSPPGSGS 720
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Db 721 SGVPGGGPIILPAAGRELPEEBELVSLQKRGGVGADPAEALRPACPPDYTLALRAPDD 780
QY 780 VPLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPTATSHNNTLPHPHSTTRV 835
Db 781 VPLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPTATSHNNTLPHPHSTTRV 836

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; APPLICANT: RANKUMAR, Jayalaxmi
 ; APPLICANT: RING, Huijun Z.
 ; APPLICANT: SANJANWALA, Madhusudan M.
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: THANGAVELU, Kavitha
 ; APPLICANT: THORNTON, Michael B.
 ; APPLICANT: TRIBOULEY, Catherine M.
 ; APPLICANT: WALLIA, Narinder K.
 ; APPLICANT: XU, Yuming
 ; APPLICANT: YANG, Junming
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: YUE, Henry
 ; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
 ; FILE REFERENCE: PI-0151 USA
 ; CURRENT APPLICATION NUMBER: US/10/274,694
 ; CURRENT FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: 60/221,837
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: 60/220,037
 ; PRIOR FILING DATE: 2000-07-21
 ; PRIOR APPLICATION NUMBER: 60/218,948
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US01/21324
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: 60/216,804
 ; PRIOR FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 12
 ; LENGTH: 801
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030143589A1 7473875CD1
 US-10-274-694-12

Query Match 90.4%; Score 4075.5; DB 12; Length 801;
 Best Local Similarity 95.1%; Pred. No. 2e-287;
 Matches 770; Conservative 3; Mismatches 18; Indels 19; Gaps 3;

QY 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGEBRFPVNTAYGRVGRRELN 60
 DB 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGEBRFPVNTAYGRVGRRELN 60
 QY 61 EILGPVVQFLGVPYATPPLGARRFQPPAPASPGVGRNATLLPACPNLHGALPAILP 120
 DB 61 EILGPVVQFLGVPYATPPLGARRFQPPAPASPGVGRNATLLPACPNLHGALPAILP 120
 QY 121 VFTDNLAAATVQNSDCLYLNLYVPTDGLTKKREATLNPPTDIRDPGKPFV 180
 DB 121 VFTDNLAAATVQNSDCLYLNLYVPTDGLTKKREATLNPPTDIRDPGKPFV 180
 QY 181 LFLHGGSYNEGTMNFDGSLAAYGNVIVATLNYRLVGLSTGDAAGNYGLDQIQ 240
 DB 181 LFLHGGSYNEGTMNFDGSLAAYGNVIVATLNYRLVGLSTGDAAGNYGLDQIQ 240
 QY 241 ALRWLSENIAHFGDGPERRITIFGSGAGASCVNLLILSHSEGLFQKAIQSGTALSSWSV 300
 DB 241 ALRWLSENIAHFGDGPERRITIFGSGAGASCVNLLILSHSEGLFQKAIQSGTALSSWSV 300
 QY 301 NTQPLKYITLAAKVCDBEDSABEVECLRRKPSRELVDQVQPARYHIAFGPVVDGVDV 360
 DB 301 NTQPLKYITLAAKVCDBEDSABEVECLRRKPSRELVDQVQPARYHIAFGPVVDGVDV 360
 QY 361 PDDPEILMQQGEFLNYDMLIGNVQEGELKFVEDSAESDGSASAFDFTVSNFVDNLYGY 420
 DB 361 PDDPEILMQQGEFLNYDMLIGNVQEGELKFVEDSAESDGSASAFDFTVSNFVDNLYGY 420
 QY 421 PGKQVLRBTIKFMYTWDNRDNGEMRRKTLIALFTDHWAPAVATAKLHADYQSPVYF 480
 DB 421 PGKQVLRBTIKFMYTWDNRDNGEMRRKTLIALFTDHWAPAVATAKLHADYQSPVYF 480

QY 481 YTFYHHCQAEGRPEWADAAGHDELPPYVGVPMVGATDLFPCNFSKNDVMSAVVMTYWTN 540
 DB 481 YTFYHHCQAEGRPEWADAAGHDELPPYVGVPMVGATDLFPCNFSKNDVMSAVVMTYWTN 540
 QY 541 FAKTGDPNQVPQDTKFTHTKPNRFEVWWSKFNKSKQYLIHGLKPRVRNYRANKVAF 600
 DB 541 FAKTGDPNQVPQDTKFTHTKPNRFEVWWSKFNKSKQYLIHGLKPRVRNYRANKVAF 600
 QY 601 WLELVPHLNLHTELFTTTTLPPYATRWPPRPAGAPGTRPPPPATLPEPEPEPGPR 660
 DB 601 WLELVPHLNLHTELFTTTTLPPYATRWPPRPAGAPGTRPPPPATLPEPEPEPGPR 660
 QY 661 AYDRPGDSRDYSTELSVTVAVGASLLFLNLTAALYYKDRRQELRCRLSPGSGS 720
 DB 661 AYDRPGDSRDYSTELSVTVAVGASLLFLNLTAALYYKDRRQELRCRLSPGSGS 720
 QY 721 GVPGGPPLLPAAGRELPEBELVSLQKRGGVGADPAEALRPACPDYTLALRAPDDV 780
 DB 721 GVPGGPPLLPAAGRELPEBELVSLQKRGGVGADPAEALRPACPDYTLALRAPDDV 780
 QY 781 PLLAPGALTLLPSGLGPPPPPPPSLHPFG 810
 DB 776 -----LSSLGPDQRP-----HPWG 791
 RESULT 4
 US-09-934-323-6
 ; Sequence 6, Application US/09934323
 ; Patent No. US20020150910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Rory A. J.
 ; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
 ; FILE OF INVENTION: FAMILY MEMBER AND USES THEREOF
 ; FILE REFERENCE: 10448-081001
 ; CURRENT APPLICATION NUMBER: US/09/934,323
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: US 60/226,774
 ; PRIOR FILING DATE: 2000-08-21
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-934-323-6
 Query Match 66.2%; Score 2986; DB 10; Length 550;
 Best Local Similarity 100.0%; Pred. No. 1.8e-208;
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 286 KATAQSGTALSSSVNYQPLKYITLAAKVCDBEDSABEVECLRRKPSRELVDQVQPA 345
 DB 1 KATAQSGTALSSSVNYQPLKYITLAAKVCDBEDSABEVECLRRKPSRELVDQVQPA 60
 QY 346 RYHIAFGPVVDGVDVDDPEILMQQGEFLNYDMLIGNVQEGELKFVEDSAESDGSAS 405
 DB 61 RYHIAFGPVVDGVDVDDPEILMQQGEFLNYDMLIGNVQEGELKFVEDSAESDGSAS 120
 QY 406 FDTVSNFVDNLYGYEGKQVLRBTIKFMYTWDNRDNGEMRRKTLIALFTDHWAPAV 465
 DB 121 FDTVSNFVDNLYGYEGKQVLRBTIKFMYTWDNRDNGEMRRKTLIALFTDHWAPAV 180
 QY 466 ATAKLHADYQSPVYFVYHHCQAEGRPEWADAAGHDELPPYVGVPMVGATDLFPCNFSK 525
 DB 181 ATAKLHADYQSPVYFVYHHCQAEGRPEWADAAGHDELPPYVGVPMVGATDLFPCNFSK 240
 QY 526 NDVMSAVVMTYWTNTAKTGDNPQVPQDTKFTHTKPNRFEVWWSKFNKSKQYLIHGL 585
 DB 241 NDVMSAVVMTYWTNTAKTGDNPQVPQDTKFTHTKPNRFEVWWSKFNKSKQYLIHGL 300
 QY 586 KPRVRNYRANKVAFWLELVPHLNLHTELFTTTTLPPYATRWPPRPAGAPGTRPPPP 645
 DB 301 KPRVRNYRANKVAFWLELVPHLNLHTELFTTTTLPPYATRWPPRPAGAPGTRPPPP 360

QY 646 PATLPPEPEPPRAYDRPQDSRDYSTELSVTVAVGASLLFLNLAFALYYKDRRQ 705
Db 361 PATLPPEPEPPRAYDRPQDSRDYSTELSVTVAVGASLLFLNLAFALYYKDRRQ 420
QY 706 ELRCRLSPGGSGVPGGGPLPAAGRELPEBELVSLQKRGGVGADPAEALRAC 765
Db 421 ELRCRLSPGGSGVPGGGPLPAAGRELPEBELVSLQKRGGVGADPAEALRAC 480
QY 766 PPDYTLALRRADDVLLAPGALTLLPSGLPPPPPPPSLHPGFPFPPPTATSHNT 825
Db 481 PPDYTLALRRADDVLLAPGALTLLPSGLPPPPPPPSLHPGFPFPPPTATSHNT 540
QY 826 LPHPHSTTRV 835
Db 541 LPHPHSTTRV 550

RESULT 5
US-09-875-353-5
; Sequence 5, Application US/09875353
; Patent No. US20020168713A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 46980, A NOVEL HUMAN NEUROLOGIN FAMILY
; FILE REFERENCE: 10448-058001
; CURRENT APPLICATION NUMBER: US/09/875,353
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/209,949
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-875-353-5

Query Match 60.9%; Score 2746; DB 10; Length 848;
Best Local Similarity 61.1%; Pred. No. 8.7e-191;
Matches 538; Conservative 101; Mismatches 138; Indels 104; Gaps 18;

QY 1 MWLLALCLVGLAGARGGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRRLN 60
Db 26 LWFSLVL--RSTQ-----APA-----PTVTHFGKLGARVELPS 60
QY 61 ELIGPVQFLGVYATPPLGARRFOPPEAPASWPGVRNATLPPACPNLHGALPAIMP 120
Db 61 ELIGPVQFLGVYATPPLGARRFOPPEAPASWPGVRNATLPPACPNLHGALPAIMP 120
QY 121 VFTNLEAATYVQNSDECLYNLYVPTD-----GPLTKRD 160
Db 121 VFTNLEAATYVQNSDECLYNLYVPTD-----GPLTKRD 160
QY 161 EATLN---PPDTIDPCKKPMFLHGGSYMEGTGNMFGSVLAAGNIVATLNRLG 217
Db 161 EATLN---PPDTIDPCKKPMFLHGGSYMEGTGNMFGSVLAAGNIVATLNRLG 217
QY 218 VLGLSTGDAQAGNYGLDQIALRWLSENIAHFGGDPERITIFGSGAGASCNVLILS 277
Db 241 VLGLSTGDAQAGNYGLDQIALRWLSENIAHFGGDPERITIFGSGAGASCNVLILS 300
QY 278 HHSEGLFQKATQSTALSSWSVNYQPKYTRLLAAKVGCDREDSABVCLARKPSREL 337
Db 301 HHSEGLFQKATQSTALSSWSVNYQPKYTRLLAAKVGCDREDSABVCLARKPSREL 360
QY 338 VQDQVQARYHAFQPVVDGWDPPDPEILMQOGEFLNYDMLGVNOGEGKFFVEDSAES 397
Db 361 VQDQVQARYHAFQPVVDGWDPPDPEILMQOGEFLNYDMLGVNOGEGKFFVEDSAES 420
QY 398 EDGVSASAFDTVSNFVNDLYGYEGKDTLRETIKFMYTDWADRDNGEMRRKTLALFTD 457
Db 457 EDGVSASAFDTVSNFVNDLYGYEGKDTLRETIKFMYTDWADRDNGEMRRKTLALFTD 457

Db 421 EDGVSAGTDFDYSVSNFVNDLYGYEGKDTLRETIKFMYTDWADRDNGEMRRKTLALFTD 480
QY 458 HQWYAPAVATKLAHAYQSPVYFTFYHCOAGSRPEWADAAGDELPHYVGVPMYGATD 517
Db 481 HQWYAPAVATKLAHAYQSPVYFTFYHCOAGSRPEWADAAGDELPHYVGVPMYGATD 540
QY 518 LFCNFSKNDVMSAVVMTYTNFAKTGDDNQVQDPTKFIHTKPNRFEVVMWSKFNSE 577
Db 541 LFCNFSKNDVMSAVVMTYTNFAKTGDDNQVQDPTKFIHTKPNRFEVVMWSKFNSE 600
QY 578 KOYLHIGLKPRVDNTRANKVAFWLSEIVLHNLHTELF---TTTTLPP---YATRW 630
Db 601 KOYLHIGLKPRVDNTRANKVAFWLSEIVLHNLHTELF---TTTTLPP---YATRW 630
QY 631 PRPPAGAPGTRPPPPATLPPPEPEPPGPRAYDRFFGDS-----RDYSTELSVTV 680
Db 660 PRPPAGAPGTRPPPPATLPPPEPEPPGPRAYDRFFGDS-----RDYSTELSVTV 712
QY 681 AVGASLLFLNLAFALYYKDRQBLRCRLSPGGSGVPGGGPLPAAGRELPEE 740
Db 713 AVGASLLFLNLAFALYYKDRQBLRCRLSPGGSGVPGGGPLPAAGRELPEE 761
QY 741 ELVSLQKRGGV-----GADPAEALRACPPDYTLALRRAPDDVLLAPGALTLLPSGL 795
Db 762 ELAALQL---GPTHHECEAGPPHDTLRLTALPDYTLILRSPODDIPLMTNITMIPNSL 818
QY 796 GPPPPPPPSLHPGFPFPPPTATSHNT-LPHPHSTTRV 835
Db 819 GPPPPPPPSLHPGFPFPPPTATSHNT-LPHPHSTTRV 848

RESULT 6

US-09-978-295A-375
; Sequence 375, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Askenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249

[illegible]

1 PRIOR FILING DATE: 1998-05-15
2 PRIOR APPLICATION NUMBER: 60/085700
3 PRIOR FILING DATE: 1998-05-15
4 PRIOR APPLICATION NUMBER: 60/085689
5 PRIOR FILING DATE: 1998-05-15
6 PRIOR APPLICATION NUMBER: 60/085579
7 PRIOR FILING DATE: 1998-05-15
8 PRIOR APPLICATION NUMBER: 60/085580
9 PRIOR FILING DATE: 1998-05-15
10 PRIOR APPLICATION NUMBER: 60/085573
11 PRIOR FILING DATE: 1998-05-15
12 PRIOR APPLICATION NUMBER: 60/085704
13 PRIOR FILING DATE: 1998-05-15
14 PRIOR APPLICATION NUMBER: 60/085697

Query Match		60.6%;	Score 2731;	DB 10;	Length 816;
Best Local Similarity		64.2%;	Pred. No. 1e-189;		
Matches 527;		Conservative 97;	Mismatches 147;	Indels 50;	Gaps 15;
QY	38	BERFPVNTAYGRVGRVRELNNELGVPVQFLGVPYATPPLGARRFOPPEAPASWPCVR	97		
DB	23	QAQYVWNTYKIRGLRTPLENEILGPVEQVIGVPIASPTGERFQPPPPSWTIGIR	82		
QY	98	NATTLPPACPNL-HGALPAIMLPVWFTNLEAAATVYQNSDECLYLNLYVPTDGLPT	156		
DB	83	NTTQFAVCPCHLDRSLHDMLEPIWFTANLDTLMTVYQDQNEDECLYLNLYVPTDGLPT	142		
QY	157	KGR-DEATINP--PDTDIRDP-GKKPVMLFEGGSYMEGTGMPFDSVLAAYGNVIVATL	212		
DB	143	KQADITISNRGEDEDLHDQNSKPKVMVYIHGGSYMEGTGMDGSLASYNVIVITI	202		
QY	213	NYRLVGLSTGDOAAKNGYGLLDQIQALRWLSENIAHFGDGPDRITIFGSGAGASCVN	272		
DB	203	NYRLGILGLSTGDOAAKNGYGLLDQIQALRWLSENIAHFGDGPDRITIFGSGAGASCVS	262		
QY	273	LLILSHHSEGLFOKAIASGTASISWSVNYQPLKTYRLLAAKVGCDREDSABAVECLRRK	332		
DB	263	LTLSHYSEGFLQKAIOSGTALSSWANYQPKYTRILADKVCNMLDITDMVECLRNK	322		
QY	333	PSREIVDDQVOPARYHIAFGVPVGDVDDPPEILMOQGEFLNYDMLIGVNOGEGKLFVE	392		
DB	323	NYKELIQTITPATVHIAFGVIGDVIIPDDPQILMEGGEFLNYDMLIGVNOGEGKLFVD	382		
QY	393	DSASEDGVASADFTVTSNFDVNLGYPEGKQVLRITIKPMYTDWADRNGEMRRKTL	452		
DB	383	GIVNEDGVTFNDFSVSNFDVNLGYPEGKQVLRITIKPMYTDWADRNGEMRRKTLV	442		
QY	453	ALFTDHWVAPAVATAKLHAYQSPVYVYTYHHCQAGRPWADAAHGDLPYVFGVPM	512		
DB	443	ALFTDHWVAPAVA-ADLHAYQSGFTYFYHHCQSEMKSADSAHGDVFPYVFGIPM	501		
QY	513	VGATDLPCNFNSKNDVMSAVMTYTWNFAKTGDPNQVPQDTKFIHTKPNRPEEVVWSK	572		
DB	502	IGTPELFCNFSKNDVMSAVMTYTWNFAKTGDPNQVPQDTKFIHTKPNRPEEVVWSK	561		
QY	573	FNSKEQVHLHGLKPRVDNVRANKYAFWELVPHLNLHTELF-TTTTTRLP-----	623		
DB	562	YNPKQQLYHLHGLKPRVDNVRANKYAFWELVPHLNLHTELF-TTTPPPPPPPPPPP	620		
QY	624	PYATRWPPPPPPAGA-PQTRPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	678		
DB	621	PPYQTR--RSPAKIWTTPKEPATIPANNPKHSDPKHTGPBETTVLIEKRYISTELSV	677		
QY	679	TVAVGASLLFLNLAFAALYKRRDRRLCRRLSPGGSGSGVPGGGLPPLAAGRELPP	738		
DB	678	TVAVGASLLFLNLAFAALYKRRDRRLCRRLSPGGSGSGVPGGGLPPLAAGRELPP	725		
QY	739	BEELVSLQKLR---GGGVADPAEARPACPDYTLALRRAPDDVPLLAGALTLLPSG	794		
DB	726	NEETMSLQKLEHDEHCELSQADHTLRLTCPPDYTLRLRRSPDDIPLMTPTNTIMPNT	785		
QY	795	LGPPPPPPPPSLHFGFPFPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	835		

Db 786 LTCMQP-----LHTPNTF-----SGQONSTNLPHGHSSTRV 816

RESULT 7
US-09-978-697-375
Sequence 375, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/064249
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2	PRIOR FILING DATE: 1998-04-29
3	PRIOR APPLICATION NUMBER: 60/083496
4	PRIOR FILING DATE: 1998-04-29
5	PRIOR APPLICATION NUMBER: 60/083499
6	PRIOR FILING DATE: 1998-04-29
7	PRIOR APPLICATION NUMBER: 60/083545
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25	PRIOR APPLICATION NUMBER: 60/084637
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27	PRIOR APPLICATION NUMBER: 60/084639
28	PRIOR FILING DATE: 1998-05-07
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30	PRIOR FILING DATE: 1998-05-07
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44	PRIOR FILING DATE: 1998-05-13
45	PRIOR APPLICATION NUMBER: 60/085582
46	PRIOR FILING DATE: 1998-05-15
47	PRIOR APPLICATION NUMBER: 60/085700
48	PRIOR FILING DATE: 1998-05-15
49	PRIOR APPLICATION NUMBER: 60/085689
50	PRIOR FILING DATE: 1998-05-15
51	PRIOR APPLICATION NUMBER: 60/085579
52	PRIOR FILING DATE: 1998-05-15
53	PRIOR APPLICATION NUMBER: 60/085580
54	PRIOR FILING DATE: 1998-05-15
55	PRIOR APPLICATION NUMBER: 60/085573
56	PRIOR FILING DATE: 1998-05-15
57	PRIOR APPLICATION NUMBER: 60/085704
58	PRIOR FILING DATE: 1998-05-15
59	PRIOR APPLICATION NUMBER: 60/085697

Query Match	60.6%;	Score 2731;	DB 10;	Length 816;
Best Local Similarity	64.2%;	Pred. No. 1e-189;		
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:	: :	
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Db	23 QAQPVVNNTKGRNGRLPTLENIILGFVQYLGVPVASPTGERRFPPEPPSWGTGR	82
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QY	98 NATTLPPACPQL-HGALPAIMLVWTTDLNLAATAVVOQSDDCYLNLIVPTEDGPIT	156
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:	: :	
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Db	83 NTPQAAYCPOHLDERSLIHDMLPIWTANLDLTIMTVVQQNEDDCYLNIIVPTEDGANT	142
:	: :	
:	: :	
QY	157 KKR-DEATLPN--PDTOIRDP-GKKPVMLFLHGGSVMYGEGTGNMFDGSLAAAGNVIAVL	212

Db 143 KKNADITSDNRGDEBHDQNSKPPWVYHGSYMEGTGMDSDSILASYGNVIVII 202
Qy 213 NYRLGVLGFLSTGDOAAKNGYLLDQIALRWLSENIAHFGDPERITIPSGAGASCYN 272
Db 203 NYRLGVLGFLSTGDOAAKNGYLLDQIALRWLSENIAHFGDPERITIPSGAGASCYN 262
Qy 273 LLLSHSHSEGLFQKAIASQGTATSSSVNYQPLKYLRLAAYKVCGRDPSABAVECLRRK 332
Db 263 LLLSHSHSEGLFQKAIASQGTATSSSVNYQPLKYLRLAAYKVCGRDPSABAVECLRRK 322
Qy 333 PSRELVDDQVQARYHAFQVVDGDDVDDPILMOQGEFLNYDMLIGNOQEGKLFYE 392
Db 323 NYKELQOITTPATYHIAFGVVDGDDVDDPILMOQGEFLNYDMLIGNOQEGKLFYE 382
Qy 393 DSAESDGVASAFDFTVSNFVNLXGYBEGKDLRETIKMYTDWADNCGEMERKTL 452
Db 383 GIVNEDGVTPNDFSVSNFVNLXGYBEGKDLRETIKMYTDWADNCGEMERKTL 442
Qy 453 ALFTDQWVAPATAKLAHAYOSPVYFYFHHCOAGRPWADAAGHDELFPYVFGVPM 512
Db 443 ALFTDQWVAPATAKLAHAYOSPVYFYFHHCOAGRPWADAAGHDELFPYVFGVPM 501
Qy 513 VGATDLFPONFSKNDVWMLSAVWYTNKATGDNQPVODTKFHTKPNRFEVWWSK 572
Db 502 IGTELFSCNFSKNDVWMLSAVWYTNKATGDNQPVODTKFHTKPNRFEVWWSK 561
Qy 573 FNSKEQYHLGLKPRVDRNYRANKVAFWLEVLPHLNLHTELF---TTTTLP----- 623
Db 562 YNPKDQYLHLGLKPRVDRNYRANKVAFWLEVLPHLNLHTELF---TTTTLP----- 620
Qy 624 -PYATWPRPPAGA-PGTRPPPPATLPPEPEPEP---GPRAYDRFPDSDSYSTELSV 678
Db 621 FPGVTR---RSPAKIWFTTKRPAITPANNPKSKDPFKTGPEDTTLVLTETKRDYSTELSV 677
Qy 679 TVAVGASLLFLNLAFALYKXDRROELRCLRSLPGSGSGSGVPGGGLLPAAAGRELP 738
Db 678 TVAVGASLLFLNLAFALYKXDRROELRCLRSLPGSGSGSGVPGGGLLPAAAGRELP 725
Qy 739 EEBLSLQK---GGGVADPABALRPACPDYTLALRALPDDVPLLPALCALTLPSG 794
Db 726 NEEINSLOMKQLEHDECELSQAHDTLRLTCLPDYTLALRALPDDVPLLPALCALTLPSG 785
Qy 795 LGPPPPPPPPSLHFGPPPPPPPTATSHNNTLPHSHSTTRV 835
Db 786 LGMQP-----LHTNTP-----SGQSNLPHGHSTTRV 816

RESULT 8

US-09-978-192A-375
; Sequence 375, Application US/09978192A
; Patent No. US20030177553A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Destrochers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertitsen, Mary E.
; APPLICANT: Giddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

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PRIOR APPLICATION NUMBER: 60/077450

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PRIOR FILING DATE: 1998-04-01

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Db 678 TIAVGASLLFLNLAFALYYKDKRKHETHRPPQRTNDIAH-----IQ 725
QY 739 EELVSLQKR-----GGGVADPAEALRPAACPDVTLALRRAPDDVPLAPGALFLPSG 794
Db 726 NEEIMSLMKOLEHDECELSQAHDTLRLTCPPDYTLTLRRSPDDIPLMTNTIWT 785
QY 795 LGPPPPPPPSLHPGPPPPPPPTATSHNTIPLPHSSTRV 835
Db 786 LTGMQP-----LHTFNTF-----SGQNSTNLPHGHSTRV 816

RESULT 9
US-09-999-832A-375
; Sequence 375, Application US/0999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/06364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
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; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-03-30
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
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; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PlC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/078936
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
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PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/081071
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558

ZTC INTERNATIONAL TRADING COMPANY

; CURRENT FILING DATE: 2001-10-16
 ; NUMBER OF SEQ ID NOS: 624
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 375
 ; LENGTH: 816
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-978-608A-375

Query Match 60.6%; Score 2731; DB 11; Length 816;
 Best Local Similarity 64.2%; Pred. No. 1e-189;
 Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;

QY	38	EEFFPVNTAYGRVGRVRELNEILGPVVQFLGVPYATPPLGARRFQPPPEAPASWPGVR	97
DB	23	QACYPVNTNYKIRGLRPLNEILGPVEQVLGVYASPTTGERRFQPPPEPSSWTGIR	82
QY	98	NATLPPACPNL-HGALPAIMLPVWFTONLEAAATYVQNSDCLYLNLYPTEDGPLT	156
DB	83	NTTQFAAVCPQHLDERSLLHMLPIWFTANLDTLMTYVQDQNECLYLNLYPTEDGANT	142
QY	157	KKR-DEATLNP--PDTDIRDP-GKPVMLFLHGGSYMEGTGMFGSVLAAYGNVIVATL	212
DB	143	KKADDTITNDGEDDEIDHONSKPVMVYIHGGSYMEGTGMFGSVLAAYGNVIVITI	202
QY	213	NYRLGVLGFLSTGDAQAGNYGLLDQIQALRWLSNIAHFGDPPERTIFGSGAGACSVN	272
DB	203	NYRLGILGFLSTGDAQAGNYGLLDQIQALRWLEENVGAFGDPKRVITFGSGAGACSVS	262
QY	273	LLILSHSGLFQKATAQSGTAISSVNYQPLKTRILLAAKVGCDREDSAEVCLRRK	332
DB	263	LLTSHSGLFQKATIQSGTALSSVAVNYQAKYTRILADKVCNMLDITDMEVCLRNK	322
QY	333	PSRELVDQVQARVHIAFGPVVDGDPVDPDEILMQQEFNLNYDMLGVNQEGELKFE	392
DB	323	NYKELIQQTITPATYHIAFGPVVDGDPVDPDEILMQQEFNLNYDMLGVNQEGELKFE	382
QY	393	DSASEDGVSAFDTVSNFVNDLYGYPEGKDVLRITIKFMYTDWADNCEMERKTL	452
DB	383	GIVDNEDGVTNDFSVSNFVNDLYGYPEGKDTLRITIKFMYTDWADKENPETERKTLV	442
QY	453	ALFTDHWVAPAVATAKLHADYQSPVYFVYFHQAGREPEWADAAGDELPHYVGVPM	512
DB	443	ALFTDHWVAPAVA-ADLHAQVGSPTFYFAFHQCSWKSWADSGDEVPYVFGIPM	501
QY	513	VGATDLFCNFKNDVMSAVNTYTNFAKTGDPNQVPQDTKFIHTKPNRFEVWMSK	572
DB	502	IGPTLFCNFKNDVMSAVNTYTNFAKTGDPNQVPQDTKFIHTKPNRFEVWMSK	561
QY	573	ENSKKQVLIHGLKPRVDRYRANKVAFWLELVPHLNLHTELF---TTTTLRP-----	623
DB	562	YNPKQVLIHGLKPRVDRYRANKVAFWLELVPHLNLHTELF-EIYOYVSTTTKVPFPPDMS	620
QY	624	-PYATRWPPRPAG-PTRRPPPPATLPPEPEPEP--GPRAYDRFPDGRDYSTELSV	678
DB	621	FPVGR--RSPAKWFTTKRPAITPANNPKSKDPHTGPDITVLTETKDYSTELSV	677
QY	679	TVAVGASLFLNLAFAALYKRRQELRCRLSPGSGSGVPGCGGLPAPAGRELPP	738
DB	678	TVAVGASLFLNLAFAALYKRRQELRCRLSPGSGSGVPGCGGLPAPAGRELPP	725
QY	739	ERELVSQVLR---GGGVGADPAALPACPDVTLALRAPDVPVLLAPGALLPLPSG	794
DB	726	NREIMSLQKQLEHDECSLAQHTLRLTCDPDVTLRLRSPDDIPMTNTMTIPTNT	785
QY	795	LGPPPPPPPLHPPGPPPPPPPTATSHNNTLPHPHSTTV	835
DB	786	LQGMQ-----LHFNTE-----SGQSNLNLPHGHSTTV	816

RESULT 12
 US-09-978-585A-375
 ; Sequence 375, Application US/09978585A

; Publication No. US20030049633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrata, Napoleon
 ; APPLICANT: Flivaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Andrew
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C15
 ; CURRENT APPLICATION NUMBER: US/09/978,585A
 ; CURRENT FILING DATE: 2001-10-16
 ; NUMBER OF SEQ ID NOS: 624
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 375
 ; LENGTH: 816
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-978-585A-375

Query Match 60.6%; Score 2731; DB 11; Length 816;
 Best Local Similarity 64.2%; Pred. No. 1e-189;
 Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;

QY	38	EEFFPVNTAYGRVGRVRELNEILGPVVQFLGVPYATPPLGARRFQPPPEAPASWPGVR	97
DB	23	QACYPVNTNYKIRGLRPLNEILGPVEQVLGVYASPTTGERRFQPPPEPSSWTGIR	82
QY	98	NATLPPACPNL-HGALPAIMLPVWFTONLEAAATYVQNSDCLYLNLYPTEDGPLT	156
DB	83	NTTQFAAVCPQHLDERSLLHMLPIWFTANLDTLMTYVQDQNECLYLNLYPTEDGANT	142
QY	157	KKR-DEATLNP--PDTDIRDP-GKPVMLFLHGGSYMEGTGMFGSVLAAYGNVIVATL	212
DB	143	KKADDTITNDGEDDEIDHONSKPVMVYIHGGSYMEGTGMFGSVLAAYGNVIVITI	202
QY	213	NYRLGVLGFLSTGDAQAGNYGLLDQIQALRWLSNIAHFGDPPERTIFGSGAGACSVN	272
DB	203	NYRLGILGFLSTGDAQAGNYGLLDQIQALRWLEENVGAFGDPKRVITFGSGAGACSVS	262
QY	273	LLILSHSGLFQKATAQSGTAISSVNYQPLKTRILLAAKVGCDREDSAEVCLRRK	332
DB	263	LLTSHSGLFQKATIQSGTALSSVAVNYQAKYTRILADKVCNMLDITDMEVCLRNK	322
QY	333	PSRELVDQVQARVHIAFGPVVDGDPVDPDEILMQQEFNLNYDMLGVNQEGELKFE	392
DB	323	NYKELIQQTITPATYHIAFGPVVDGDPVDPDEILMQQEFNLNYDMLGVNQEGELKFE	382
QY	393	DSASEDGVSAFDTVSNFVNDLYGYPEGKDVLRITIKFMYTDWADNCEMERKTL	452
DB	383	GIVDNEDGVTNDFSVSNFVNDLYGYPEGKDTLRITIKFMYTDWADKENPETERKTLV	442


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QY 453 ALFTDHOWAPATAKLHAYOSPVYFYFHHCOAEGRPWADAAGDELPHYVGVPM 512
; PRIOR FILING DATE: 1997-11-13
Db 443 ALFTDHOWAPAVA-ADLHAQYSPYFYFHHCOSEMKPSWADSAHGVYVFGIPM 501
; PRIOR FILING DATE: 1997-11-21
QY 513 VGATDLFPCNFSKNDVMSAVNVTWNTFAKTGDPNQPVQDTKFIHTKXPNRFEVYVWSK 572
; PRIOR FILING DATE: 1998-03-10
Db 502 IGTTELFSCNFSKNDVMSAVNVTWNTFAKTGDPNQPVQDTKFIHTKXPNRFEVYVWSK 561
; PRIOR FILING DATE: 1998-03-11
QY 573 FNSKEQYLIHGLKPRVDRNYRANKVAFWLELVPHLNLHTELF---TTTTLRLP----- 623
; PRIOR FILING DATE: 1998-03-11
Db 562 YNFDQYLIHGLKPRVDRHYRATKFAWLELVPHLNLN-ELFQVSVTTTKVPPDDMTS 620
; PRIOR FILING DATE: 1998-03-12
QY 624 -PYATRWPPPPAGA-PGTRRRPPPPATLPPEPEPEP---GPRAYDRFPDSDRSTELSV 678
; PRIOR FILING DATE: 1998-03-12
Db 621 FPYGTR---RSPAKIWPTTKRPAITFANNPKSKDPKGTGPDFTVLITKDYSTELSV 677
; PRIOR FILING DATE: 1998-03-13
QY 679 TVAVGASLLFLNLAAALYKEDRQELRCRLSPGSGSGVPGGGLLPAAGRELP 738
; PRIOR FILING DATE: 1998-03-20
Db 678 TIAGASLLFLNLAAALYKEDRQELRCRLSPGSGSGVPGGGLLPAAGRELP 725
; PRIOR FILING DATE: 1998-03-20
QY 739 EELVSLQKLR-----GGVGADPAEALRPACPPDYTLALRRAPDDVPLIAPGALTLLPSG 794
; PRIOR FILING DATE: 1998-03-25
Db 726 NEEMSLQKLEHDEHCESSLQAHDTLRLTCTPDYTLRLRSPDDIPLMTPTITWINT 785
; PRIOR FILING DATE: 1998-03-25
QY 795 LGPPPPPPPSLHPPGFFPPPPPTATSHNNTLPHPHSTTRV 835
; PRIOR FILING DATE: 1998-03-25
Db 786 LTGMQP-----LHTFNTF-----SGQONSTNLPHGHSTTRV 816
; PRIOR FILING DATE: 1998-03-25

RESULT 13
US-09-978-191A-375
; Sequence 375, Application US/09978191A
; Publication No. US2003050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03

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RESULT 14

US-09-978-403A-375
Sequence 375, Application US/09978403A
Publication No. US2003050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;

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QY 98 NATTLFPACPNL-HGALPATMLPWFTDNLBAATYVQWSEDCLYNLVYPTEDGFLT 156
DB 83 NTQTAAVCPQHLDRSLHMLPWFNTANLDTLMTYVQDQNECLYNIYVPTEDGANT 142
QY 157 KKR-DEATLNP--PPTDIRDP-GKKFVMLFLHGGSYMEGTGNTMFDGSLAAYGNVIVATL 212

DB 143 KKNADDITSNDRGEDEIHQNSKXPVMVYIHGGSYMEGTGNTMIDGSLASYNVIVITI 202
QY 213 NYRLGVLGFLSTGDOAAKNGNYLLDQIQALRWLSNIAHFQGGDPRIITFGSGAGASCVN 272
DB 203 NYRLGVLGFLSTGDOAAKNGNYLLDQIQALRWIEENVGAFGGDPKEVITFGSGAGASCVS 262
QY 273 LILSHHSEGLFQKAIAGSTRAISSWVNYQPLKYTRLLAAKVGCDREDSABAVECLARK 332
DB 263 LTLTSHYSEGLFQKAIQSGTALSSWAVNYQPAKTRILADKVGCMMLDITDMVCECLANK 322
QY 333 PSRELVDQDQPARVHIAFGPVVDGDDVVDDEIILMOQGEFLNYDMLIGVNOGEGKLFVE 392
DB 323 NYKELIQTTITATYHIAFGPVIDGDIVDDPQILMEQGEFLNYDMLIGVNOGEGKLFVD 382
QY 393 DSAESEDGVSASAFDTVSNFVDNLYGYPEBGKVLRRTIKFMYTIDWARDNGEMRKILL 452
DB 383 GIVDNEEDGVTNDFDVSFVNDNLYGYPEBGKDTLRITIKFMYTIDWADKENPETERKTIV 442
QY 453 ALFTDHWVAPAVATAKLHADYQSPVVFYTFVHHQASGRPEWADAAGHDELPPYVFGVPM 512
DB 443 ALFTDHWVAPAVA-ADLHAQYGSYTYFYAFVHHQSEMKPSWADSAGDEVPYVFGIPM 501
QY 513 VGATDLFFCNFSKNDVMSAVVMYTNFNAKTGDPNQVPQDTKFIHTKPNRFEVVMWSK 572
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QY 573 FNSKEQYVHLGLKPRVRDNYRANKVAFWLELVPHLHNLHTLP-----TTTTL 623
DB 562 YNPKOQLYHLGLKPRVRDHYRATKVAFWLELVPHLHNLN-EIYOYVSTTTKVPDPMWS 620
QY 624 -PYATRWPPRPAGA-PGTRRPPPPATLPPPEPEPP---GPRAYDRFPDGRDYSTELSV 678
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QY 739 EELVSLQLK---GGGVGADPAEALRACPDVYTLALRRAPDDVPLAPGALTLLPSG 794
DB 726 NEEIMSLQWQLEHDEHESLOAHDTLTLTCDPDYTLRLRSPDIPMLTNTITMIPNT 785
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deshoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC25
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 CURRENT FILING DATE: 2001-10-16
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 PRIOR APPLICATION NUMBER: 60/084640

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 17:13:07 ; Search time 4890.86 Seconds
(without alignments)
12463.166 Million cell updates/sec

Title: US-09-934-323-3

Perfect score: 2508

Sequence: 1 agtggctctggcgtgtg.....actccaccactgggtatag 2508

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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7: em_estro:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	991.8	39.5	3853	11 AK039018	Mus muscu
2	740	29.5	1884	11 BC028738	BC028738 Homo sapi
3	733.6	29.3	1157	12 BM477185	BM477185 AGENCOURT
4	699.8	27.9	790	14 CA324321	CA324321 UI-M-FY0-

5	682.8	27.2	981	13	BU542698	AGENCOURT
6	674.6	26.9	919	13	BQ891968	AGENCOURT
7	667.2	26.6	735	10	BF058856	7k35e09.x
8	661.8	26.4	879	13	BQ947939	AGENCOURT
9	656.4	26.2	708	14	CD349431	UI-M-FY0-
10	652.6	26.0	739	13	BQ769293	UI-M-FY0-
11	645.8	25.7	755	14	CD348520	UI-M-FY0-
12	643.4	25.7	1155	13	BQ278029	AGENCOURT
13	636.8	25.4	784	14	CD526398	UI-M-FY0-
14	636.6	25.4	807	14	CD348683	UI-M-FY0-
15	629.4	25.1	729	13	BQ771190	UI-M-FY0-
16	628.4	25.1	795	14	CA316129	UI-M-FY0-
17	628.2	25.0	660	12	BI046856	ME3-FN020
18	626.2	25.0	1066	13	BQ920779	AGENCOURT
19	621.2	24.8	804	14	CD355788	UI-M-FY0-
20	620.8	24.8	910	13	BU931333	AGENCOURT
21	619.2	24.7	873	12	BG920355	602825882
22	618.2	24.6	770	12	BM944282	UI-M-EHOP
23	617.6	24.6	741	14	CA328689	UI-M-FY0-
24	617.4	24.6	719	13	BQ180305	UI-M-EXO-
25	614	24.5	715	13	BQ180670	UI-M-EXO-
26	613.4	24.5	780	14	CA316667	UI-M-FW0-
27	606.2	24.2	692	10	BE952199	UI-M-CD0-
28	602.8	24.0	727	14	CB526164	UI-M-FY0-
29	597.8	23.8	689	13	BU708515	UI-M-FY0-
30	595.2	23.3	736	14	CB249514	UI-M-EXO-
31	593.6	22.9	679	14	CB248107	UI-M-FY0-
32	593.2	22.9	733	14	CA316458	UI-M-FW0-
33	567.2	22.6	714	12	BM963021	UI-M-EQ0-
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35	549.6	21.9	680	14	CD355677	UI-M-FY0-
36	549	21.9	709	12	BM951227	UI-M-EH0-
37	546	21.8	788	12	BI687443	603315171
38	545.6	21.8	699	14	CA324959	UI-M-FY0-
39	537.2	21.4	647	14	CB524511	UI-M-FY0-
40	530.8	21.2	766	14	CA749282	UI-M-FY0-
41	526	21.0	528	9	AI337820	qt29e04.x
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43	524.6	20.9	612	13	BU057485	UI-M-FY0-
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45	508	20.3	580	9	AW291374	UI-H-BI2-

ALIGNMENTS

RESULT 1
AK039018
LOCUS
DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length
enriched library, clone:A230085M13 product:NEUROLIGIN 3 ISOFORM
HNL3 homolog [Homo sapiens], full insert sequence.

ACCESSION AK039018
VERSION AK039018.1 GI:26332978
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636

REFERENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159


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Qy 483 -----GGGACGCTCAATCCGCCAGACACAGATATCCGTGACCCCTGGGAAAGACCTGTGCA 538
Db 766 TAGCGGATAATGACGGGGATGAAGATGAAGACATCCGAGACAGTGGTGTAAACCTGTGCA 825
Qy 539 TGTGTTTCTCCATGGCGGCTCTACATGAGAGGGGACCGGAAACATGTTGATGGCTCAG 598
Db 826 TGGTCTACATCCAGAGGCTCTTACATGGAAGAAACAGGAAACATGATTGATGGCGATG 885
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Db 886 TTCTTGCAAGTTAGGCAACGTCATCGTCATCAACCTCAACTATCGGGTCGGGGTCTAG 945
Qy 659 GTTTTCTCAGACCGGGGACAGGCTGCAAAAGGCAACTATGSGCTCTGGACCATCC 718
Db 946 GTTTCCTGAGCATGGAGATCAGGCTGCCAAGGGCAACTATGSGCTCTTGTATCAATCC 1005
Qy 719 AGGCCCTGCGCTGCTCAGTGAAGAAACATCGCCCACTTTGGGGGCAACCCGAGCGTATCA 778
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Db 1126 CTGAGGGGCTTTTCCAGAGGGCCATCATCCAAAGTGGCTCTGTCTATCTAGCTGGCTG 1185
Qy 899 TCAACTACCAAGCGCTCAAGTACACGCGGTCTGTCAGCAGCAAGGTGGGCTGTGACCGAG 958
Db 1186 TGAAC'TACCAACAGTGAAGTATACCAAGTTGCTGGCAGAGAAAGTGGGCTGTAACGTCC 1245
Qy 959 AGACAGTGTGAAGTGTGAGATGCTGCGCGGAGAGCCCTCCCGGAGCTGGTGAAC 1018
Db 1246 TGGACACTTGGATATGTTGGATGTTCTTCGACAAAGAGTGCAGAGGAGCTGGTAGAAC 1305
Qy 1019 AGACGCTGACGCTGCCCGCTACCAATCGCTTTGGGCGGTGGTGGATGGCGAGCTGG 1078
Db 1306 AGNACATTCAGACAGCCCGCTACCATGTGGCTTTGGCCCTGTGATGATGATGTCA 1365
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Db 1366 TTCTGATGACCTGAGATCCTTATGAGCAGGAGAGTTCTCTCAACTATGATATCATGC 1425
Qy 1139 TCGCGTCAACAGGAGAGGCTCAAGTTCGTGGAGGACTCTGCAGAGAGCGAGAGC 1198
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Qy 1199 GTGTGTCTGCGAGCGCTTTGACTTCACTGTCTCTCAACTTTGTGGCAACCTGTATGGCT 1258
Db 1486 GTGTCTCGGCACTGACTTTGACTACTCTCTCTCAATTTTGTGGCAATCTGTATGGCT 1545
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Db 1546 ATCTGAGGATAGGACACCTCGGAGAGACTATCAAGTTATGATATAGGACTGGGCGAG 1605
Qy 1319 ACCGGACATGCGAATGCGCGCAAAACCTGTGCGCTCTTTACTGACCAACCAAT 1378
Db 1506 ACCGAGACACCTGAGACCGCGGTAAACACTGTGTGGCACTTTCATGACCAACCAT 1665
Qy 1379 GGTGGCACAGCTGTGGCACTGCCAAGCTGCAACCGCGACTACCAAGTCTCCCGTCTACT 1438
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Qy 1619 ACTTCGCCAAGACTGGGACCCCAACAGCGGTCGCGCAGGATACCAAGTTCTATCCACA 1678
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Qy 1739 ATCTGCACATAGGCTGAAGCCACGCTGCTGACAACTACCGGCCCAACAAGGTGGCT 1798
Db 2026 ACTTTCATCTCGGCTGAACCAAGGTTCTGTATCATTTACCGGCCACAAAGGTAGCT 2085
Qy 1799 TCTGCTGAGACTCGTGCCTCCACCTGCAACACCTGCAACAGAGCTC-----TTCA 1849
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Qy 1850 CACCAACACGCGCTGCTCCTACCGCAGCGCTG-----GCCGCTCTGTCCTCC 1900
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Qy 1901 CCGTGGCGCCCGGCGCACACGCGGCCCGCCCTGCGCACCTGCTCCCGAGCCCG 1960
Db 2206 ACGCCAAGACTTGGAGCACCAAGCGCGCGGATTTTACCTGCTTACAGCAATGAGAATG 2265
Qy 1961 AGCCGAGCCCGGCCCAAGGGCTATGA-----CCGTTCCCGGGGACTCACGGG 2011
Db 2266 CCGCTGGGTCTGGAATGGGACCAAGGATGCGGGGCCACTCTCTGGTTGAGAACCTCGAG 2325
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Qy 2072 TCCTGGCCTTTGCTCCCTCTTACTACAAAGCGGAGACCGCGGACAGAGCTGCGGTGACGGC 2131
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Qy 2132 GGCTTAGCCACCTGGCGGCTCAGGCTGCGCTGCGTGGTGGGGCCCCCTGCTCCCG 2191
Db 2446 AGCTTAGCCCCCAAGGGGAACTGGTGC-----CCCTG 2478
Qy 2192 CCGGGGCGGTGAGCTGCCACAGAGGAGGAGTGTGTCACTCAGCTGAGTGAAGCGGGTG 2251
Db 2479 AATTGGNACTGCTCCGAGGAGGAGCTGGCAGCATTAAGTTGGTCCCACTCACCATG 2538
Qy 2252 GTGGCTCGGGGCGGACCTTCGCGAGGCTGTGCGCTGCTGCGCGCGCGACTACACCC 2311
Db 2539 AATGTGAGCGCGTCCCGCCACATGACACACTTGCCTCACAGCACTGCCGACTATACCC 2598
Qy 2312 TGGCCTGCGCGGCGCACCGGACGATGCTCTTTGGCCCCCGGGGCCCTGACCCCTGC 2371
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Qy 2372 TGCCAGTGGCTCG 2386
Db 2659 TTCTTAATTCCTCG 2673
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RESULT 2

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LOCUS      1884 bp      mRNA      linear      HTC 01-MAY-2002
DEFINITION Homo sapiens, Similar to neurologin 3, clone IMAGE:526328, mRNA.
ACCESSION  BC028738
VERSION     BC028738.1  GI:20380993
KEYWORDS   HTC.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1884)
AUTHORS    Strausberg, R.
```


Qy	1638	CCCAACACAGCCCGTGC	CGGATACCAAGTTCATCCACCAAGCCCAATCGCTTCGA	1697
Db	373	CCCAACACAGCCCGTGC	CGGATACCAAGTTCATCCACCAAGCCCAATCGCTTCGA	432
Qy	1698	GGAGGTGGTGTGAGCAAA	TTCAACAGCAAGGAGAGCAGTATCTGCATAGAGCCTGAA	1757
Db	433	GGAGGTGGTGTGAGCAAA	TTCAACAGCAAGGAGAGCAGTATCTGCATAGAGCCTGAA	492
Qy	1758	GCACGCGTGC	GTGACAACTACCGCGCCCAACAAAGGTGGCTTCTGTGCTGGAGCTCTGGCC	1817
Db	493	GCACGCGTGC	GTGACAACTACCGCGCCCAACAAAGGTGGCTTCTGTGCTGGAGCTCTGGCC	552
Qy	1818	CCACCTGCACAACTGC	CACAGGAGCTCTTACCACACACAGCGCTGCCTCCCTACGC	1877
Db	553	CCACCTGCACAACTGC	CACAGGAGCTCTTACCACACACAGCGCTGCCTCCCTACGC	612
Qy	1878	CACGCGCTGC	CGCCCTCGT - CCCCCCGCTGGCGCCCGGGGCACACGCGCCCGCCCGC	1936
Db	613	CACGCGCTGC	CGCCCTCGT - CCCCCCGCTGGCGCCCGGGGCACACGCGCCCGCCCGC	672
Qy	1937	CTGCGACCTTGCTCC	CGAGCCGAGCCCGAGCCCGAGCCCGG - CCCAAGGGCCCTATGACCGCTT	1994
Db	673	CTGCGACCTTGCTCC	CGAGCCGAGCCCGAGCCCGAGCCCGG - CCCAAGGGCCCTATGACCGCTT	732
Qy	1995	CCCCGGGGACTCAC -	GGGACTACTCCACGAGCTGAGCGTCAACCGTGGCCGTGG - GTGCG	2052
Db	733	CCCCGGGGACTCAC	GGGAGTACTCCACGAGCTTACGTCACCGTGGCCGTGGAGTGGC	792
Qy	2053	TCCTCTCTC -	TTCTCTCAACATCTGTGCC - - - TTTGTGTCCTCTACTACAAGCGGG - AC	2106
Db	793	TCCTCTCTCTCTCT	CAACATCTGTGGCCCTTTTGTGTCCTCTCTATACAAGCGGGAGCC	852
Qy	2107	CGCGCGCAGAGCT -	CGGTGTGAGGGCGCTTACGCCACCTGG - CGGCTCAGGCTCTGG -	2162
Db	853	GGCGGAGAAACTGT	CGCGGCGAGCGCGCTTACGCCCTTACGCCCTTACGGCGGTTACGGCTCCGGG	912
Qy	2163	-CGTGCTGTGTGGGCG	CCCCCTGCTCCCGCGCGGG 2197	
Db	913	CGGGGCGCTGTGGG	GGGGCCCCCTGCTCCCGCCCCG 948	

RESULT 4

CA324321

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA324321

UI-W-FYO-cdp-g-21-0-UI.r1 NIH BMAP_FYO Mus musculus cDNA clone

IMAGE: 6822670 5', mRNA sequence.

CA324321

CA324321.1 GI:24542419

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 790)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgaabs@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

The following repetitive elements were found in this cDNA sequence: 21-63, >GC rich/Low_complexity (matched complement)

Seq primer: pyx-5.

Location/Qualifiers

1..790

FEATURES

source

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1CM2561 row: f column: 18
High quality sequence start: 14
High quality sequence stop: 486.

FEATURES

Location/Qualifiers
1..919
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:6377489"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
BASE COUNT 187 a 290 c 275 g 167 t
ORIGIN

Query Match 26.9%; Score 674.6; DB 13; Length 919;
Best Local Similarity 98.0%; Pred. No. 2.2e-115; Indels 0; Gaps 0;
Matches 683; Conservative 0; Mismatches 14;

QY 355 CTGCTGTGTGGTTCACGCAACTTGGAGCGCGCCACCTACGTGCGAAGACGAGC 414
DB 1 CTGCTGTGTGGTTCACGCAACTTGGAGCGCGCCACCTACGTGCGAAGACGAGC 60
QY 415 GAGGACTGCTGTACCTCAACCTCTAGTGCACCGAGGACGCTCGCTCAGAAAAA 474
DB 61 GAGGACTGCTGTACCTCAACCTCTAGTGCACCGAGGACGCTCGCTCAGAAAAA 120
QY 475 CGTGACGAGGCGAGCTCAATCCGCGACAGACAGATATCCGTGACCTTGGGAAGAGCCT 534
DB 121 CGTGACGAGGCGAGCTCAATCCGCGACAGACAGATATCCGTGACCTTGGGAAGAGCCT 180
QY 535 GTGATGTGTTTCCATATGCGGCTCTCTATGAGGAGGACCGGAAACATGTTGATGGC 594
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DB 241 TCAGTCTGCTGCTATGCAAGCTGATGAGCAGCTCAACTACCGTCTTGGGGTG 300
QY 655 CTCGGTTTCTCAGCACCGGGACGAGCTGCAAAAGGCAACTATGGGCTCTTGACGAG 714
DB 301 CTCGGTTTCTCAGCACCGGGACGAGCTGCAAAAGGCAACTATGGGCTCTTGACGAG 360
QY 715 ATCCAGGCGCTGCGCTGCTCAGTGAAACATCGCCACCTTTGGGGGCGACCCGAGCGT 774
DB 361 ATCCAGGCGCTGCGCTGCTCAGTGAAACATCGCCACCTTTGGGGGCGACCCGAGCGT 420
QY 775 ATCACCATTCTTGGTTCCGGGCGAGGGGCTCTCTGCGCTCAACCTTCTGATCTCTCCAC 834
DB 421 ATCACCATTCTTGGTTCCGGGCGAGGGGCTCTCTGCGCTCAACCTTCTGATCTCTCCAC 480
QY 835 CATTGAGAGGCTGTTCCAGAGGCGCATGCCAGAGTGGCAGCCGATTTCCAGCTGG 894
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QY 895 TCTGTCAACTACGAGCGCTCAAGTACACGCGGCTGCTGGCAGCAAGGTTGGGCTGTGAC 954
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QY 1314 GCGCGACCGGCAATGCGCAATGCGCGCAAAACCTGCTGGGCTCTTTACTGACCA 1373
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DB 253 CCAATGGTGGCAACAGCTGTGGCCACTGCGCAAGCTGCGAGCGGACTACAGTCTCCCGT 312
QY 1434 CTACTTTTACACCTTCTACCAACCTGCGCAGGAGGCGCGCTGAGTGGGCGAGATGC 1493
DB 313 CTACTTTTACACCTTCTACCAACCTGCGCAGGAGGCGCGCTGAGTGGGCGAGATGC 372
QY 1494 GCGCGACCGGATGAATGCTGCTTGTGGCGTGCCTGAGTGGGCGAGATGC 1553
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QY 1554 CTTCCCTGTAACCTTCCAAAGATGAGCTGCTGCTGAGTGGGCGAGATGC 1613
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QY 1614 GACCAACTTCGCAAGACTGGGACCCCAACACGCGGTCGCGAGGATACCAAGTTTCA 1673
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QY 1734 GCAGTATCTGCATAGGCTGAAAGCAGCGCTGCTGCAACTACCGGCGCAACAGGT 1793
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QY 1794 GGGC--TTTGGGTGAGCTCGTG-CCCACTGCGC-AACCTGCGACAGAGCTCTTCA 1849
DB 673 GGGCCTTTTGGGTGAGCTCGTGCCCGCCACCTGCGACAACTGCGAGGAGCTCTTC 732
QY 1850 CCACCAACAGCGCTGCTTCCCTGACGCGAGCGCTGCGCGCTCTGCTCCCGCTGGCG 1909
DB 733 CCACCAACAGCGCGCTGCTTCCCTGACGCGAGCGCTGCGCGCTCTGCTCCCGCTGGCG 792
QY 1910 CCGCGGACACACCG 1969
DB 793 CCGCGGCG 852
QY 1970 CCGG 1973
DB 853 CCGG 856

RESULT 6
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LOCUS BO891968 919 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8695255 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6377489
5', mRNA sequence.
ACCESSION BO891968
VERSION BO891968.1 GI:22283982
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 919)
AUTHORS NTH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

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QY 1015 GACGAGAGCTGACGCTGCCCTACCATCGCT 1051
Db 661 GACGAGAGCTGACGCTGCCCTACCATCGCT 697

RESULT 7
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DEFINITION similar to TR:962888 Q62888 NEUROLIGIN 2.; mRNA sequence.
ACCESSION BF058856
VERSION BF058856.1 GI:10812752
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 735)
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moekaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
FEATURES
Location/Qualifiers
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strand cDNA was primed with a Not I - oligo (dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGCGACATTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTV73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 159 a 233 c 204 g 137 t 2 others
ORIGIN
Query Match 26.6%; Score 667.2; DB 10; Length 735;
Best Local Similarity 97.0%; Pred. No. 4.9e-114;
Matches 689; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
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QY 445 CCCACCGAGGAGCTGCGCTCACAAAAAAGCTGACGAGCGAGCTCAATCGCCAGAC 504
Db 61 CCCACCGAGGAGCTGCGCTCACAAAAAAGCTGACGAGCGAGCTCAATCGCCAGAC 120
QY 505 ACAGATATCCGTGACCTCGGAGAGACCTGTGATGCTTTCTTCCATGCGGCTCCTAC 564
Db 121 ACAGATATCCGTGACCTCGGAGAGACCTGTGATGCTTTCTTCCATGCGGCTCCTAC 180
QY 565 ATGAGGAGCGCCGAAACATGTTTCATGGCTCAGTCTGCTGCTTGGCAACGTCATT 624

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Db 181 ATGAGGAGCGCCGAAACATGTTTCATGGCTCAGTCTGCTGCTATGGCAACGTCATT 240
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Db 301 GCAAAAGGCAACTATGGGCTCCTGGACCAAGCCCTGCGCTGGCTCAGTGAAGAAC 360
QY 745 ATGCGCCACATTGGGGGCGACCCCGAGCGGTATCACCATTCTTGGTTCCGGGGCAGGGGCC 804
Db 361 ATGCGCCACATTGGGGGCGACCCCGAGCGGTATCACCATTCTTGGTTCCGGGGCAGGGGCC 420
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Db 421 TCCTGCGCTCAACCTTCTGATCTCTCCACCATTTCAGAGGGCTGTTCAGAGAGGCCATC 480
QY 865 GCCCAGAGTGGCAGCCGCAATTCAGCTGTCTGTCACTACCGCGCTCAAGTACAG 924
Db 481 GCCCAGAGTGGCAGCCGCAATTCAGCTGTCTGTCACTACCGCGCTCAAGTACAG 540
QY 925 CGGCTGCTGCGCAGCAAGGTGGGCTGTGACCGAGAGGACAGTGTGAGAGCTGTGAGTGT 984
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Db 601 CTGCGCCGGAAGCCCTCCGGGAGCTGGTGGACCGAGACGTCGACGCTGCCCGTACAC 660
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Db 661 ATCACTGATGCGCCGCTGGTGGTGGATAGTACGCTGTCCGCCATGACCTCTGA 709

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RESULT 8
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LOCUS AGENCOURT_8795167 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6427691
DEFINITION 5', mRNA sequence.
ACCESSION BO947939
VERSION BO947939.1 GI:22363417
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2613 row: b column: 12
High quality sequence stop: 575.
Location/Qualifiers
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/clone_lib="NIH MGC 101"
/note="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:

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XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 171 a 315 c 240 g 153 t

ORIGIN

Query Match 26.4%; Score 661.8; DB 13; Length 879;
Best Local Similarity 89.3%; Pred. No. 5.1e-113; Indels 4; Gaps 4;
Matches 758; Conservative 0; Mismatches 87; Indels 4; Gaps 4;
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QY 1226 CTGCTCCAACTTTGTGACAACCTGTATGGCTACCCGGAAGGCAAGATGTGCTTCGG 1285
DB 72 CTGCTCC-AC-TTTGTGACAACCTGTATGGCTACCCGGAAGGCAAGATGTGCTTCGG 130
QY 1286 AGACCATCAAGTTTATGACACAGACTGGCGCGACCGGCAATGGCGAAATGGCGCGCA 1345
DB 131 AGACCATCAAGTTTATGACACAGACTGGCGCGACCGGCAATGGCGAAATGGCGCGCA 190
QY 1346 AAACCTGCTGCGCTTTTACTGACCAACCAATGGGTGGCAACAGCTGTGGCCACTGCCA 1405
DB 191 AAACCTGCTGCGCTTTTACTGACCAACCAATGGGTGGCAACAGCTGTGGCCACTGCCA 250
QY 1406 AGCTGACGCGGACTACCACTCTCCGCTACTTTTACACCTTACCACTGACCACTGCCAG 1465
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QY 1466 CGAGGGCGCGCTCAGTGGGAGATGGCGGCGACGGGGATGAAGTGCCTTATCTTTTG 1525
DB 311 CGAGGGCGCGCTCAGTGGGAGATGGCGGCGACGGGGATGAAGTGCCTTATCTTTTG 370
QY 1526 GGTGTCATATGGTGGTGGCGACGACCTTCTCCCTGTAACTTCTCCAGATGACGTCA 1585
DB 371 GGTGTCATATGGTGGTGGCGACGACCTTCTCCCTGTAACTTCTCCAGATGACGTCA 430
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DB 431 TGCTCAGTGGCGTGTGATGACCTACTGACCAACTTCCGCAAGCTGGGACCCCAACC 490
QY 1646 AGCCGGTGGCGGAGATACCAAGTTTATCCACACCAAGCCCAATGCTTGGAGAGTGG 1705
DB 491 AGCCGGTGGCGGAGATACCAAGTTTATCCACACCAAGCCCAATGCTTGGAGAGTGG 550
QY 1706 TGTGAGCAAAATTCACAGCAGGAGAGAGTATCTGCATAGGCTGAAGCCAGCG 1765
DB 551 TGTGAGCAAAATTCACAGCAGGAGAGAGTATCTGCATAGGCTGAAGCCAGCG 610
QY 1766 TGCGTGACAACTACCGCGCCCAACAGGTGG-CTTTCTGGCTGGAGCTGTGCCCCCA-CCT 1823
DB 611 TGCGTGACAACTACCGCGCCCAACAGGTGGCTTTCTGGCTGGAGCTGTGCCCCCACT 670
QY 1824 GCACAACTGACACGG-AGCTTTCACCAACACACAGCGGCTGTCTTCCCTACGCCAGC 1882
DB 671 GCACAACTGACACGGAGCTTTCACCAACACACAGCGGCTGTCTTCCCTTACGCCCC 730
QY 1883 GTTGGCGGCTGTCTTCCCGCTGTGGCGCCGCGGACACGCGGCGCCGCGCTGCCA 1942
DB 731 AGCGCTGGCGGCTGTCTTCCCGCTGTGGCGCCGCGGACACAGCGGCGGCG 790
QY 1943 CCTGCTCCGAGCCCGAGCCCGGAGCCCGGCGCCCAAGGGCTATGACGCTTCCCGGG 2002
DB 791 CCGCGCGCGGCTGGCCCAACCTTGGCTTCCGAGCCCGGAGCCCGGAGTCCCGGG 850
QY 2003 ACTCAGGG 2011
DB 851 GCCCAAGG 859

RESULT 9
CD349431

LOCUS
DEFINITION

ACCESSION
CD349431

VERSION
KEYWORDS

SOURCE
ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD349431 708 bp mRNA linear EST 29-MAY-2003
UI-W-F10-cfq-b-14-0-UI-r1 NIH_BMAP_F10 Mus musculus cDNA clone
IMAGE: 6854415 5', mRNA sequence.

CD349431.1 GI:31140946

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 708)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousef.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

The following repetitive elements were found in this cDNA

sequence: 16-58, >GC_richLow_complexity (matched complement)

Seq primer: pYX-5.

Location/Qualifiers

1..708

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE: 6854415"

/tissue_type="whole brain"

/dev_stages="embryo 13.5,14.5,16.5,17.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP_FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonafide, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is ACCGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): Gene Discovery in the

Developing Mouse Nervous System", supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

BASE COUNT 126 a 242 c 222 g 117 t

ORIGIN

Query Match 26.2%; Score 656.4; DB 14; Length 708;
Best Local Similarity 95.5%; Pred. No. 5e-112;
Matches 675; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 40 GCTCAACGCGGGGGGGGGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 99

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QY 100 GCGAGCTTCGCGAGAGCGCTTCCTCGGTGGTGAACACAGCGCTACGCGGAGTGGCGGT 159

DB 61 GCGAGCTTCGCGAGAGCGCTTCCTCGGTGGTGAACACAGCGCTACGCGGAGTGGCGGT 120

QY 160 GTGCGCGCGAGCTCAACACAGATCCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 219


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121 GTGCGGCGGAGCTCAACAGAGATCTTGCGCGGCTGTGAGTCTTTGGGCGTGCC 180
220 TACGCCACGCGCCCTGGGCGCGCGCTTCAGCGCGCTAGCGCGCGCGCTGTGG 279
181 TACGCCACGCGCGCTTTGGGCGCGCGCTTCAGCGCGCTAGGACCTGCTGTGG 240
280 CCGCGCTGGCGCAACGACACACCTGCGCGCGCGCTGCGCGAGAACCTGACGCGGGG 339
241 CCGCGCTGGCGCAACGACACACCTGCGCGCGCGCTGCGCGAGAACCTGACGCGGGC 300
340 CTGCGCGCGCATGCTGCTGTGTGTTACCGAACAATTTGAGGGGCGCGCACCTAC 399
301 CTGCGCGCGCATGCTGCTGTGTGTTACCGAACAATTTGAGGGGCGCGCACCTAC 360
400 GTGCAGAACACGAGCGAGGAGTCTGCTACTCAACTCTACCTGCGCGCGCGCGAGCGGT 459
361 GTGCAGAACACGAGCGAGGAGTCTGCTACTCAACTCTACCTGCGCGCGCGAGCGGT 420
460 CCGCTCACAAAAAACGTGACGAGCGAGCGCTCAATCCGCGAGACACAGATATCGGTGAC 519
421 CCGCTCACAAAAAACGTGACGAGCGAGCGCTCAATCCGCGAGACACAGATATCGGTGAC 480
520 CTTGGGAGAGCTGTGATGCTGTTCTTCATGGCGGCTCTACATGAGGGGACCGGA 579
481 TCTGGGAGAAACCGGTGATGCTGTTCTACAGCGCGGCTCTACATGAGGGGACCGGG 540
580 AACATGTTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
541 AACATGTTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
640 TACGCTCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
601 TACGCTCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
700 GGGCTCTGAGACAGATCCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746
661 GGGCTCTGAGACAGATCCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707

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RESULT 10
BQ769293
LOCUS
DEFINITION
  UI-M-F10-byp-j-01-0-UI-r1 NIH BMAP_F10 Mus musculus cDNA clone
  IMAGE:5721312 5', mRNA sequence.
ACCESSION
  BQ769293
VERSION
  BQ769293.1 GI:21977767
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished
  Contact: Robert Strausberg, Ph.D.
  Email: cga@bbs-remail.nih.gov
  Tissue Procurement: Dr. Jim Lin, University of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
Seq primer: pYX-5.
Location/Qualifiers
  1..799
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6"

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FEATURES
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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_F10"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: Ecor I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCACGAC. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
BASE COUNT 160 a 238 c 230 g 168 t 3 others
ORIGIN
Query Match 26.0%; Score 652.6; DB 13; Length 799;
Best Local Similarity 90.1%; Pred. No. 2.6e-11; Indels 0; Gaps 0;
Matches 697; Conservative 0; Mismatches 77;
QY 767 CCGAGCGTATCACCATCTTTGGTTCCGGGGCAGGGGCTCTCGTCAACCTTTGTATCC 826
Db 1 CTGAACGATCATCTATCTTTGGTCTGGTGCAGGGGCTCTCTGTTCAACTTGTGTATCC 60
QY 827 TCTCCACCATTCAGAGGGCTGTTCCAGAGGCGCATGCCAGAGTGCGCCGCAATTT 886
Db 61 TTTCCACCATTCAGAGGACTGTTCCAGAGGCGCATGCTCAAGTGGTATGCGCATTT 120
QY 887 CCAGTGGTCTGTCAAATPACAGCGCTCAAAGTACACGCGGCTGTGTCAGCGCAAGTGG 946
Db 121 CCAGTGGTCTGTCAAATPACAGCGCTCAAAGTACACGCGGCTGTGTCAGCGCAAGTGG 180
QY 947 GCTGTGACGAGAGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1006
Db 181 GCTGTGACGAGAGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 240
QY 1007 AGCTGGTGACGAGACGCTGAGCGCTGCGCGCTACCATCGCCCTTTGGGCGCGGTGTGG 1066
Db 241 AGCTAGTGGACGAGATGTACAGCTGCGCGCTACCATTTGCGCTTTGGGCGCTGTGGTGG 300
QY 1067 ATGGGACGCTGTCCCGATGACCTGTAGATCTCTATGTCAGCGAGGAGAAATTCCTCACT 1126
Db 301 ACGGCGAGGTANTCCCTGATGACCCCGAGATCTCTATGCAACAGGGGAAATTCCTCACT 360
QY 1127 ACGATGCTCATCGCGCTCAACGAGGAGAGGGGCTCAAGTTCGTGAGGACTCTGCAG 1186
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QY 1187 AGAGCGAGGACGCTGTGCTGCCAGCGCTTTGACTTCATGTTCTCAACTTTGTGGACA 1246
Db 421 AGAGTGGAGCGGTGTGCTGCCAGCGCTTTGACTTCATGTTCTCAACTTTGTGGACA 480
QY 1247 ACTGTATGGCTACCGGAGGAGGATGCTTCGGGAGACCATCAAGTTTATGTACA 1306
Db 481 ACTTGTACGGGTACCCAGAGGCAAGGCGTCTTCGAGAGACCATCAAGTTTATGTACA 540
QY 1307 CAGACTGGGCGCGACCGGACCAATGCGGAAATGCGCGCGCAAAACCTGTGCGGCTCTTTTA 1366
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QY 1367 CTGACACCAATGGGTGGACCCAGCTGTGGCCATGTCGCCAGTGCACCGGACTACCACT 1426
Db 601 CCGACCAACAGTGGGTGCGCGCGGTGTGCGCACCGCCCAAGCTGCATCGGACTACCACT 660
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Db 661 CCCCCGTCTACTTTTACACTTTTACCACTCCAGGAGAGGGCGGCGGAGGTGG 720
QY 1487 CAGATCGCGGCGACGGGAGTGAACCTGCCTATGCTTTGGCGTCCCATGTTGG 1540
Db 721 CAGACGACGACGACGGGACGAGTGCCTACGTTCTTTGGTGGCCCATGGTGG 774

RESULT 11
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UI-M-FY0-cfo-g-15-0-UI_r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE: 6853768 5', mRNA sequence.
CD348520
ACCESSION CD348520.1 GI:31140035
VERSION 1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 755)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP).
Seq primer: pYX-5.
FEATURES
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/mol_type="mRNA"
/strain="C57BL/6"
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/clone="IMAGE: 6853768"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
BASE COUNT 156 a 213 c 214 g 170 t 2 others
ORIGIN
Query Match 25.7%; Score 645.8; DB 14; Length 755;
Best Local Similarity 90.9%; Pred. No. 4.7e-110;
Matches 686; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 508 GATATCCGTGACCTCGGAGAGACCTGTGATGCTGTTTCCATGCGGCTCCTACATG 567
Db 1 GATATCCGGGACTCTGGGAGAGAACCGGTGATGCTGTTTCTACACGGGCTCCTACATG 60
QY 568 GAGGGGACCGGAACATGTTTCGATGGCTAGTCTGCTGCTCCTATGCAACGTCATTGTA 627

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Db 61 GAAGGACACCGGAACATGTTTACGCGCTCAGTCTGGCTGCCCATGGAATTCATCGTA 120
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Db 121 GTCACACTCACTACCGTCTTGGGGTGTCTGGTTTTCTCAGCACTGGTGACCGGCTGCA 180
QY 688 AAAGGCAACTATGGGCTCTCTGGACAGATCCAGGCGCTGCGCTGAGTGAATAAATC 747
Db 181 AAAGGCAACTATGGGCTCTCTGGACAGATCCAGGCGCTGCGCTGAGTGAATAAATC 240
QY 748 GCCCACTTTGGGGGCGACCCCGAGCGTATCACCATCTTTGGTTCCGGGGCAGGGCCCTCC 807
Db 241 GCCCACTTTGGAGGTGACCCCTGAACGATCACTATCTTTGGGTCTGGTGACGGGCTCC 300
QY 808 TCGTCAACCTTTCTGATCTCTCCCACTTCCAGAGGGCTGTTCCAGAGGCCATCGCC 867
Db 301 TGTGTCAACTCTGCTGATCTCTTCCCACTTCCAGAGGACTGTTCCAGAGGCCATTCCT 360
QY 868 CAGAGTGGCACCGCATTTCCAGCTGGTCTGTCACTACCACTACCGCCCTCAAGTACACGGG 927
Db 361 CAAAGTGGTACTGCCATTTCCAGCTGGTCTGTCACTACCACTACCGCCCTCAAGCACACGGG 420
QY 928 CTGCTGGCAGACCAAGTGGGCTGTGACCGAGAGGACAGTGTGAAGCTGTGGAGTGTCTG 987
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QY 988 CCCCAGAGCCCTCCCGGAGCTGGTGACAGAGAGCTGGTGGAGCGCTGCCCTTACACATC 1047
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QY 1048 GCCTTTGGGCGGTGGTGAGTGGGACCTGGTCCCGATGACCTGAGATCTCTATGACAG 1107
Db 541 GCCTTTGGGCGGTGGTGAGCGGACGTANTCCCTGATGACCCCGAGATCTCTATGCAA 600
QY 1108 CAGGAGAGAACTCTCACTACGACATGCTCATCGCGCTCAACACGAGGAGAGGCGCTCAAG 1167
Db 601 CAGGCGGAACTCTCACTACGACATGCTCATTTGGTGTCAACACGAGAGAGGCTCTCAAG 660
QY 1168 TTCGTGGAGGACTCTGACAGAGCGGAGCGGTGTGTCTGCGAGGCGCTTTGACTTCACT 1227
Db 661 TTCGTGGAGGACTCTGACAGAGAGTGAAGACGCTGTCTGTCGCGGCTTTGACTTCACT 720
QY 1228 GTCTCCAACTTTGTGCAACACTGTATGGCTACCC 1262
Db 721 GTCTCCAACTTTGTGCAACACTTTGTACGGGTACCC 755

BO278029 1155 bp mRNA linear EST 07-MAY-2002
AGENCOURT 7061669 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5804959
5', mRNA sequence.
BO278029
VERSION BO278029.1 GI:20488237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1155)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ruben Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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QY 300 CACCTCTCCCGCCGCTGCGCAGAACCTGACGGGGCGCTCCCGCCATCATGCTGCC 359
 Db 121 CACCTCTCCCGCCGCTGCGCAGAACCTGACGGGGCGCTCCCGCCATCATGCTGCC 180
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 Db 181 TGTGTGTTTACCGAACAATGAGGGGGCGGCACTAGTGCAGAAACAGAGCGAGA 240
 QY 420 CTGCTCTACTCAACCTCTACGTGCGCCACCGAGGAGCGTCCGCTCACAAAAACGTGA 479
 Db 241 CTGCTCTACTCAACCTCTACGTGCGCCACCGAGGAGCGTCCGCTCACAAAAACGTGA 277
 QY 480 CGAGGAGCGCTCAATCCGCGACACAGATATCCGTGACCCCTGGGAAGAGCCTGTGAT 539
 Db 278 -----GATATCCGGGACTCTGGGAAGAAACCGGTGAT 309
 QY 540 GCTGTTTCTCCATGGGGCTCTACATGGAGGGAGCGGAAACATGTTGATGGCTCAT 599
 Db 310 GCTGTTTCTACAGGGGGCTCTACATGGAGGGAGCGGAAACATGTTGATGGCTCAT 369
 QY 600 CTTGGCTGCTATGGCAACGCTCATTTAGCCACGCTCAACTACCGTCTTGGGGTGTCTCG 659
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 QY 780 CATCTTTGTTCCGGGGCAGGGCTCTCTGCTGCAACTTCTGATCTCTCCACCATTC 839
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 QY 900 CAATACACCGCTCAAGTACACGGGGTGTCTGGCAGCAAGGTGGGCTGTGACCGAGA 959
 Db 670 CAATACACCGCTCANGTACACGGGGTGTCTGGCAGCAAGGTGGGCTGTGACCGAGA 729
 QY 960 GGACAGTCTGAGCTGTGAGTGTGTGCGCCGGAAGCCCTCCCGGAGCTGGT 1014
 Db 730 AGACAGCACTGAAGCTGTGAGTGTGTGCGCCGGAAGCTCTCCCGGAGCTAGT 784

RESULT 14
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 IMAGE: 6855212 5', mRNA sequence.
 VERSION CD348683
 KEYWORDS CD348683.1 GI:31140198
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 807)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-t@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousef1.html
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: pYX-5.

FEATURES

Location/Qualifiers
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 /mol_type="mRNA"
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 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_FYO"
 /note="Torgan: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGAGCAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
 BASE COUNT 162 a 236 c 238 g 170 t 1 others
 ORIGIN

Query Match 25.4%; Score 636.6; DB 14; Length 807;
 Best Local Similarity 89.6%; Pred. No. 2.4e-108;
 Matches 706; Conservative 0; Mismatches 80; Indels 2; Gaps 2;
 QY 753 CTTTGGGGGACCCCGAGCGTATCACATCTTTGGTTCGGGGCAGGGCTCTGCGT 812
 Db 1 CTTTGGAGGTGACCTGAACGATCATCTATCTTTGGGTCTGGTGCAGGGGCTCTGCT 60
 QY 813 CAACCTCTGATCTCTCCACCATTCAGAGGCTGTTCAGAGGCGCATTCGCCAGAG 872
 Db 61 CACTTGTGATCTTTCCACCACTCAGAGGACTGTTCAGAGAGCCATTTGCTCAAG 120
 QY 873 TGGCAGCGCATTTCCAGCTGCTGTCAACTACACGCGCTCAAGTACACGCGCTGCT 932
 Db 121 TGGTACTGCCATTTCCAGCTGCTGTCAACTACACGCGCTCAAGTACACGCGCTGCT 180
 QY 933 GGCAGCCAAAGTGGGCTGTGACGAGAGGACAGTGTGAGCTGTGGAGTGTTCGCCCG 992
 Db 181 GCGGCGCAAGTGGGCTGTGACCGAGAAGACAGCACTGAAGCTGTGGAGTGTTCGCCCG 240
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 Db 241 GAAGTCTTCCCGGAGCTAGTGGACAGGATGTACAGCTGCCCGCTACACATTCGCTT 300
 QY 1053 TGGCCCGCTGGTGTGATGGCGACAGTGTCCCGATGACCTGAGATCTCTATGACGAGGG 1112
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 QY 1113 AGAATTCCTCAACTACACATGCTCATCGCGCTCAACAGGAGAGGGCTCAAGTTCGT 1172
 Db 361 GGAATTCCTCAACTACACATGCTCATTTGTTGTCACACAGGAGAGGGTCTCAAGTTCGT 420
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 Db 481 CAATCTTGTGACAACTCTGTATGCTACCCGAGGCAAGGATGTCTTCGGAGGACCAT 540

QY 1293 CAAGTTTATGTACACAGACTGGCGCCGACCGGACAAATGGCGAAATGGCGCGCAAAACCCCT 1352
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 QY 1353 GTTGGCGCTCTTACTGACACCAATGGGTGGGACACAGCTGTGGCACTGCCAAGCTGCA 1412
 Db |||||
 QY 601 GTTGGCGCTCTTACTGACACCAATGGGTGGGACACAGCTGTGGCACTGCCAAGCTGCA 660
 Db |||||
 QY 1413 CGCGGACTACAGTCTCCGCTGTCTTACTTTTACACCTTCTACCACTTCTACCACTGCGAGCGGAGGG 1472
 Db |||||
 QY 1473 CGCGGCTAGTGGGAGAGTCCGCGGACCGGAGTGAAGTCCCTAAGTCTTTGGCGTGC 1532
 Db |||||
 QY 720 CGCGGAGAGTGGGAGAGAGCGGCGGACCGGAGAGCTG-CCTACGCTTTTGGTGTGCC 778
 Db |||||
 QY 1533 CATGTGG 1540
 Db |||||
 QY 779 ATGTGGG 786
 Db |||||

RESULT 15
 BQ771190
 LOCUS
 DEFINITION
 UI-M-F10-byx-f-03-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone
 IMAGE:6400514 5', mRNA sequence.
 BQ771190
 BQ771190.1 GI:21979666
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 REFERENCE
 1 (bases 1 to 729)
 AUTHORS
 NIH-MGC http://mgi.nhl.nih.gov/
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished
 COMMENT
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pyX-5.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6400514"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_hosts="DRI0B (11 phage resistant)"
 /clone_lib="NIH_BMAP_F10"
 /note="Organ: Brain; Vector: pyX-Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 to the protocol of Benton and Davis, 1978. The library was
 size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with Not I and then cloned
 directionally into pyX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CAGCCAGCAG. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
 Developing Mouse Nervous System, supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."
 BASE COUNT 149 a 205 c 206 g 168 t 1 others
 ORIGIN
 Query Match 25.1%; Score 629.4; DB 13; Length 729;
 Best Local Similarity 91.8%; Pred. NO. 5.2e-107;
 Matches 666; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 QY 535 GTGATGCTGTTTCTCCATGCGCGCTCTCATGAGAGGAGCCGGAACATGTTTCGATGGC 594
 Db 1 GTCATGCTGTTTCTACACGCGGCTCTCATGAGAGGAGCCGGAACATGTTTCGCGGC 60
 QY 595 TCAGTCTGCTGCTATGAGCAACGTCATTTAGCAGCAGCTCAACTACCGTCTTGGGTG 654
 Db 61 TCAGTCTGCTGCTATGAGCAATGTATCGTAGTCACACTCAACTACCGTCTTGGGTG 120
 QY 655 CTGCGTTTCTCAGCACCGGGGACCGAGCTGCAAAAGGCAACTATGGGCTCTCTGGACCAG 714
 Db 121 CTGCGTTTCTCAGCACTGTGTGACAGGCTGCAAAAGGCAACTATGGGCTCTCTGGACCAG 180
 QY 715 ATCCAGCCCTGCGTGGTCTAGTGAACAATCGCCCACTTTGGGGCGGACCCCGAGCGT 774
 Db 181 ATCCAGCCCTGCGTGGTCTAGTGAACAATCGCCCACTTTGGGGCGGACCCCGAGCGC 240
 QY 775 ATCAGCATCTTGGTTCGCGGCGAGGCGCTCTCGGTCAACCTCTGTATCTCTCCAC 834
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 QY 895 TCTGTCAACTACAGCGCGCTCAAGTACACCGGCTGCTGCGAGCAGCTGGAGTGGATGGGAC 1074
 Db 481 GACCAGGATGTACAGCGCTGCGCGCTACCAATTTGCCCTTTGGGCGCTGTGTGGAGCGGAC 540
 QY 1075 GTGGTCCCGATGACCTCGAGATCTCATGACAGGAGGAGATTCCTCAACTACGACATG 1134
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 QY 1255 GGCTACCC 1262
 Db 721 GGGTACCC 728

Search completed: February 19, 2004, 04:51:21
 Job time : 4894.86 secs

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Db 2220 TGGCTGAGCTCGTGGCCCACTGCAACCTGCAACAGCAGGAGTCTTCAACACACAG 2279
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QY 1981 GCCTATGACGCTTCCCGGGGACTCACGGGACTACTCCACGAGCTGAGCGTCAACG 2040
Db 2400 GCCTATGACGCTTCCCGGGGACTCACGGGACTACTCCACGAGCTGAGCGTCAACG 2459
QY 2041 GCGTGGGTGCTCCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
Db 2460 GCGTGGGTGCTCCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2519
QY 2101 CGGACCGCGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2160
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Db 2580 GGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2639
QY 2221 GAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2280
Db 2640 GAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2699
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QY 2341 CTTCTTTGGGCGCGCGGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
Db 2760 CTTCTTTGGGCGCGCGGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2819
QY 2401 CCACCGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2460
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RESULT 3
US-10-274-694-30
; Sequence 30, Application US/10274694
; Publication No. US20030143589A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BRUNS, Christopher M.
; APPLICANT: DAS, Debopriya
; APPLICANT: DING, Li
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: HAFALIA, April J.A.

APPLICANT: KEARNEY, Liam
APPLICANT: KHAN, Farrah A.
APPLICANT: LAL, Preeti G.
APPLICANT: LEE, Ernestine A.
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Yan
APPLICANT: NGUYEN, Damiel B.
APPLICANT: PATTERSON, Chandra S.
APPLICANT: RAMKUMAR, Javalaxmi
APPLICANT: RING, Huijun Z.
APPLICANT: SANJANWALA, Madhusudan M.
APPLICANT: TANG, Y. Tom
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THORNTON, Michael B.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: WALIA, Narinder K.
APPLICANT: XU, Yuming
APPLICANT: YANG, Junming
APPLICANT: YAO, Monique G.
APPLICANT: YUE, Henry
; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
; FILE REFERENCE: PI-0151 USA
; CURRENT APPLICATION NUMBER: US/10/274,694
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/221,837
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/220,037
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/218,948
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US01/21324
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/216,804
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2663
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030143589A1 7473875CB1
US-10-274-694-30

Query Match 90.3%; Score 2265.4; DB 13; Length 2663;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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 QY 2041 GCGTGGGTGCTCCCTCTCTTCTTCTAAACATCTGGGCTTTGCTGCGCTCTTACTACAAG 2100
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 Db 2337 GCGTGGCTGGTGGGCGGCGGCTGCTTCCCGCGCGGCGGCTGAGCTGCCACAGAGGAG 2396
 QY 2221 GAGCTGGTCTCACTGCGAGCTGAAGCGGGTGGTGGCGGCGGAGCCCTGCGG 2275
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RESULT 4

US-09-978-295A-374
 ; Sequence 374, Application US/09978295A
 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: KJavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napiez, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05

; PRIOR APPLICATION NUMBER: 60/084414
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084441
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 ; PRIOR APPLICATION NUMBER: 60/084637
 ; PRIOR FILING DATE: 1998-05-07
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 ; PRIOR APPLICATION NUMBER: 60/084640
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 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 36.4%; Score 912.2; DB 10; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.5e-206;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

Qy 108 CGGCGAGGCGCTTCCGCTGTGTGACACGGCTACGGCGAGTGGCGGTGCGGGG 167
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 Qy 168 CGAGCTCAACACAGATCTCGGCGCCCGCTGTCAGTCTTGGGGTGGCGGTGCGCCAC 227
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 Qy 228 GCGCGCCCTGGGCGCGCGCTTCCAGCGCTGAGCGCGCGCGCTGCGCGCGCGGT 287
 Db 232 ACCCGCCACTGGAGAGGCGGTTTCAGCGCGCGCGCGCGCGCGCGCTTCTCTGGACTGGCAT 291
 Qy 288 GCGCAACGCGCACCCCTGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 344
 Db 292 CCGAAATACTACTGAGTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 351
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 Qy 405 GAACAGAGCGAGCTGCTGT 464
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 Qy 465 CACAAAAAAGCTGACGAGGCG-----ACGCTCAATCCGCGCGCGCGCGCGCGCGCG 515
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 Qy 573 GACCGAAACATGTTTCATGGCTCAGTCTGGCTGCTATGCGCAACGCTTATGTAGCCAC 632
 Db 592 CACCGGCAACATGATTCACCGGAGCATTTTGGCAAGTACGAAACGCTCATCGTGTATCAC 651
 Qy 633 GCTCAACTACCGTCTTGGGTGCTGCTTTCTCAGCACCGGGGACGAGTGTGCAAAAGG 692
 Db 652 CATTAACCTACCGTCTGGGAATACTAGGGTTTTTAAGTACCGGTACCGAGCAGCAAAAGG 711
 Qy 693 CAACATATGGCTCTGACACAGATCCAGGCGCTGCGCTCAGTCAATAAATCATGCGCCA 752
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RESULT 5

US-09-978-697-374
 ; Sequence 374, Application US/09978697
 ; Patent No. US20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Shexman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C27
 ; CURRENT APPLICATION NUMBER: US/09/978,697
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 36.4%; Score 912.2; DB 10; Length 3113;

Best Local Similarity 64.7%; Pred. No. 2.5e-206;

Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGCGGAGGAGCGCTTCCCGGTGGTGAACACAGCGCTTACGGGCGAGTGCGGGGTGGCGGG 167
 DB 112 CAGCCNAGCACAGTATCCAGTTGTCAACACAAATATGCAAAATCCGGGGCTAAGAAC 171
 QY 168 CGAGCTCAACACAGAGATCCTGGGCGCGGTCTGTGAGTCTTTGGGGGTGCGCTACGCCAC 227
 DB 172 ACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCCTC 231
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Db 1969 AATCACTCTCTCCCAACATCCCAACCACTTAAGGACCTTCAAAAACAGGCGCTGAGGA 2028
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Qy 2163 GGTGCTGTGGTGGGCGCCCTGCTTCCCGCGCGCGCGCTGAGTGGCCACAGAGGAGGA 2222
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Qy 2283 GGGCGCTCGCTGCGCGCGCGGCTACACCTGCGCGCTGCGCGGCGACCGGACGATGTGCC 2342
Db 2305 GAGGTGACCTGCGCGCGGAGACTACACCTCACTGCGCGCGTGGCGAGATGATATCC 2364
Qy 2343 TCTTGTGGCGCGCGGCGCTTGAACCTGCTGCGCGAGTGGCGCTG 2385
Db 2365 ACTTATGACGCAAAACACCATCATCATGATTCCAAACACACTG 2407

RESULT 6

US-09-978-192A-374
; Sequence 374, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06

QY 1653 GCGGAGGATACCAAGTTTCATCCACACCAAGCCCAATCGTTTCGAGGAGGTGGTGTGAG 1712
 Db 1669 TCTCAGGATACCAAGTTTCATCCACACCAAGCCCAATCGTTTCGAGGAGGTGGTGTGAG 1728
 QY 1713 CAAATTCACACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1772
 Db 1729 CAAATTCACACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1788
 QY 1773 CAAATTCACACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1832
 Db 1789 TCACTACCGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1848
 QY 1833 GCA-----CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1893
 Db 1849 GAGCAGAGATATTCAGATATTCAGATATTCAGATATTCAGATATTCAGATATTCAGAT 1908
 QY 1884 CTGGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1943
 Db 1909 ATTTCCTATGACACCGGCGGAGTCTCCGCGCAAGATATGCGCAACCAACCAACCGCC 1968
 QY 1944 CTGCTCTCCGAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1992
 Db 1969 AATCACTCTGTCGCAACATCCCAACACTCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2028
 QY 1983 CTATGACGCTTCCCGGCGGAGTCTACGCGGAGTCTACGCGGAGTCTACGCGGAGTCTAC 2042
 Db 2029 CACAACTGCTCTATTGAAACCAAGAGATATTCACCAAGATATTCACCAAGATATTCAC 2088
 QY 2043 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2102
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 QY 2103 GGACGGGCGGAGGAGTGGCTGAGCGGCTTACGCGGCTTACGCGGCTTACGCGGCTTACG 2162
 Db 2149 GGACAAAGGCGGAGGAGTGGCTGAGCGGCTTACGCGGCTTACGCGGCTTACGCGGCTT 2208
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 Db 2365 ACTTATGACGCAACCAACCACTCACCATGATTCACAAACACACTG 2407

RESULT 7

US-09-999-932A-374
 ; Sequence 374, Application US/099999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C63
 ; CURRENT APPLICATION NUMBER: US/09/999,832A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
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Query Match 36.4%; Score 912.2; DB 10; Length 3113;

Best Local Similarity 64.7%; Pred. No. 2.5e-206;

Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

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Db	172	ACCGTTACCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGT	CCCCCTATGCCCTC	231
QY	228	CGCGCCCTGGGCGCGCCCGCTTCCAGCGCGCTGAGGCGCCCGCTGT	GTGCGCGGGGT	287
Db	232	ACCCCCCACTGAGAGAGGCGGTTTCAGCCCCCAAGAACCCCGCTCT	CTGTGACTGGCAT	291
QY	288	CGCACAACGCCACCCCTGCCCGCGCGTGTCCGCGAACCTGCAACG	---GGGCGCTGCC	344
Db	292	CGGAATACTACTCAGTTTGTCTGTGTGTGCGCCCGCAGCACCTGT	GATGAGATCCTTACT	351
QY	345	CGCCATCATGCTGCTGTGTGTTCACCGACAACTTGGAGGCGCGCC	CGCCACCTACGTCA	404
Db	352	GCATGACATGTGCGCCATCTGGTTACGCCCAATTTGGATACTTTG	TGATGACCTATGTTCA	411
QY	405	GAACACGAGCGGAGTCTGCTGTACCTCAACCTCTAGTGCCCGCC	CGGAGGACGCTCGCT	464
Db	412	AGATCAAAATGAGACTGCCCTTACTTAAACATCTAGTGCCCGC	CGGAAGATGGAGCAA	471
QY	465	CACAAAAAAGTACGAGGCGG-----ACGCTCAATCCGCGCAC	CACAGATATCCG	515
Db	472	CACAAAGAAAAACGAGATGATATAACGAGTAATGACCGTGTG	GAAGACGAGATATTC	531
QY	516	TGACCCCTG---GGAAGAGCGCTGTGATGCTGCTTTCTCCATG	CGCGCTCCTACATGAGGG	572
Db	532	TGATCAGAACAGTAGAAGAGCCGCTCATGCTCTATATCATCG	GGGAGTCTTACATGGAGG	591

APPLICANT: Kljavin, Ivar J.
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APPLICANT: Tumas, Daniel
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
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PRIOR APPLICATION NUMBER: 60/083545
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PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/085582
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 36.4%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%; Pred. No. 2,5e-206;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

Qy 108 CGCGAGGAGCGTTCCTCCGGTGTGAACACGCGCTACGGCGGAGTGGCGGTGGCGG 167
Db 112 CAGCAAGCACAGTATCCAGTTGTCACACAAATATGCAAAATCCGGGGCTAAGAAC 171
Qy 168 CGAGCTCAACACAGAGATCTCGGCGCGCTGCGAGTTCTTGGGGTGGCGTACGCCAC 227
Db 172 ACCGTTACCAATGAGATCTTGGGTCAAGTGGAGAGTACTTAGGGTCCCTTATGCCTC 231
Qy 228 GCGGCCCTCGGGCGCGCGCTTCCAGCGCGCTGAGGCGCGCGCTCGTGGCGCGGCGT 287
Db 232 ACCCCCACTGGAGAGAGGCGGTTTCAGCCCCCAGAAACCCCGCTCCTCGACTGGCAT 291
Qy 288 GCGCAAGCCACACCTCGCGCGCGCTGCGCGAGAACCTGCAGC---GGGCGCTGCC 344
Db 292 CCGAAATACATACAGTTCTGCTGTGTCGCCCCAGACCTCGATGAGATCTCTTACT 351
Qy 345 CGCCATCATGCTGCTGTGGTTTCAACGACAACTTGGAGGCGCGCGCCACCTACGTGCA 404
Db 352 GCATGACATGCTGCCATCTGGTTTACCGCCAATTGGATACCTTGTGATGACCTATCTCA 411
Qy 405 GAACGAGGAGGAGTCTGCTGTACCTCAACCTTACGTGCCACCGAGGACGGTCCGCT 464
Db 412 AGATCAAAATGAGACTGCTTACTTAAACATCTAGTGCCTCCACGAGATGGAGCCAA 471
Qy 465 CACAAAAAACGTCAGGAGCG-----ACGCTCAATCCGCGCAGACACATATCCG 515
Db 472 CACAAAGAAACACAGATGATATACGAGTATGACCGTGGTGAAGACAAATATCA 531
Qy 516 TGACCCCTG---GGAAGAGCGTGTGATGCTGTTTCTCCATGGCGGCTCTACATGAGGG 572
Db 532 TGATCAGAAACAGTAAAGACCGCTCATGGTCTATATCCATGGGGGATCTTACATGGAGGG 591
Qy 573 GACCGAAACATGTTCCGATGCTCAGTCCCTGGCTGCTATGGCAACGTCATTGTAGCCAC 632

Db 592 CACCGGCACATGATTGACGGCAGCATTTTGGCAAGCTACGGAACGTCATCTGTATCAC 651
Qy 633 GCTCAACTACCGTCTTGGGTGCTCGGTTTCTCAGCACCGGGGACAGGCTCAAAAGG 692
Db 652 CATTAACCTACCGTCTGGATATCTAGGTTTAACTACCGGTGACCGGACGCAAAAGG 711
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Db 772 CTTTGGCGGGGACCCCAAGAGAGTACCATTCTTGGCTCGGGGCTCGGGCTCTCTGT 831
Qy 813 CAACCTTCTGATCTCTCCACCATTCAGAAAGGCTGTTCCAGAAAGGCTATCGCCACAG 872
Db 832 CAGCCTGTTGACCTGTCTCCACTACTCAGAAAGGCTCTTCCAGAAAGGCTATCTCAGAG 891
Qy 873 TGGCACCGCCATTTCCAGCTGGTCTGTCACTACAGCGCTCAAGTACACGCGGCTGCT 932
Db 892 CGGCACCGCCCTGTCCAGCTGGGAGTGAACCTACAGCGCGCCCAAGTACACTCGATATT 951
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Qy 1413 CGCGACTACAGTCTCCGCTTACTTACACCTTCTACACCACTGCGAGGCGGAGG 1472
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Qy 1473 CGGGCTCAGTGGGAGATGCGGCGACCGGGATGAACCTGCGCTTATGTTCTTGGCGTGCC 1532
Db 1489 GAAGCCAGCTGGGAGATTCGGCCCATGGTATGAGTCTCCCTATGTTCTTGGCATCCC 1548
Qy 1533 CATGTGGTGGCAGCGACCTCTTCCCTCTTAACTTCTCCAGAAATGACGTCATGCTCAG 1592
Db 1549 CATGATCGTCCCGAGCTCTTCACTTGTGTTAACTTTTCCAAAGAACGACGTCATGCTCAG 1608
Qy 1593 TGCGGTGTGATGACCTACTGGAACCACTTCGCAAGACTGGGACCCCAACAGCCGCT 1652
Db 1609 CGCGGTGTGATGACCTACTGGAACCACTTCGCAAGACTGCTGATCAAAATCAACAGT 1668
Qy 1653 GCGCGAGGATACCAAGTTTCATCCACCAAGCCCAATGCTTTCGAGGAGGTGGTGTGAG 1712

1669 TCCTCAGGATACCAAGTTTCATTTCACACAAACCCACCGCTTTGAAGAAGTGGCTGGTC 1728
1713 CAAATTCACAGCAGAGAGCAGTATCTGCATAGGCTGAAGCCACGCTGGCTGA 1772
1729 CAAGTATAATCCCAAGACCAAGCTCTATCTGCATATGGCTTGAACCCAGAGTGAGAGA 1788
1773 CAACTACCGCGCCACAAAGGTGGCTTCTGGCTGGAGCTCGTGCCCACTGCAACACCT 1832
1789 TCACCTACCGGGCAACGAAGTGGCTTCTGGTTGGAACCTGTTCTCTCATTTGCACAACT 1848
1833 GCA-----CACGAGCTCTTACACACACACAGCGCTGCTCTCTACGCGCAGCG 1883
1849 GAACGAGATATTCAGATATGTTTCAACACACCAAGGTTCTCCACACAGCATGATC 1908
1884 CTGGCGGCTGCTCCCGCTGGCGCCCGGCGACACGCGCGCCCGCGCGCTGCGCAC 1943
1909 ATTTCCTATGCAACCGCGGATCTCCCGCCAGATATGGCCACACCAACGCCACG 1968
1944 CTGCTCCCGAGCCGAGCCGAGC-----CCGCCCCAAGGGC 1982
1969 AATCACTCTGCGCAACAATCCCAACACCTCTAAGGACCTTCACAAACAGGGCTGAGGA 2028
1983 CTATGACCGCTTCCCGGGAGCTCAGGAGCTACTCCAGGAGCTGAGCGTCACCGTGGC 2042
2029 CAACTGCTCTATTGAACCAACAGAGATTTCCACCGNATTAAGTGTACCAATTC 2088
2043 CGTGGGTGCTCTCTCTCTTCTCAACATCTGGCTTTGCTGCTCTCTACTACAAGC 2102
2089 CGTGGGGGCTCGCTCTCTCTCTCAACATCTAGCTTTTGGCGGCTGTACTACAAA 2148
2103 GACCGGGGAGGAGCTGGGTGAGGGGCTTACCCACTGCGGCTCAGGCTCTGG 2162
2149 GGAACAGAGGCGCATAGACTACAGGGGCGCCAGTCCCGAGAGAAACACCAATGA 2208
2163 CGTGCCTGTGGGGGCGCCCTGCTCCCGCGGGCGCTGAGCTGCCACAGAGAGGA 2222
2209 TATCGTCTACATCCAGAACGAAGATCATGCTCTGAGAGTGAAGAGCTGGAACGA 2268
2223 GCTGGTGTCACTGAGCTGAAGGGGTGGTGGCTGGGGGCGACCTGCGGAGCTCT 2282
2269 TCAGGAGTGTAGTCTCGAG-----GCACAGACACACT 2304
2283 GCGCCCTGCTGCGCCCGGCTGACTACACCTGCTGCTGCGCGGGCAGCGAGTGTGCC 2342
2305 GAGCTCACTGCGCCGCGAGACTACACCTCAGCTGCGCGGCTGCGCGAGTGACATCC 2364
2343 TCTTTTGGCCCGGGGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2385
2365 ACTTATGCGCCAAACACCATCACCATGATGATTCACAAACACACTG 2407

RESULT 9

US-09-978-608A-374
; Sequence 374, Application US/09978608A
; Publication No. US20030045462A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 374
; LENGTH: 3113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-374

Query Match 36.4%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%; Pred. No. 2.5e-206;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGCGAGGAGCGCTTCCCGTGGTGAACACGGCTACGGCGAGTGGCGGTGGCGGCG 167
Db 112 CAGCCAAGCACATATCCAGTTGTCAACACAAATATGCAAAATCCGGGGCTTAAGAAC 171
QY 168 CGAGCTCAACACAGAGATCTGGGCGCCCTGCTGCAGTTCTTTGGGCGTGCCCTACGCCAC 227
Db 172 ACCTTACCAATAGATCTTGGTCCAGTGGAGCAGTACTTAGGGGTCCCTTATGCCTC 231
QY 228 GCGCGCCCTGGGCGCGCGCTTTCAGCGCTGAGGCGCCCGCTCTGTGGCGCGCGCT 287
Db 232 ACCCGCCACTGGAGAGAGCGGTTTCAGCGCCCGAGAACCCCGCTCTCTGTGGACTGGCAT 291
QY 288 GCGCAACGCCACACACCTGCGCGCCCGCTGCGCGCAGAACCTCAGCG---GGCGGTGCC 344
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QY 345 CGCCATCATCTGCTGTGTGTTACCGACAACCTTGGAGGCGCGCCACCTACGTGCA 404
Db 352 GCATGACATCTGCCCATCTGGTTTACCGCAATTTGGATCTTTGATGACCTATGTTC 411
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QY 516 TGACCTCTG---GGAGAGCTGTGATGCTGTTCTCCATGGCGGCTCTTACATGGAGGG 572
Db 532 TGATCAGACAGTAAGAAGCCCGTCACTGCTATATCCATGGGGGATCTTACATGGAGGG 591
QY 573 GACCGGAAACATGTTCCATGGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
Db 592 CACCGGCAACATGATTCAGCGGCACTTTTGGCAAGCTACGGAACCTCATCGTGATCAC 651
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Db 712 CAACCTATGGGCTCTCGGATCAGATTCAGACCTGCGGTGGATTCAGGAGATGTGGGAGC 771
QY 753 CTTTGGGGGCGACCCCGAGCGATATCAACATCTTTGGTTCGGGGCAGGGGCTCTCTCGGT 812

Db	772	CTTTGGCGGGGACCCCAAGAGAGTGAACAATCTTTTGGCTCGGGGGCTCGGGGCTCTCTGTGT	831
Qy	813	CAACCTTTCTGATCTCTCCACCATTCAGAAAGGGCTGTTCCAGAAGCCATCGCCACAG	872
Db	832	CAGCCTGTTGACCCCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGCCATCATTCAGAG	891
Qy	873	TGGACACGCCATTTCCAGCTGGTCTGTCAACTACCAGCGCTCAAGTACACGCGGCTGCT	932
Db	892	CGGACACGCCCTGTCCAGCTGGGCAGTGAATACACGCGCGCAAGTACACTCGGATATT	951
Qy	933	GGACGCCAAGGTGGGCTGTGACCGAGAGGACAGTGCTGAAGCTGTGAGTGTCTTGCGCCG	992
Db	952	GGCAGACAAGGTGGCTGCACATGCTGTGACACCAACCGCATGGTAGAATGCCTCGGGA	1011
Qy	993	GAAGCCCTCCGGGAGCTGGTGGACAGGAGCTGTCAGCTTCCCGCTTACCACTATCGCCTT	1052
Db	1012	CAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCGCGCCACCTTACCACATAGCCTT	1071
Qy	1053	TGGGCCCGTGGTGGATGGCAGCTGGTCCCGGATGACCTGAGATCTCATGTCAGAGGG	1112
Db	1072	CGGCGCGGTGATCGACGCGCAGCTCATCCAGACGACCCCCAGATCTGTATGGAGCAGG	1131
Qy	1113	AGAATTCCTCAACTACACATGTCTATCGGCGTCAACACGGGAGAGGGCTCAAGTTCTGT	1172
Db	1132	CGAGTTCTCTCAACTACACACTCATGCTGGGCGTCAACCAAGGGGAAAGGCTGAAGTTCTGT	1191
Qy	1173	GGAGGACTCTGCAGAGACGAGACGGTGTGTGTCGACGCGCTTTTGACTTCTACTGCTCTC	1232
Db	1192	GGACGGCATCTGTGATTAACGAGACGGTGTGACGCCACGACTTTTGACTTCTCCGTGTC	1251
Qy	1233	CAACTTTTGGACAACTGTATGCTACCCGGGAAGCAAGGATGTGCTTCGGGAGACCAT	1292
Db	1252	CAACTTCGTGGACAACTTTTACGCTACCTGAGGGGAAAGACACTTTGCGGAGACTAT	1311
Qy	1293	CAAGTTTATGTACACAGACTGGGCGGACCGGCAATGGCGGAAATGGCGCGCAAAACCTT	1352
Db	1312	CAAGTTTATGTACACAGACTGGGCGGCAATAGGAAACCCCGGACGCGGCGGAAACCTT	1371
Qy	1353	GCTGGCGCTCTTTACTGACCACCAATGGGTGGCACACAGCTGTGGCCACTGCCAAGCTGCA	1412
Db	1372	GGTGGCTCTCTTTACTGACCAACCAAGTGGTGGCCCGCGCGTGGCC---GCCGACCTGCA	1428
Qy	1413	CGCGACTACAGTCTCCGTCTACTTTTACACTTCTACCACTGCGCAGCGCGGAGGG	1472
Db	1429	CGGCACTAGCGGTCCCCCACTACTTCTATGCTCTCTATCATCACTGCCCAAGCAAAAT	1488
Qy	1473	CCGCGCTGAGTGGGACAGATCGGCGCACGGGATGAATCCCTATGTCTTTTGGCGTGCC	1532
Db	1489	GAAGCCAGCTGGCAGATTCGGCCCATGTGTATGAGTCCCTATGTCTTTCGGCATGCC	1548
Qy	1533	CATGGTGGGTGCCACCGACCTCTTCCCTGTAACTTCTCAGAATGAAGTCAATGCTCAG	1592
Db	1549	CATGATCGGTCCCAACGAGCTCTTTCAGTTGTAACCTTTTCCAGAAAGCAAGCTCATGCTCAG	1608
Qy	1593	TGCGGTGTCATGACCTACTTGGACCAACTTCCGACAGACTGGGACCCCAACACAGCGGT	1652
Db	1609	CGCGGTGGTCATGACCTACTTGGACCAACTTCCGCAAACTGGTGATCCAATCAACAGT	1668
Qy	1653	CGCGCAGGATACCAAGTTTCATCCACACCAAGCCCAATCGCTTCGAGAGAGTGTGTGGAG	1712
Db	1669	TCCTCAGGATACCAAGTTTCATTCACACAAACCAACCCGCTTTTGAAGAGTGGCTGGTC	1728
Qy	1713	CAAAATCAACGACGAGAGACGATATCTGCAATAGGCTTGAAGCCAGCGGTGCTGTA	1772
Db	1729	CAAGTATATTCCTCAAGACCAAGTCTATCTGCAATTTGGCTTTGAAACCCAGAGTGAAGA	1788
Qy	1773	CAACTACCGGCGCAACCAAGGTGGCTTCTGGCTGGAGCTCGTGGCCCACTGTCACAACTT	1832
Db	1789	TCCTACCGGCAACGAAGTGGCTTCTGTTGGAACTCGTTCTCTCATTTTGACAACTT	1848
Qy	1833	GCA-----CACGGAGCTTTTCAACCAACCAACCGCGCTCGCTCCCTTAOCGCACGGG	1883
Db	1849	GAACGAGATATTCCAGTATGTTTCAACCAACCAAAAGTTTCTCCACCAACATGACATC	1908

1984	QY	CTGCGCGCTGTCTCCCGCGTGGCGCCCGGGGACACAGCGGGGCCCGCGCGCTGCAC	1943
1909	DB	ATTTCCCTATGGCACCCGGCGATCTCCGGCAAGATATGGCAACCAACGCGCCAGC	1968
1944	QY	CCTGCTCCCGAGCCCGAGCCCGAGC-----CCGGCCCCAAGGGC	1982
1969	DB	AATCACTCCTGCCAACANTCCCAACACTCTAAGGACCTCACAAAACAGGGCTGAGGA	2028
1983	QY	CTATGACGGCTTCCCGGGGACTCACGGGACTACTCCACGAGCTGAGCGTCAACCTGGC	2042
2029	DB	CACAACCTGTCTCTATTGAAACCAACAGAGATTATTCACCGAAATTAAAGTGTCAACATTC	2088
2043	QY	CGTGGGTGCTCCCTCTCTCTCTCAACTCTCTGGGCTTTTGCTGGCCTCTACTACAAAGC	2102
2089	DB	CGTGGGGCGTGGTCTCTCTCTCAACATCTAGCTTTTTCGGGCGCTGTACTACAAA	2148
2103	QY	GGACCGGGGAGAGAGTGGCGGTGACGGCGGCTTAGCCCACTTGGCGGGCTCAGGCTCTGG	2162
2149	DB	GGACAAGAGGGCCATGAGACTCACAGGCGCCCGAGTCCCACAGAAACACCAAAATGA	2208
2163	QY	CGTGCTGTGGGGGCCCCCTGTCTCCCGCGGGGCGGTGAGTGTGCCACACAGAGGAGGA	2222
2209	DB	TATCGCTCATCCAGAACGAAGAGATCATGTCTCTGCAGATGAAGCAGCTGGNACAGA	2268
2223	QY	GCTGGTGTCACTGAGCTGAAGCGGGGTGTGTGGTGTGGGGCGGACCTGCCGAGGCTCT	2282
2269	DB	TCACGAGTGTGAGTCGTGCAG-----GCACACACACACT	2304
2283	QY	GCGCCCTGCTGCCCGCCGACTACACCTTGGCCCTGCGCGGGGACCGGACGATGTGC	2342
2305	DB	GAGCTCACCTGCGCCGCGAGACTACACCTTCACGCTGCGCGCGGTGCGGCAGTGCATCCC	2364
2343	QY	TCTCTGGCCCCCGGGGCCCTGACCTCTGTGCCCAAGTGGCTG	2385
2365	DB	ACTTATGACGCGCAAAACCACTCATCCACTGATTCACAAACACACTG	2407

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RESULT 10
US -98-978-585A-374
; Sequence 374, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deencovets, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: Secured and Trans
; TITLE OF INVENTION: Acids Encoding t
; FILE REFERENCES: P2630P1C15

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; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILLING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      36.4%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%; Pred. No. 2.5e+206;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGGCGAGGAGCGCTCCCGTGTGTGAACGGGCTACGGCGAGTGCAGCGGTGTGCGGCG 167
DB 112 CAGCAGACAGATCCAGTTGTCAACACAATATGCAAAATCGGGGCGCTAAGAAC 171
QY 168 CGAGCTCAACACAGAGATCCTGGGCGCGGTGFGCAGTTCTTTGGGCGGTGCCTACGGCAC 227
DB 172 ACGGTTACCCAATAGATCTTGGGTCCAGTGGAGCAGTACTTATGGGTGCCCTATGCGCTC 231
QY 228 GCGCGCCCTGGGCGCGCGCTTCCAGCGCGCTGAGGGCGCCGCTCTGTGGCGCCGCGGT 287
DB 232 ACCCCCACTGGAGAGGCGGTTTCAGCCCCAGAACCCCGCTCTCTTGGAGTGGCAT 291
QY 288 GCGCAACGCCACACACCTCCCGCCCGCTGCCCGCAGAACCTGCACG---GGCGGTGCC 344
DB 292 CGAAATACTACTCACTTGTGCTGTGTGCCCGCCAGCACCTGGATGAGAGATCCTTACT 351
QY 345 CGGCATCATGCTGCCTGTGTGGTTACCGACAACTTGGAGGCGGCCGCCACCTACGTGCA 404
DB 352 GATGACATGCTGCCCATCTGGTTTACCGCCAAATTTGGATACTTTGTATGACCTTATGTTCA 411
QY 405 GAACCAAGCGAGGACTGCTGTACCTCAACTCTACGTGCCCCACCGAGGACCGTCCGCT 464
DB 412 AGATCAAAATGAAGACTGCTTTTACTTAAACATCTACGTGCCCAACGAGATGGAGCAA 471
QY 465 CACAAAAAACGTGACGAGGCG-----AGCTCAATCCGCCACACACAGATATCCG 515
DB 472 CACAAAGAAAACGCGAGATGATATACGATATAGACCGTGTGTGAAGACGAAGATATCA 531
QY 516 TGACCCCTG---GGAAGAAGCCTGTATGTGTCTTCTCCATGGCGGCTCTTACATGAGGG 572
DB 532 TGATCAGACAGTAAGAGCCCGTCTATGTCTATATCCATGGGGATCTTTACATGGAGGG 591
QY 573 GACCGAACAATGTTTCATGGCTCAGTCTGCTGCTATGGCAAAGTCAATTGTAGCCAC 632
DB 592 CACCGCACATGATTGACGGCAGCATTTGGCAAGCTACGGAAACGTCACTCGTATCAC 651
QY 633 GCTCAACTACCGTCTTGGGGTGTCCGGTTTCTCAGCACCGGGGACAGGCTCCAAAAGG 692
DB 652 CATTACTACCGTCTGGAACTACTAGGGTTTAAGTACCGGTGACAGGACGCAAAAGG 711
QY 693 CAACATAGGCTCCTCGAACAGATCCAGGCCCTGCGCTGGCTCAGTGAAGAACATCGCCCA 752
DB 712 CAACATAGGCTCCTCGATCAGATTCAGACACTGCGGTGGATTTGAGGAGAAATGTGGAGC 771
QY 753 CTTTGGGGGCGACCCGAGCGTATCAACATCTTTGGTTCCGGGCGAGGGGCTCTCTCGGT 812
DB 772 CTTTGGCGGGACCCCAAGAGTGTACCATCTTTTGGCTCGGGGGCTGGGGCTCTCTGT 831
QY 813 CAACCTTCTGATCCTCTCCCAACATTCAGAAGGGCTGTTCCAGAGGCCATTCGCCACAG 872
DB 832 CAGCCTGTTGACCCCTGTCCCACTACTCAGAAGGTCTCTTCAGAAGGCCATCATTCAGAG 891
QY 873 TGCAACCGCCATTTCCAGCTGTGTGTCAACTACACGCGCTCAAGTACACGCGGCTGCT 932
DB 892 CGGACCGCCCTGTCCAGCTGGCAGTGAATACACAGCGCGCCAGTACACTCGGATATT 951
QY 933 GGCAGCCAAAGGTGGGTGTGACCGAGAGGACATGTGTGAAGCTGTGAGTGTCTTGCCCGC 992
DB 952 GGCAGACAAGCTCGGTGTCAATGATGTGGACACCAACGACATGATGAATGCTCTCGCGAA 1011

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Db 1012 CAAGAACTACAGAGAGCTATCCAGCAGACCATACCCCGGCCACCTACACATAGCCTT 1071
QY 1053 TGGSCCGTGGTGGATGGCGACGTGGTCCCGATGACCTGATCTCATGCGAGAGG 1112
Db 1072 CGGGCCGGTGTATCGACGGCGAGCTATCCAGACGACCCCGATCTCTATGGAGCAGG 1131
QY 1113 AGAATTCCTCAACTACAGATGCTCATPCGCGCTCAACAGGGAGAGGGCTCAAGTTCTT 1172
Db 1132 CGAGTTCTCTCAACTACAGATGCTATGCTGGCGCTCAACAGGGAGAGGGCTGAAGTTCTT 1191
QY 1173 GGAGGACTCTGAGAGAGCGAGAGCGGTGTCTGCGAGCGCTTTGACTTCACTGCTCTC 1232
Db 1192 GGACGGGATCGTGATACAGAGAGCGGTGTGACGCCAAGCATTTGACTTCTCCGTGTC 1251
QY 1233 CAACCTTTGTGGACAACCTGTATGGCTACCCGGAAGGCAAGGATGTGCTTCGGGAGACCAT 1292
Db 1252 CAACCTCGTGGACAACCTTTACGGCTACCTCTGAAGGMAAGACACTTTGCGGAGACTAT 1311
QY 1293 CAAGTTTATGTACAGACTGGGCGGACCGGAGCAATGGGMAATGCGCGCAAAACCTT 1352
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QY 1353 GCTGGCGCTCTTTACTGACCAACCAATGGGTGGCAGCTGTGGCCACTGCCAAGCTGCA 1412
Db 1372 GTTGGCTCTCTTTACTGACCAACCAAGTGGGTGGCCCGCGTGCGCC---GCCACTGCA 1428
QY 1413 CGCGACTACAGCTCTCCGCTACTTTTACACCTTTACCACTACCTGCGAGCGGAGG 1472
Db 1429 CGCGAGTACGGCTCCCGCACTACTTCTATGCTTCTATCATCACTGCCAAGCGAAT 1488
QY 1473 CGGCGCTGAGTGGCAGATCGGCGACGGGATGAATGCCCTATGCTTTGGCGTGC 1532
Db 1489 GAAGCCGAGTGGCGAGATTGGCGCCATGTGTATGAGTCCCTATGCTTTCGGCATCC 1548
QY 1533 CATGGTGGTGGCCACCGACCTCTTCCCTGTAACTTCTCCAAGATGAGCTCATGCTCAG 1592
Db 1549 CATGATCGTCCACCGAGCTCTTCACTGTAACTTTCCAGAACGAGCTCATGCTCAG 1608
QY 1593 TGCGTGGTATGACTTACGACCACTTCCGCAAGACTGGGAGACCCCAACAGCGGT 1652
Db 1609 CGCGTGGTATGACTTACGACCACTTCCGCAAGACTGGGAGTCCAAATCAACCACT 1668
QY 1653 GCGCAGATACCAAGTTCTACACACCAAGCCAACTCGCTTCAGAGAGTGTGTGGAG 1712
Db 1669 TCCTCAGATACCAAGTTCTATCACAAACCCACCGCTTTGAAGAGTGGCTGGTC 1728
QY 1713 CAATTCACAGCAAGAGAGAGTATCTGCATAGGCTGAAGCCACGGTGGCTGA 1772
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Db 1849 GAACGAGATATTCAGTATGTTTCAACAAACCAAGAGTTCTCCACACGAGATGATC 1908
QY 1884 CTGGCGCTCTGCTCCCGCTGGCGCCCGGCGCACAGCGCGCGCCCGCGCTGCCAC 1943
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QY 1944 CTTGCTCCCGAGCGGAGCCGAGC-----CGGGCCCAAGGCG 1982
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QY 2043 CGTGGGTGCTCTCTCTCTCAACATCTCGGCTTGTGCTGCTCTCTACAGCG 2102

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Db 2149 GGACAAGAGGCGCCATGAGACTCAGAGGCGCCAGTCCCGAGAGAAACACCAATGA 2208
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Db 2209 TATCGCTCACATTCAGAACAGAGATCATGTCTCTGAGATGAAGCAGCTGGAAACGA 2268
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Db 2269 TCACGAGTGTGAGTGGCTGAG-----GCACAGACACACT 2304
QY 2283 GCGCCTGCTCCCGCGCGACTACCTGGCCCTGCGCGGCGACCGGACGATGTGCC 2342
Db 2305 GAGGCTCACCTGCGCGCGAGACTACCTCAGCTGCGCGGCTCGCCAGATGATCATCCC 2364
QY 2343 TCTCTTGGCCCCGGGGCGCTGACCTGCTGCCAGTGGCGCTG 2385
Db 2365 ACTTATGACGCCAAACACCATCATCATGATTCCAAACACACTG 2407

RESULT 12

US-09-978-403A-374
; Sequence 374, Application US/09978403A

; Publication No. US20030050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-03-10

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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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QY	108	CGCGCAGAGCGCTTC	CGCGTGTGTGAACACGGCTACGGCGCAGTGTGCGGGTGTGCGGCG	167	
Db	112	CAGCCACACAGATAT	CAAGTTGTCAACAATAATTATGGCAAAATTC	CGGGCGCTTAAGAAC	171
QY	168	CGAGCTCAACACAGAT	CTCTGGGCCCCGCTGTGCAGTTCTTTGGCGGTGCCCTACGGCCAC	227	
Db	172	ACCGTTACCCAAATG	ATCTTGGGTCCAGTGGAGCAGTACTTTAGGGTCCCCCTATGCGCTC	231	
QY	228	GCGCGCCCTGGGCGCC	CGCGCTTCAGCCGCTGAGGCGCCGCGCTGTGTGGCGCGGGGT	287	
Db	232	ACCCGCCACTCGAGAG	AGCGGGTTTTCAGCCCCCAGAACCCCGCTCCTCTGCACTGGCAT	291	
QY	288	GCGCAAAGCCACACCT	CGCGCCGCGCTGCCCGCAGAACCTGTCAAG--	GGGCGCTGCC	344
Db	292	CGAAATACTACTCAG	TTTGTCTGTGTGCCCCCAGCACCTTGATGAGATCCTTACT	351	
QY	345	CGCCATCATGCTGCT	GTGTGTGTACCCGACAACTTGGAGGCGCGCCACCTACGTGCA	404	
Db	352	GCATGACATGCTGCC	ATCTGGTTTACCGCAATTTGGATACTTTTGATGACTATGTTC	411	
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QY	465	CACAAAAAAGCTGAC	AGGCGG-----ACGCTCAATCCGCCAGACACAGATATCCG	515	
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QY	573	GACCGGAACATGTT	TCGATGGCTCAGTCTCGGCTGCTATGSCAACGTCATTGTAGCCAC	632	
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QY	633	GCTCAACTACCGTCT	TGGGGTGTCTGGGTTTCTCAGCACCGGGACGAGGTGCAAAAGG	692	
Db	652	CATTAACTACCGT	CTGGGATCTAGGGTTTTTAAGTACCGGTGACGAGCAGCANAAGG	711	
QY	693	CAACTATGGGCTCT	GTGACAGATCCAGGCCCTGCGCTCGCTCAGTGAATAATCGGCCA	752	
Db	712	CAACTATGGGCTCT	GTGATCAGATTCAAGCACTGCGGTGGATTGAGGAATGTGGGAGC	771	
QY	753	CTTTGGGGCGACCC	CGAGCGTATCACCATCTTTGGTTCCGGGCGAGGGGCTCCTCGGT	812	
Db	772	CTTTGGCGGGACCC	CAAGAGATGACATCTTTGGCTCGGGGGTGGGGGCTCCTGTGT	831	
QY	813	CAACCTTCTGATCT	CTCCACCAATTCAGAAAGGCTGTTCCAGAAAGGCCATCGGCCAGAG	872	
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QY	873	TGGCACCGCCATTT	CCAGCTGGTCTGTAACACTACGCGCTCAAGTACAACGCGCTGCT	932	
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QY	933	GGCACCGCAAGTG	GGGCTGTGACCGAGAGGACAGTGTGTAAGCTGTGAGTGTCTGTGCGCG	992	
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QY	993	GAAGCCCTCCCG	GAGGTGGTGGACAGGACGCTGCAGCCTGCCGCTACCAATCCGCTT	1052	

Db 2089 CGTCGGGGCGTCCTCTCTCTCAACATCTTAGCTTTTGGGGCGGTGTAACAATAA 2148
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QY 2283 GCGCCCTGCTGCGCGCCCGACATACACCTGGCGCTGCGCGGGCAGCGGACGATGCGC 2342
Db 2305 GAGGCTCACCTGCGCGCCGACAGATACACCTCAGCTGCGCGGTGCGGACGATGACATCC 2364
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Db 2365 ACTTATGCGGCAACACCATCACCATGATCCAAACACACTG 2407

RESULT 13

US-09-978-564A-374

; Sequence 374, Application US/09978564A

; Publication No US20030050241A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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Query Match 36.4%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%; Pred. No. 2.5e-206;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
QY 108 CGCGAGAGAGCGCTTCCCGGTGGTGAACACACGCGCTACGCGGCGAGTGC CGGGTGTGGCGG 167
Db 112 CAGCCACAGACAGTATCCAGTTGTCAACACAAATATGCAAAATCCGGGGCTTAAGAAC 171
QY 168 CGAGCTCAACAGAGATCCTGGGCGCGGTGTGAGTGTCTTGGGGTGGCGGCTTACGCCAC 227
Db 172 ACCGTTACCCATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGTCCCGCTATGCGCTC 231
QY 228 GCGGCGCTGGGCGCGCGCTTCCAGCGGCTCAGCGCGCGCGCTCGTGGCGCGCGGT 287
Db 232 ACCCGCCACTGAGAGAGAGCGGTTTCAGCGCCAGAACCCCGCTCTCTGGACTGGCAT 291
QY 288 GCGCAACGCCACCAACCCCTGCGCGCGCTGCGCGAGAACCTGCAAG---GGGCGCTGCC 344
Db 292 CCGAAATACTACTCAGTTTGTCTGTGTGCGCCCGCAGCACCTGGATGAGAGATCCTTACT 351
QY 345 CGCCATCATGCTGCTGTGTGTTTCAACGACAACTTGGAGGCGCGCGCGCTAGTGCA 404
Db 352 GCATGACATGCTGCCCATCTGTTTACCGCAATTTGGATACTTTTGATGACCTATGTTCA 411
QY 405 GAACAGAGCGAGAGACTCGCTGTACTCAACCTCTACCTGCGCCACCGAGGAGCGTCCGCT 464
Db 412 AGATCAAAATGAAGACTGCCITTTACTTAAACATCTACGTGCGCCACGGAAGATGGAGCAA 471
QY 465 CACAAAAAAGCTGACGAGGCG-----ACGCTCAATCGCCGACACACAGATATCGG 515
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QY 516 TGACCCCTG---GGAAGAAAGCTGTGATGCTGTGTTCTCCATGCGGCTCTACATGGAGG 572
Db 532 TGATCAGACAGTAGAAGCGCGTCTATGTTCTATATCATGGGGATCTTACATGGAGG 591
QY 573 GACCGAAACATGTTGATGGCTAGTCTCGCTGCTTATGGCAACGTCATTGTAGCCAC 632
Db 592 CACCGCAACATGATTGACCGCAGCAITTTGGCAAGCTTACGAAACGTCATCGTATCAC 651
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Db 652 CATTAACCTACCGTCTGGGAATAGTGGGTTTTTAAGTACCGGTGACCGAGGAGCAAAAG 711
QY 693 CAACCTATGGGCTCTCGGACAGATCCAGGCGCTGCGCTGCGTCAAGTGAACATCGCCCA 752
Db 712 CAACCTATGGGCTCTCGGATCAGATTCAAGCACTGCGGTGAGTTGAGGAGATGTTGGAGC 771
QY 753 CTTTGGGGGACCGCGAGCGTATCACCATTCTTGGTTCCGGGGGAGGGGCTCTGCGT 812
Db 772 CTTTGGGGGACCGCGAGAGAGTGAACATCTTTGGCTCGGGGCTGGGGGCTCTGTTGT 831
QY 813 CAACCTCTGATCTCTCCCAACCAATTGAGAAGGCTGTTCCAGAAGGCCATCGCCCAAG 872
Db 832 CAGCCTGTTGACCTGTCTCCACTACTCAGAGGTTCTTCCAGAAGGCCATCTCAGAG 891
QY 873 TGGCACCGCCATTTCCAGCTGCTGTGCACTACAGCGGCTCAAGTACAGCGGCTGCT 932
Db 892 CGGCACCGCCCTGTCTCAGCTGGGAGTGAACCTACAGCGCGCCCAAGTACACTCGGATAT 951
QY 933 GGCACGCAAGGTGGGCTGTGACCGGAGAGAGTGTGAAGCTGTGGAGTGTCTGCGCG 992
Db 952 GGCAGCAAGGTGGGCTGCAACATGCTGGACACCAAGGACATGTAGTATGCTTGGCGAA 1011
QY 993 GAAGCCCTCCCGGAGCTGGTGGACCGAGAGCTGCGAGCTCCCGCTACCACTACGCTT 1052

Db 1012 CAAGAACTCAAGAGGCTCATCAGCAGACCATCACCCCGGCACACTCAACATAGCCTT 1071
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Db 1252 CAATTTTGTGAACAACTGTATGCTGCGCGTCAACCAAGGGAGAGGCTCAAGTTGCT 1311
Qy 1293 CAAGTTTATGTACACAGACTGGGCCCGACCGGACATGCGAAATGCGCGCGCAAAACCT 1352
Db 1312 CAAGTTTATGTACACAGACTGGGCCCGATTAAGGAAACCCCGGAGACCGCGGGAACCT 1371
Qy 1353 GCTGGGCTCTTTACTGACCAACATGGGTGGACCAAGTGTGGCACTGCGCAAGCTGCA 1412
Db 1372 GGTGGCTCTCTTTACTGACCAACAGTGGGTGGGCCCGCGGTGGCC---GCCGACCTGCA 1428
Qy 1413 CGCGGACTACAGTCTCCGCTCTACTTTTACACCTTCTACCACTCTACCACTGCGAGG 1472
Db 1429 CGCGGACTAGGCTCCCGCACTTCTATGCTCTTATCATCTGCTCACTGCAAGCGAAT 1488
Qy 1473 CGCGCTGAGTGGGCGAGATCGCGCGCAGCGGAGTGAAGTCCCTATGTCTTTGGGCTGCC 1532
Db 1489 GAAGCCAGCTGGCGAGATTCGGCCCATGATGAGTCCCTATGTCTTCGGCATCCC 1548
Qy 1533 CATGGTGGTGCACACGACCTTCCCTGTGTAATCTTCAAGATGACGTATGCTGAG 1592
Db 1549 CATGATCGTCCACCGAGCTCTCAAGTTGTAACTTTTCAAGAACGACGTATGCTGAG 1608
Qy 1593 TGCGTGGTCACTGACTTACTGACCACTTCGCGCAAGACTGGGGACCCCAACCGCGGT 1652
Db 1609 CGCGTGGTCACTGACTTACTGACCACTTCGCGCAAGACTGGGGACCCCAACCGAGT 1668
Qy 1653 GCGCAGGATACCAAGTTCTACACACCAAGCCCAATGCGTTGAGGAGGTTGGTGGAG 1712
Db 1669 TCCTCAGGATACCAAGTTCTACACCAAAACCCCGCTTTGAAGAAGTGGCTGGTC 1728
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Db 1789 TCATACCGGCGCAACAAAGTGGCTTCTGGTTGGAACCTGTTCTCATTTGCACAACTT 1848
Qy 1833 GCA-----CAGGAGCTTTACGACACACGCGCTGCTTCCCTACGCGCGG 1883
Db 1849 GAACGAGATATTCAGTATGTTTCAACAAACAAAGAGTTCTTCCACGAGATGACATC 1908
Qy 1884 CTGGCCGCTCTGCTCCCGCTGGCGCCCGGCGCACAGCGCGCCCGCGCGCTGCCAC 1943
Db 1909 ATTCCCTATGGCACCGCGGATCTCCGCGCAGATATGGCCCAACCAACGCGCCAGC 1968
Qy 1944 CTGGCTCCGAGCGCGAGCCCGAGC-----CGGCGCCAAAGGC 1982
Db 1969 AATCACTCTCGCAACAAATCCCAACACTCTAAGGACCTTCAAAACAGGGGCTGAGGA 2028
Qy 1983 CTATGACCGTCTCCCGGAGCTACGCGGACTACTCAGCGAGCTCAGCGTCACTGGC 2042
Db 2029 CAACTGTCTCTATTGAACCAACGAGATTTATTCACGAAATTAAGTGTACCAATGC 2088
Qy 2043 CGTGGGCTCTCTCTCTCTCTCAACATCTGGCTTGTGCTTCTACTACAGCG 2102
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Qy 2103 GGACCGCGCAGAGAGTGTGGGTGACGGCGGCTTAGCCACCTGCGCGGTCTAGGCTCTGG 2162
Db 2149 GGACAGAGCGCGCATGAGACTCACAGCGCGCCCGAGTCCCAGAGAAACACCAATGA 2208
Qy 2163 CGTCCCTGGTGGGGGCCCTGCTCCCGCGCGGCGGTGAGTGCACACAGAGGAGGA 2222
Db 2209 TATCGCTCATCATCCAGAACGAGAGATCATGTCTCTCAGATGAGCAGTGGACAGGA 2268
Qy 2223 GCTGTGTCTCTGAGTGAAGGGGGTGTGGCGTGGGGCGGACCTTCCCGAGGCTCT 2282
Db 2269 TCACGAGTGTGAGTGGTGCAG-----GCACACGACACACT 2304
Qy 2283 CGGCGCTGCTGCGCGCGGACTACACCTGCGCGGCTGCGCGGCGACCGGACGATGCGC 2342
Db 2305 GAGGCTCACCTGCGCGCGGAGACTACACCTCAGCTGCGCGGTGCGCAGATGATCATCCC 2364
Qy 2343 TCTCTTGGCGCGCGCGGCGCTGACCTGCTGCGCGAGTGGCGCTG 2385
Db 2365 ACTTATGAGCGCAACACCATCATCATGATTCCAAACACACTG 2407

RESULT 14

US-09-999-833A-374
; Sequence 374, Application US/09999833A
; Publication No. US20030054405A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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62	PRIOR FILING DATE: 1998-04-15
63	PRIOR APPLICATION NUMBER: 60/082568

; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 36.4%; Score 912.2; DB 11; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.5e-206;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY	108	CGCGAGGAGCGCTTCCGCGTGTGACACGCGCTACGCGCGAGTGC	1053	TGGCCCGTGTGGATGGCGACGTGGTCCCGCATGACCTTCAGATCCT
DB	112	CACCAAGACAGATATCCAGTTGTCAACAAATATGCGAATATCCG	1072	CGGSCCGTGATCGACGCGACGTATCCCGACAGACCCCGATCTG
QY	168	CGAGCTCAACACAGAGATCCTGGGCGCGCTCGTGACAGTTCTT	1113	AGAATTCCTCAACTACGACATGCTCATCGCGCTCAACACGAGAG
DB	172	ACCGTTACCAATAGATCTTGGGTCCAGTGGAGCAGTACTTAGG	1132	CGAGTTCTCAACTACACATCATGCTGGGCGTCAACAAAGGGAAG
QY	228	GCAGCCCTGGGCGCGCGCTTCAGCGCGCTGAGCGCGCGCTCG	1173	GGAGGACTCTGCAGAGAGCAGGACGCTGTGTCTTGCAGCGCTTT
DB	232	ACCCCGCCTGGGAGAGGCGGTTTCAGCGCGCGCGCGCTTCCT	1192	GGACGCGATCGTGATTAACGAGGACGCTGTGACGCCCAACGAC
QY	288	GCACAAAGCGCACACCGCTCGCGCGCGCTCGCGCGAGAACCT	1233	CAACTTTGTGGACAACTGTATGGCTTACCGGAGGCAAGATGTG
DB	292	CGCAATATCTACTACGTTTCTGCTGTGTCGCGCGCGCGCTTC	1252	CAACTTCGTGGACAACTTTTACGCTACCTTGAAGGGAAGACAC
QY	345	CGCCATCATGCTGCTGTGTGTTTACCGACAACTTGGAGGCGCG	1293	CAAGTTTATGTACACAGACTGGCGCGACCGGGAATGGCGGAAT
DB	352	GCATGACATGCTGCTGCTTACCTTACCGCGCAATTTGGGATA	1312	CAAGTTTATGTACACAGACTGGCGCGATAGGAAACCCGAGAGC
QY	405	GAACACAGAGGAGGACTGCTGTACCTCAACCTTCTACGTCGCC	1353	GCTGGCGCTCTTTACTGACCAATGGGTGGCAACAGTGTGGCCAC
DB	412	AGATCAAAATGAAGACTGCTTCTTAAACATCTACGTCGCCCA	1372	GGTGGCTCTCTTTACTGACCACTGGTGGCGCGCGCGCTGGCC
QY	465	CACAAAAAAGCTGAAGAGCGG-----ACGCTCAATCCGCCA	1413	CGCGACTACGAGTCTCCGCTCTACTTTTACACCTTCTACACACT
DB	472	CACAAAGAAAGCGAGATGATATAAGAGTATGACCGTGTGAGAG	1429	CGCGAGTACGGTCTCCCGACCTACTTCTATGCTTCTATCATCT
QY	516	TGACCTG---GGAAGAAGCTGTGATGCTTTTCTCCATGCGGCT	1473	CCGCGCTGAGTGGGCGAGATCGGCGCACGCGGAGTGAATGCTC
DB	532	TGATCAGAACAGTAGAGCCGCTCATGTCTATATCCATGGGGAT	1489	GAAGCCGAGCTGGGCGAGATTCGCGCCATGCTGATGAGTCCCT
QY	573	GACCGGAAACATGTTGATGGTTCAGTCTGCTGCTATGGCAAGT	1533	CATGGTGGGTGGCACCGACCTCTTCCCTGTAACTTCTCCAGATG
DB	592	CACCGGCAACATGATTGACGCGAGCATTTTGGCAAGCTACGGA	1549	CATGATCGGTCCCAACGAGCTCTTCAAGTGTAACTTTTCCAGAA
QY	633	GCTCAACTACGCTTTGGGCTGCTCGGTTTCTACAGCGGGGACG	1593	TGCGCTGGTCAATGACACTTCTGGACCAACTTCGCGCAAGACT
DB	652	CATTAACTACCGCTTGGGAATCTAGGGTTTAAAGTACCGGTG	1609	CGCGTGGTCAATGACCTTCTGAGCAACTTCGCGCAAACTGGTG
QY	693	CAACTATGGGCTCTTGACACAGATCCAGGCGCTGCGCTCAGTG	1653	GCSCAGGATACCAAGTTTATCCACCAAGCCCAATCGCTTCGAG
DB	712	CAACTATGGGCTCTTGATCAGATTCAAGCACTGCGGTGATTT	1668	TCCTCAGGATACCAAGTTTATTCACAAACCCACCGCTTTGAAG
QY	753	CTTTGGGGGACCGCGAGGATATACCATTTTGGTTTCGGGGAGG	1712	CAAAATTCACAGCAAGGAGAGAGTATCTGCAATAGGCTGAAGC
DB	772	CTTTGGGGGACCGCGAGGATGACCATTTTGGCTCGGGGCTTCT	1728	CAAGTATATCCCAAGACAGCTCTATCTGCAATATGGCTTGAAC
QY	813	CAACTTCTGATCTCTCCACCATTCAGAGGCTGTTCCAGAGGCC	1772	CAACTACCGCGCCCAAGGTGGCTTCTGGCTGGAGTCTGTCGCC
DB	832	CAGCTGTTGACCTGTCCCACTACTCAGAGGTCTTCTCCAGAGG	1788	TCAGTATATCCCAAGACAGCTCTATCTGCAATATGGCTTGAAC
QY	873	TGGCACCGCATTTTCCAGCTGGTGTGTCAACTACAGCGCGCTC	1832	CAACTACCGCGCCCAAGGTGGCTTCTGGCTGGAGTCTGTCGCC
DB	892	CGGACCGCGCTGTCACAGCTGGGAGTGAATACCAAGCGCGCG	1848	TCAGTATATCCCAAGACAGCTCTATCTGCAATATGGCTTGAAC
QY	933	GGCAGCAAGGTGGCTGTGACCGAGAGGACGTGTGAGCTGTGG	1883	GCA-----CACGGAGCTTTCACACCAAGCTCTGCTTCCCTAC
DB	952	GGCAGCAAGGTGGCTGTGACCGAGAGGACGTGTGAGCTGTGG	1898	GAACGAGATATTCAGTATGTTTCAACCAAGGTTCTTCCACCA
QY	993	GAAGCCCTCCGGGAGCTGGTGGACAGGAGCTGCGCGCTGCGG	1943	CTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB	1012	CAAGAACTACAGAGGCTCATCCAGAGGACCATCACCGCGCGC	1968	ATTTCCCTATGGCACCGCGGATCTCCCGCAAGATATGCGCAAC
QY	1052	GAAGCCCTCCGGGAGCTGGTGGACAGGAGCTGCGCGCTGCGG	1982	CTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB	1071	CAAGAACTACAGAGGCTCATCCAGAGGACCATCACCGCGCGC	2028	AATCACTCTGCGCAACATCCCAACACTCTAAGGACCTTCAAAA


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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      36.4%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%; Pred. No. 2.5e-206;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGGCGAGGAGCGCTTCCCGGTGGTGAACAGCGCTACGGCGAGTGGCGCGGTGTGCGCGG 167
DB 112 CAGCAGACAGATCCAGTTGTCAACACAAATATGGCAAAATCCGGGCGCTTAAGAC 171
QY 168 CGAGCTCAACAAACAGATCCCTGGGCCCGGTGGTGTCTTGGCGGTGCGCTTACGCCAC 227
DB 172 ACCGTTACCAATAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCGTC 231
QY 228 CGCGCCCTGGGCGCGCTTCCAGCGCGCTGAGCGCGCGCGCTGCTGGCGCGCGGT 287
DB 232 ACCCGCCACTGGAGAGGCGGTTCAGCCCCAGAACCCCGCTCTCTCTGGATGCGAT 291
QY 288 CGCAACGCCACCACTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 344
DB 292 CGAAATACTACTCAGTTTGTGCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 351
QY 345 CGCATCATGCTGCTGTGTTTCAAGGAACTTGGAGGCGCGCGCGCGCGCGCGCGCGCG 404
DB 352 GCATGACATGCTGCGCGCTGTTTACCGCGCAATTTGGATACTTTGATGACCTATGTTC 411
QY 405 GAACCAAGCGGAGGAGTGCCTGTACTCAACCTTACGTGCGCGCGCGCGCGCGCGCGCG 464
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QY 465 CACAAAAAAGCGTACGAGGCGG-----ACGCTCAATCCGCGCGCGCGCGCGCGCGCG 515
DB 472 CACAAAGAAAAACGAGATGATATAACGAGTAATGACCGGTGGTGAAGACGAAGATATTC 531
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DB 532 TGATCAGAACAGTAAAGAGCGCGCTCATGCTTATCCATGGGGGATCTTACATGAGG 591
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QY 633 GCTCACTACCGCTTGGGTGCTCGGTGTTTCTCAGCACCGCGCGCGCGCGCGCGCGCG 692
DB 652 CATTAACCTACCGCTGCGGATFACAGGTGTTTAACTACCGGTGACCGAGCAAGG 711
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DB 892 CGGCACCGCGCTGCTCCAGTGGGAGTGAACCTACAGCGCGCGCGCGCGCGCGCGAT 951
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DB 952 GCGAGCAAGGTGGGCTGTGCACTGCGGACACCGGACATGTTAGATGCTCTGCGGAA 1011
QY 993 GAAGCCCTCCCGGAGTGTGGACCGAGGAGTGCAGCGCTTCCCGCGCTTACCAATCGCT 1052
DB 1012 CAAGAACTACAAGGAGTCTATCCAGAGAGCCATCCCGCGCGCGCGCGCGCGCGCT 1071
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QY 1072 CGGCGCGGTGATCGACGGCGACGTCTATCCAGACGACCCCGACATCCTGATGAGCAAG 1131
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QY 1113 AGAATTCCTCAACTACGACATGCTCATCGCGCTCAACAGGAGAGGGCTCAAGTTGCT 1172
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QY 1173 GGAGGACTTGCAGAGAGCGAGAACGGTGTGCTGCCAGCGCTTTGACTTCACTGTCTC 1232
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QY 1192 GGACGGCATCGTGGATAACGAGGACGCTGTGACGCCCAAGACTTTGACTTCTCCGTGC 1251
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QY 1233 CAATTTTGTGGAACAACCTGTATGGCTACCGGAAGCGAAGGATGCTCTCGGAGACCAT 1292
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QY 1353 GCTGGCGCTCTTTACTGACCAACCAATGGGTGGACAGCTGTGGCCACTGGCCAGTGCA 1412
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Db |||||

Search completed: February 19, 2004, 11:54:13
Job time : 824.794 secs

128 TGGTGAACACGGCTACGGCGAGTGGCGGTGGTGGCGGAGCTCAACACGAGATCC 187
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Qy 188 TGGGCCCCGTCGTGAGTCTTTGGGGTGGCCCTACGCAACGGCCGCGGCGCCGCC 247
Db 594 TGGGGCTGTGACCAATACTGGGGTGGCCCTACGCAACGGCCGCGGAGAAC 653
Qy 248 GCTTCAGCCGCTGAGGCGCCGCTGCTGGCCGCGGCTGGCAACGCCACCCCTGC 307
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Qy 308 CGCCGCCCTGCGCGAGAACCTGACGGGGCGCTGCCGCCATCATGCTGCTGTGT 367
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Qy 368 TCACGACAACTTGGAGGGCGCCGCACTCATGTCAGAACACGAGGAGGACTGCCTGT 427
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Db 1974 CTTGCAACTTCTCCAGAAATGATGTTATGCTCAGTGTCTGCTCATGACCTATGACCA 2033
Qy 1619 ACTTGCACAGACTGGGACCCCAACAGCGGTGCGGAGGATACCAAGTTCATCCACA 1678
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Db 2334 ATGCAAGACTGGAGCACCAAGCGCCAGCCATCTCACTGCTTACAGCAACGAGAATG 2393
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Qy 2371 CTGCCCCAGTGGCCTGG 2386
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RESULT 2
US-09-491-356C-6
; Sequence 6, Application US/09491356C
; Patent No. 656061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF X013
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 4436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: n is not determined
US-09-491-356C-6

Query Match 34.7%; Score 871; DB 4; Length 4436;
Best Local Similarity 67.6%; Pred. No. 8.5e-153;
Matches 1294; Conservative 0; Mismatches 565; Indels 54; Gaps 3;

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Qy 1932 GCGGCT 1973
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Db 2785 CCAGGATGAGGGCCACTCTCTGGTGGAGAACCTCGTGACTACTCCACTGAAATTAAGTGT 2844
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RESULT 3
US-09-491-356C-3
; Sequence 3, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-491-356C-3

Query Match 28.8%; Score 723.4; DB 4; Length 1764;
Best Local Similarity 67.4%; Pred. No. 1.6e-125; Indels 69; Gaps 1;
Matches 1073; Conservative 0; Mismatches 451;

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Qy 188 TGGGCGCCGCTCGTGCAGTTCCTTGGCGGTGCCCTACGCCACGCGCCCTCGGCGCCGCGC 247
Db 261 TGGGCGCTGTGACCAATACCTGGGGTGGCTACGAGCTCCCGGATCGGCGAGAAC 320
Qy 248 GCTTCAGCGCGCTGAGGCGCGCCCTCGTGGCGCGGCTGGCAACGCAACACCTGTC 307
Db 321 GTTCTCGCCCTTGAACCAACCCCATCTGCTGGTGGGATCCGGAACGCCACACACTTTC 380
Qy 308 GCGCGCGCTGCGCGGAGAACCTGACGGGGCGCTCCCGCCCATCATGCTGCTGTGGT 367

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Qy 368 TCACGACAACTTGGAGGCGCGCCACCTAGCTCAGAACCCAGAGCGAGAGTCCCTGT 427
Db 441 TCATGCGCAACTTGGATATCGTGGTCTTATCATCCAGGAGCCCAACGAGACTCTCT 500
Qy 428 ACTCAACCTTACGTGGCCACCGAGGAGCTGCTCCTCAAAAAAAGCTGACGAGGGA 487
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Qy 488 CGCTCAATCCG----- 498
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Db 621 TAGCGGATAATGACGGGATGAAGATGAAGACATCCGGGACAGTGGTGTCTAAACCCGTCA 680
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Db 921 CTGCTTTGGCTCGGCGCATTTGGTGCATCTCTGCTCAGCTCCTCAGTGTGCATCAT 980
Qy 839 CAGAGGGCTGTTCAGAGAGCCATCGCCAGAGTGGCAGCGCCCATTTCCAGCTGCTG 898
Db 981 CAGAGGACTTTTCCAGAGAGCCATCTCAAAAGTGGCTCTGCTCTGCTCAGCTGGCTG 1040
Qy 899 TCAACTACGAGCGCTCAAGTACACGCGGCTCTGGCAGCCAGGCTGGTGTGACCGAG 958
Db 1041 TGAACCTACCACCAAGTGAAGTACACCGCTCTGGCAGACAAAGTGGGCTGTAATGTGC 1100
Qy 959 AGGACAGTCTGAAGTGTGGAGTGTCTGGCGCGGAAGCCCTCCCGGAGCTGGTGGACC 1018
Db 1101 TGGACACCGTGGATATGGTGGACTGTCTTCGGCAAAAGAGTGCCAAAGAGCTGGTAGAGC 1160
Qy 1019 AGGACGTGCAGCTGCGCGCTACCACTCGCTTTGGGCGCGGTGGTGGATGGCGACGTGG 1078
Db 1161 AGGACATCCAGCGAGCGCGCTACACGCTGGCTTTGGCCCTGTGATTGATGGTATGTC 1220
Qy 1079 TCCCGATGACCTCGAGATCTCTATGAGCGAGGAGAAATTCCTCACTACGACATGCTCA 1138
Db 1221 TTCTGATGACCTCGAGATCTCTATGAGCGAGGCGAGTTCCTCACTATGACATCATGC 1280
Qy 1139 TCGGGCTCAACAGAGAGAGGCGCTCAAGTTCTGCGAGAGCTCTCGACAGAGCGAGGACG 1198
Db 1281 TAGGTGTCAACAGCGCGAGGGTCTCAAGTTTGTGAAGGGGTGGTGGACCTGAGGATG 1340
Qy 1199 GTGTGTCTGCCAGCGCTTTGACTTCACTGTCTCAACTTTGTGGAACCTGTATGGCT 1258
Db 1341 GTGTCTCTGCCACTGACTTTGACTATTCCGTCTCCAAATTTGTGGACAATCTGTATGGCT 1400
Qy 1259 ACCCGAAGCGAGATGTGCTTCGGGAGACCATCAAGTTTATGTATACAGACTCGGCGC 1318
Db 1401 ATCTGAGGTAAGGACACCTTCGAGAGACCATCAAGTTTATGATATACAGACTGGGAG 1460
Qy 1319 ACCGGACAAATGGCGAAATGCGCGCAAAACCTGCTGGCGCTCTTTACTGACCAACCAAT 1378
Db 1461 ACCGTGACAACCTGAGACCCCGCGTAAACACTGGTGGCACTCTTCTACTGACCAACCACT 1520

QY 1379 GGGTGGCAACAGCTGTGGCCACTGCAAGCTCACCGGAGTACAGTCTCCCGTCTACT 1438
 DB 1521 GGGTGGAGCCCTCAGTGGTGAAGCGGATCTGATGCCGCTACGGCTCGCTACTACT 1580
 QY 1439 TTTCACCTTTACCACTACCTCCAGCGGAGGGCCGCTGAGTGGGAGATCGGGC 1498
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 QY 1559 CTTGTAACCTTCCAAGATGACGTGCTCA 1591
 DB 1701 CCTGCAACTTCTCCAAGATGATGTTATGCTCA 1733
 RESULT 4
 US-09-491-356C-4
 ; Sequence 4, Application US/09491356C
 ; Patent No. 6566061
 ; GENERAL INFORMATION:
 ; APPLICANT: Philibert, Robert A.
 ; APPLICANT: Ginns, Edward I.
 ; APPLICANT: Delisi, Lynn
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
 ; FILE REFERENCE: 9465.6US11
 ; CURRENT APPLICATION NUMBER: US/09/491,356C
 ; PCT APPLICATION NUMBER: PCT/US99/09365
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR FILING DATE: 1998-04-29
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 2818
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-491-356C-4
 Query Match 27.9%; Score 700.4; DB 4; Length 2818;
 Best Local Similarity 66.4%; Pred. No. 3e-121;
 Matches 1079; Conservative 0; Mismatches 491; Indels 54; Gaps 3;
 QY 790 TCGGGGCAAGGGGCTCTGCTGCTCAACCTTCTGATCTCTCCACCACTCAGAGGGCTG 849
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 QY 850 TTCCAGAGGCCATCGCCAGAGTGGCAGCGCATTTCCAGTGTCTGTCAACTACCAG 909
 DB 62 TTCCAGAGGCCATCATCAAGTGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
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 QY 1150 CAGGGAGAGGGCTCAAGTTCGTGAGGACTCTGACAGAGAGAGAGAGAGTGTGTCTGCC 1209
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 QY 1270 AAGATGTGCTTCGGAGACCAATCAAGTTTATGTAACAGACTGGGCGGACCGGCAAT 1329
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 QY 1330 GGGAAATGCGCGCAAAACCTTGTGGGCTCTTTTACTGACCAACAAATGGGTGGACCA 1389
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 QY 1390 GCTGTGGCCACTCCCAAGTGTGACGCGGACTACAGTCTCCCGTCTACTTTTACCTTC 1449
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 QY 1450 TACCACCACTGCCAGCGGAGCGCGCTGAGTGGGCGAGATGCGGCGACCGGGATGAA 1509
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 QY 1510 CTGCCCTATGCTTTTGGCGTCCCATGCTGGGTGGCGACCGACTCTTCCCTGTAACTTC 1569
 DB 722 GTACCCCTATGTTTGGGTTCCTATGTAGGCGCCACTGACCTTTTCCCTGCAACTTC 781
 QY 1570 TCCAAGATGAGTCACTGCTGAGTGGGCTGATGATGATGATGATGATGATGATGATGAT 1629
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 QY 1630 ACTGGGGACCCCAACAGCGGCTGCGGAGGATACCAAGTTTATCCACCAAGCCCAAT 1689
 DB 842 ACTGGGGATCCCAACAGCGGCTGCGGAGGATACCAAGTTTATCCACCAAGCCCAAT 901
 QY 1690 CGCTTCGAGAGTGTGTGGAGCAATTCACAGCAAGAGAGAGAGATCTGTCACATA 1749
 DB 902 CGCTTTGAGGAGTGGCTGCTCCAAATATACATCCCGGAGACGAGCTTACCTTCAATC 961
 QY 1750 GGCCTGAAGCCAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1809
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 QY 1810 CTGCTGCCCACTGTCAACACTGTGACAGGAGCTC-----TTCAACCAACCAACG 1860
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 DB 1202 TGAACCGGGACCAAGGATCAGGCGCACTCTCTGTTGGAGAACCTCTGCTGCTGCTGCTGCT 1261
 QY 2023 GAGCTGAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2082
 DB 1262 GAATTAAGTGTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
 QY 2083 GCTGCCCTTACTTCAAGCGGGACCGCGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2142
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 QY 2143 CTTGGGCGCTCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2202
 DB 1382 CAGCGGGAGCGGGCT-----CCCGAGTGGAGCT 1414
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OTHER INFORMATION: Bovine pancreatic cholesterol esterase cDNA

PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: 08/462,884
PATENT FILING DATE: 1995-06-05
PUBLICATION DATE: 1997-04-29

US-09-347-878-33

Query Match 5.8%; Score 145.6; DB 4; Length 1905;
Best Local Similarity 53.0%; Pred. No. 1.3e-18;
Matches 335; Conservative 0; Mismatches 294; Indels 3; Gaps 1;

QY	581	ACATGTTCCATGCGTCAGTCCTGGTGGCTATGGCAAGTCATTTAGCCAGCTCAACT	640
DB	452	ACCTTACACGCGGAGGAGATTGCCACAGGGGCAAGTCATCGTGTGTCAGTTCAACT	511
QY	641	ACCGTCTTGGGTGCTCGGTTTCTCAGCACCGGGGACCAGGCTCCAAAGGCAACTATG	700
DB	512	ACCGCGTTGGGCGCTTCTCAGCACCGGGGACTTCCAACTGCCAGTAATATG	571
QY	701	GGCTCTGACAGATCCAGGCGCTCGGCTGCTCAGTGAAACATGCCCACTTTGGGG	760
DB	572	GGCTTTGGGATCAGCACATGGCCATGCTTGGGTGAAGAGAACATTCAGGCGCTTCGGAG	631
QY	761	GGGACCCCGAGCGTATCAACATCTTGGTTCGGGGGAGGGGCTCTCTGCTCAACCTTC	820
DB	632	GAGACCCGACACATCACTCTTTGGGAGTCGCGGGAGCGGCGGCTCTCTGTC	691
QY	821	TGATCTCTCCACCATTCAGAAAGGCTGTTCCAGAGGCGCATGCCAGAGTGCCACG	880
DB	692	AGACCCCTCTCTCCCTACACAAAGGCGCTCATCAAGCGAGCCATCAGCCAGAGTGAGTGG	751
QY	881	CCATTTCCAGCTGGTCTGTCACTACACCGCGCTCAAGTACACCGGCTGCTGGCAGCA	940
DB	752	GTTTGTGCGCTTGGGCGCATTCAGAGGACCCCTCTTCTGGGCTAAAGGATTGCAGAGA	811
QY	941	AGGTGGGCTGTGACCGAGAGGACAGTGTGAGCTGTGAGTGTGTCGCGGAGCGCCT	1000
DB	812	AGGTGGGCTGCCCGCTGGACGACACACAGATGGCTGGGTGCTGAAGATCACTGACC	871
QY	1001	CCGGGAGCTGTGACACGAGAGCTGACGCTGCGGCTTACCATCGCTTTGGGCGCG	1060
DB	872	CCCGTGCGCTGACG---CTGGGCTATAAGCTGCGGCTGGGAGCGGAATACCCCAAGC	928
QY	1061	TGGTGGATGGGACGCTGTGCTCCCGATGACCTGAGATCTCATGACGAGGAGAAATTC	1120
DB	929	TGCACTATCTGCTCTTGTGCTCCCGTCATGATGGAGACTTATCCCTGATGACCCGTC	988
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DB	989	ACCTGTACGCCAAACCGCGGACGTCGACTATAGCGGGGACCAATGACATGACGCGCC	1048
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RESULT 7

US-08-462-884A-2
Sequence 2, Application US/08462884A
Patent No. 5624836

GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
TITLE OF INVENTION: Esterase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 10 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,884A
FILING DATE: Unknown
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1907 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 100..129
OTHER INFORMATION: /note= "complementary sequence to
OTHER INFORMATION: oligonucleotide probe"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1824
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1907
OTHER INFORMATION: /note= "Bovine pancreatic
OTHER INFORMATION: cholesterol esterase cDNA"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..30
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 31..1821
US-08-462-884A-2

Query Match 5.8%; Score 145.6; DB 1; Length 1907;

Best Local Similarity 53.0%; Pred. No. 1.3e-18;
Matches 335; Conservative 0; Mismatches 294; Indels 3; Gaps 1;

QY	581	ACATGTTCCATGCGTCAGTCCTGGTGGCTATGGCAAGTCATTTAGCCAGCTCAACT	640
DB	452	ACCTTACACGCGGAGGAGATTGCCACAGGGGCAAGTCATCGTGTGTCAGTTCAACT	511
QY	641	ACCGTCTTGGGTGCTCGGTTTCTCAGCACCGGGGACCAGGCTGCAAAAGGCAACTATG	700
DB	512	ACCGCGTTGGGCGCTTCTCAGCACCGGGGACTTCCAACTGCCAGTAATATG	571
QY	701	GGCTCTGACAGATCCAGGCGCTCGGCTGCTCAGTGAAACATCGCCCACTTTGGGG	760
DB	572	GGCTTTGGGATCAGCACATGGCCATGCTTGGGTGAAGAGAACATTCAGGCGCTTCGGAG	631
QY	761	GGGACCCCGAGCGTATCAACATCTTGGTTCGGGGGAGGGGCTCTCTGCTCAACCTTC	820
DB	632	GAGACCCCGACACATCACTCTTTGGGAGTCGCGGGAGCGGCGGCTCTCTCTGCG	691
QY	821	TGATCTCTCCACCATTCAGAAAGGCTTCCAGAGGCGCATGCCCAAGTGCCACCG	880
DB	692	AGACCCCTCTCTCCCTACACAAAGGCGCTCATCAAGCGAGCCATCAGCCAGAGTGAGTGG	751
QY	881	CCATTTCCAGCTGGTCTGTCACTACACCGCGCTCAAGTACACCGGCTGCTGGCAGCA	940
DB	752	GTTTGTGCGCTTGGGCGCATTCAGAGGACCCCTCTTCTGGGCTAAAGGATTGCAGAGA	811

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RESULT 8

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US-08-461-881B-2
; Sequence 2, Application US/08461881B
; Patent No. 5792832
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic Cholesterol Esterase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehrnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL USA
; COUNTRY: IL USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" hard disc
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461.881B
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; REFERENCE/DOCKET NUMBER: 89,852-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/913-0001
; TELEFAX: 312/913-0002
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1908 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 100..129
; OTHER INFORMATION: /note= "complementary sequence to
; OTHER INFORMATION: oligonucleotide probe"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1824
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1908
; OTHER INFORMATION: /note= "Bovine pancreatic
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; OTHER INFORMATION: cholesterol esterase cDNA"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..30
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 31..1821
; US-08-461-881B-2
; Query Match 5.8%; Score 145.6; DB 1; Length 1908;
; Best Local Similarity 53.0%; Pred. No. 1.3e-18;
; Matches 335; Conservative 0; Mismatches 294; Indels 3; Gaps 1;
QY 581 ACATGTTCCATGGCTCAGTCTCGGCTGCTATGGCAACGTCATTTAGCAGCCTCAACT 840
Db 452 ACCTCTACACGCGGGAGGAGATTGCCACACGCGGGCAACGTCATCGTGTGCAGTTCACT 511
QY 641 ACCGCTCTTGGGGTGTCTCGGCTTTTCTCAGCACCGGGGACCAGGCTGCACAAAGGCAACTATG 700
Db 512 ACCGCTTGGGGCTTCTCAGCACCGGGGACTTCCAACTCCAGGTAACATATG 571
QY 701 GGCTCTCGACACAGATCCAGGCGCTGCGCTGAGTGAAGAAACATCGCCCACTTTGGGG 760
Db 572 GCCTTTGGGATCAGCACATGGCCATTTGCTTGGGTGAAGAGGAAACATTTAGGCGCTTCGGAG 631
QY 761 GCGACCCCGAGCGTATCACCATCTTTGGTTCGCGGGCAGGGGCTCTCTGCGTCAACCTTC 820
Db 632 GAGACCCCGACACATCACCTCTTTGGGAGTTCGCGGGGCGCCAGCGTCTCTCTGC 591
QY 821 TGATCTCTCCACCATTCAGAAAGGCTGTTCCAGAAAGCCATCGCCCAAGTGGACCG 880
Db 692 AGACCCCTCTCTCCCTACAAAGGCGCTCATCAAGCGAGCCATCAGCCAGAGTGGAGTGG 751
QY 881 CCATTTCCAGCTGCTGTCTCACTACAGCCGCTCAAGTACACGCGGCTGCTGGCAGCCA 940
Db 752 GTTTGTGCGCTTGGGCAATCCAGAGACCCCTCTTTGGGCTAAAGGATTCAGAGA 811
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; RESULT 9
; US-09-123-960-2
; Sequence 2, Application US/09123960
; Patent No. 5981299
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehrnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
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; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" hard disc
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,881
; FILING DATE: June 5, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; REFERENCE/DOCKET NUMBER: 89,852-K
; TELEPHONE: 312/913-0001
; TELEFAX: 312/913-0002
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1908 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 100..129
; OTHER INFORMATION: /note= "complementary sequence to
; OTHER INFORMATION: oligonucleotide probe"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1824
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..1908
; OTHER INFORMATION: /note= "Bovine pancreatic
; OTHER INFORMATION: cholesterol esterase cDNA"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..30
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 31..1821
; US-09-123-960-2

Query Match 5.8%; Score 145.6; DS 2; Length 1908;
Best Local Similarity 53.0%; Pred. No. 1.3e-18;
Matches 335; Conservative 0; Mismatches 294; Indels 3; Gaps 1;

QY 581 ACATGTTTCATGGCTCAGTCCTGGCTGCTATGGCAAGTCATTGTAGCCAGGCTCAACT 640
Db |||||
QY 452 ACCTTACACGGGGAGGAGATTGCCACACGGGGCAACGTCATCGTGTGCTCAACT 511
Db |||||
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Db |||||
QY 512 ACCGGTTGGCCCTTGGGCTTCTCAGCACCGGGGACTCCAACTGCCAGTCACTATG 571
Db |||||
QY 701 GCGTCTCGACAGATCCAGGCCCTCGGCTGCTCAGTGAAGAAATCCGCCCACTTTGGG 760
Db |||||
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QY 632 GAGACCCCGACACATCACCTCTTTGGGAGTCGGCGGAGGCCCGCAGCTCTCTCTGC 691
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QY 821 TGATCTCTCCACCATTCAGAAAGGCTGTTCCAGAGGCCATCGCCCGAGTGGCACCG 880
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QY 692 AGACCTCTCTCCCTACAAAGGGCCTCATCAAGCGAGCCATCAGCCAGAGTGGAGTGG 751
Db |||||

881 CCAITTCAGCTGCTGTCAACTACAGCGCGCTCAAGTACACGCGGCTGCTGCGAGCA 940
Db |||||
752 GTTTGTCCCTTTGGGCACTCCAGCAGGACCCCTCTTCTGGGCTAAAGGATTCGAGGA 811
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QY 1181 CTGCAGAGAGCGAGACGCTGTGTCTGCCAGC 1212
Db 1049 ACCTCTTTGTCGGGATGAGCGTGCACGCCATC 1080

RESULT 10
US-08-445-050-8
; Sequence 8, Application US/08445050
; Patent No. 5763739
; GENERAL INFORMATION:
; APPLICANT: Blaesberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Hernell, Olle
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stroemqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5763739el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,050
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,691
; FILING DATE:
; APPLICATION NUMBER: SE 9300686-4
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300722-7
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner Ph.D., Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2184 base pairs

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; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; TISSUE TYPE: mammary gland
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 82..2088
 ; OTHER INFORMATION: /label= Variant_1
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 151..2085
 ; FEATURE:
 ; NAME/KEY: repeat_region
 ; LOCATION: 1756..2052
 ; FEATURE:
 ; NAME/KEY: repeat_unit
 ; LOCATION: 1756..1788
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 ; LOCATION: 2020..2052
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Query Match 5.3%; Score 132.4; DB 1; Length 2184;

Best Local Similarity 48.8%; Pred. No. 3.5e-16;

Mismatches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;

QY	581	ACATGTTTCGATGGCTCAGTCCTGGCTGCTATGGCAAGCTCATTTAGCCACGCTCAACT	640
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QY	641	ACGCTTGGGTGCTCGTCTTCTCAGACCGGGGACAGGCTGCAAAAGCAACTATG	700
Db	578	ACCGTGTGCGCCCTTGGGTTCTCAGCACTGGGGAGCCCAATCTGCCAGGTAACATG	637
QY	701	GGCTCTGACAGATCCAGGCGCTCGCTGCTCAGTGAAACATCGCCCACTTTGGG	760
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Db	758	AGACCTCTCTCCCTTACAAAGAGGCTCATCTCGGAGGCTATCGCCAGAGCGGCTGG	817
QY	881	CCATTTCCAGCTGGTCTGTCTCAACTACAGCCGCTCAAGTACACGGGCTGTGGCAGCA	940

Db	818	CCCTGAGTCCCTGGGTATCCAGAAAAACCACTCTTCTGGGCCAAAAAGTGGCTGAGA	877
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Db	878	AGTGGGTTGCCCTGTGGGTGATCCGCCAGGATGCCCAAGTGTCTGAAGGTACTGATC	937
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QY	1058	CCGTGTGGATGGGACGTGCTCCCGATGACCTCGAGATCTCTCATGACGAGGGAGAAT	1117
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Db	1118	TCCTCGCAGATCGGATGCTCCGATCAACGAGGCAAGAGTCAAGAGTCAAGGAGG	1177
QY	1238	TTGTGGACAACTGTATGGCTACCCGGAAGCAAGATGTCTCGGG-----AGACCA	1291
Db	1178	ACTTCTACAAAGCTGTGCTGAGTTCACAAATCACCAAGGGGCTCAGAGCGCCAGACA	1237
QY	1292	TCAGTTTATGACAGACTGGGCGGACGGGACATGGCGAATGGCCGCAAAACCC	1351
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QY	1352	TGCTGGCGCTCTTT-----ACTGACCACTTGGTGGCAGCAGCTGTGGCCACTGCCA	1405
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QY	1406	AGTGCACCGGACTACCACTCTCC---GTCTATTTTACACTTCTACCACTGCTGC	1462
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QY	1463	AGCGGAGGCGCGCTGAGTGGGAGATGCGCGCAGCGGATGAACCTGCTATGCT	1522
Db	1418	GGATGCCCTTACCCCAATGGTGGGGCGCACCATGACATGACATTCAGTACGTTT	1477
QY	1523	TTGGCGTCCCATGGTGGTGCACCGACCTTTCCCTGTAACTTCTCCAAAGATGACG	1582
Db	1478	TCGGGAAGCCCTTGGCCACCCCTACCGGGCTACCGGCCCAAGACAGGACAGTCTTAAG	1537
QY	1583	TCATGCTCAGTCCGCTGCTATGACCTACTGACCACTTCCGAGACTGGGGACCCCA	1642
Db	1538	CCATGATCG-----CCTACTGACCAACTTTGCCAAAAACAGGGGACCCCA	1582
QY	1643	AC 1644	
Db	1583	AC 1584	

RESULT 11

; US-08-204-691-8
 ; Sequence 8, Application US/08204691
 ; Patent No. 5827683
 ; GENERAL INFORMATION:
 ; APPLICANT: Blasekberg, Lars
 ; APPLICANT: Edlund, Michael
 ; APPLICANT: Hansson, Lennart
 ; APPLICANT: Hernell, Olle
 ; APPLICANT: Lundberg, Lennart
 ; APPLICANT: Stromqvist, Mats
 ; APPLICANT: Toernell, Jan
 ; TITLE OF INVENTION: No. 5827683el Polypeptides
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: White & Case
 ; STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2184 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: 82..2088
OTHER INFORMATION: /label= Variant_T
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 151..2085
FEATURE:
NAME/KEY: repeat region
LOCATION: 1756..2052
FEATURE:
NAME/KEY: repeat unit
LOCATION: 1756..1788
FEATURE:
NAME/KEY: repeat unit
LOCATION: 1789..1821
FEATURE:
NAME/KEY: repeat unit
LOCATION: 1822..1854
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NAME/KEY: repeat unit
LOCATION: 1921..1953
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NAME/KEY: repeat unit
LOCATION: 1954..1986
FEATURE:
NAME/KEY: repeat unit
LOCATION: 1987..2019
FEATURE:

NAME/KEY: repeat unit
LOCATION: 2020..2052
US-08-204-691-8
Query Match
5.3%; Score 132.4; DB 1; Length 2184;
Best Local Similarity 48.8%; Pred. No. 3 se-16;
Matches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;
Qy 581 ACATGTTTCGATGGCTCAGTCTCGCTGCTCCCTATGATGCAACGTCAATGTAGCCACGCTCAACT 640
Db |||||
Qy 518 ACCTGTATGACGGCGAGGAGATGCCACACGCGGAAACGTCATCGTGGTCACTTCACTTCAACT 577
Db |||||
Qy 641 ACCGTCTTGGGGTCTCGGTTTCTCAGCACCCGGGACCAAGGCTGCCAAAAGGCAACTATG 700
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Qy 1058 TGTAGCCCAACGCGCGCATCGACTATATAGCAGGACCAACACATGAGCGGCCACA 1117
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Db |||||
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Db |||||
Qy 1352 TGCTGGGCTCTTT-----ACTGACCAAAATGGGTGGGACCCAGCTGTGGCCACTGCCA 1405
Db |||||
Qy 1298 CTGTGGTGGACTTTGAGACCGATGTCTCTTCTGTGGTGGCCACCGAGATTGCCCTAGCCC 1357
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 Db 1583 AC 1584

RESULT 12
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 ; Sequence 31, Application US/09347878C
 ; Patent No. 6376210
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuan, Chong
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
 ; FILE REFERENCE: 25885-1651
 ; CURRENT APPLICATION NUMBER: US/09/347,878C
 ; CURRENT FILING DATE: 1999-07-06
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 31
 ; LENGTH: 2344
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (9)...(2252)
 ; FEATURE:
 ; OTHER INFORMATION: Human cholesterol esterase cDNA
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: M85201/GenBank
 ; US-09-347-878-31

Query Match 5.3%; Score 132.4; DB 4; Length 2344;
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 Db 805 AGGTGGGTTCCTCTGTGGGTGTGCGCCAGAGTGCCTGAGGTACTGATC 864
 Qy 1001 CCGGGAGCT---GGTGGACAGGAGCTGCAGCTGCCCGCTTACCACATCGCTTTGGG 1057
 Db 865 CCGAGCCCTGACGCTGGCTATAGGTGCCCTGGCAGGCTGGAGTACCCCTGCTGC 924

Qy 1058 CCGTGTGGATGCGGACGTGGTCCCGGATGACCCCTGAGATCCTCATGACGAGGAGAAAT 1117
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 ; Sequence 1, Application US/08445050
 ; Patent No. 5763739
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaeckberg, Lars
 ; APPLICANT: Edlund, Michael
 ; APPLICANT: Hansson, Lennart
 ; APPLICANT: Hernel, Oile
 ; APPLICANT: Lundberg, Lennart
 ; APPLICANT: Stromqvist, Mats
 ; APPLICANT: Toernell, Jan
 ; TITLE OF INVENTION: No. 5763739el Polypeptides
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: White & Case
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 10036-2787
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/445,050

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FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA: SE 9300722-7
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2428 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: 82..2319
OTHER INFORMATION: /product= "bile-salt-stimulated
OTHER INFORMATION: lipase"
FEATURE:
NAME/KEY: exon
LOCATION: 985..1173
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NAME/KEY: polyA_signal
LOCATION: 2397..2402
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US-08-445-050-1		

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Best Local Similarity	48.8%; Pred. No. 3,6e-16;
Matches	528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;
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QY	641 ACCGTCTTGGGTGCTCGGTTTCTCAGCACCGGGACCAAGGCTGCAAAAGGCAACTATG 700
Db	578 ACCGTCTGCGCCCTTGGTTCCTCAGCACTGGGACGCCAATCTGCCAGGTAACTATG 637
QY	701 GGCTCTCTGACACAGATCCAGGCCCTCGCTGAGTGAACATCGCCCATCTTGGGG 760
Db	638 GCCTTCGGGATCAGCATGCGCCATTGCTTGGGTGAAGAGGAATATCGCGCCTTCGGGG 697
QY	761 GCACCCCGAGCTATCACCATCTTTGGTTCGGGGCAGGGGCTCTCGTCAACCTTC 820
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QY	881 CCATTTCCAGTGGTCTGTCAACTACACCGCTCAAGTACACGCGGCTCTCGCGAGCCA 940
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Db	878 AGTGGGTTGCCCTGTGGGTGATGCCGCCAGGATGCCCAGTGTCTGAAGGTTACTGATC 937
QY	1001 CCCGGAGCT--GGTGGACAGGACGTGACGCTCCCGCTACCACTACGCTTTGGGC 1057
Db	938 CCCGAGCCCTGACGCTGGGCTATAAGGTCCCGCTGGCAGGCTTGGAGTACCCCATGCTGC 997
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Db 998 ACTATGTGGCTTCCTCCCTGTCAATGATGGAGACTTCATCCCGCTGACCCGATCAACC 1057
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; Patent No. 5827683
; GENERAL INFORMATION:
; APPLICANT: Blaeckberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Harnell, Olie
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stroemqvist, Mats
; APPLICANT: Toerrell, Jan
; TITLE OF INVENTION: No. 5827693el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,691
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300686-4
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300722-7
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner Ph.D., Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: mammary gland
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..2319
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Db 1583 AC 1584

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Job time : 135.731 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 16:42:38 ; Search time 605.415 Seconds
(without alignments)
1182.718 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2508	100.0	2508	24	Human carboxylesterase
2	2508	100.0	4667	24	Human carboxylesterase
3	2506.4	99.9	4622	24	Human drug coding
4	2500	99.7	4763	24	Human drug metabol
5	2443.6	97.4	2523	22	Human MBSF4 polype
6	2265.4	90.3	2663	24	Human drug metabol
7	1013	40.4	2865	24	3 isoform protein
8	1010	40.3	4233	21	cdna sequence of h

9	930.4	37.1	4975	23	AA574457	DNA encoding novel
10	924	36.8	924	21	AA574457	Human ORF ORF498
11	912.2	36.4	3112	21	AA574457	Human PRO701 prote
12	912.2	36.4	3113	20	AA574457	Human PRO701 nucle
13	912.2	36.4	3113	21	AA574457	Human PRO701 UNQ3
14	912.2	36.4	3113	25	AA574457	CDNA encoding huma
15	886.2	35.3	3454	25	AA574457	CDNA encoding novel
16	886.2	35.3	3751	25	AA574457	CDNA encoding novel
17	871	34.7	4436	21	AA574457	CDNA sequence of h
18	870.2	34.7	3502	24	AA574457	Human neurotrophin
19	751.8	30.0	4365	25	AA574457	CDNA encoding novel
20	751.2	30.0	815	23	AA574457	CDNA encoding novel
21	723.4	28.8	1764	21	AA574457	CDNA sequence of h
22	721.8	28.8	2183	21	AA574457	CDNA sequence of h
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24	697.4	27.8	2362	22	AA574457	Human cdna sequenc
25	697.4	27.8	2362	25	AA574457	CDNA encoding novel
26	697.4	27.8	2362	25	AA574457	CDNA encoding novel
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41	697.4	27.8	2362	25	AA574457	CDNA encoding novel
42	697.4	27.8	2362	25	AA574457	CDNA encoding novel
43	697.4	27.8	2362	25	AA574457	CDNA encoding novel
44	697.4	27.8	2362	25	AA574457	CDNA encoding novel
45	697.4	27.8	2362	25	AA574457	CDNA encoding novel

ALIGNMENTS

RESULT 1
ABA95200
ID ABA95200 standard; cdna; 2508 BP.

AC ABA95200;
XX
XX 10-JUN-2002 (first entry)
DE Human carboxylesterase family member, 33410 coding sequence.

KW Carboxylesterase; 33410; cytochrome; cardiant; dermatological; human;
KW antidiabetic; antirheumatic; antiarthritic; antiarrhythmic; vasotropic;
KW vulnary; neuroprotective; antiinflammatory; antitumor; antidiabetic;
KW antiallergic; antiviral; hepatotropic; nephrotropic; anti-HIV; gene;
KW antiparkinsonian; tuberculostatic; hypotensive; antithrombotic;
KW neurotropic; antitense therapy; angiogenesis; gene therapy; ss.

OS Homo sapiens.

XX
XX Key Location/Qualifiers
FH CDS 1..2508
FT /*tag= a
FT /product= "33410 polypeptide"

XX WO200216616-A2.

XX 28-FEB-2002.

XX 21-AUG-2001; 2001WO-US26091.

XX 21-AUG-2000; 2000US-226774P.

XX (MILL-) MILLENNIUM PHARM INC.
 XX Curtis RAJ;
 XX WPI; 2002-257916/30.
 XX P-PSDB; ABB07675.
 XX
 PT New carboxylesterase nucleic acid 33410, useful for the treatment and
 PT diagnosis of immune, cardiovascular, reproductive and cancerous
 PT disorders -
 XX
 XX Claim 1; Page 108-110; 123pp; English.
 XX
 CC The invention provides a novel carboxylesterase family member, designated
 CC 33410. Compounds that binds to or modulate the activity or expression of
 CC 33410, are useful for treating or preventing a disorder such as cellular
 CC proliferative or differentiative, neural, cardiovascular, prostatic, skin
 CC brain and skeletal muscular disorders, protein-protein interaction
 CC disorders, signal transduction disorders, immune (e.g. diabetes and
 CC rheumatoid arthritis), reproductive disorders, cardiovascular (e.g. hypertension,
 CC atherosclerosis, coronary artery disease, arrhythmia, ischemic heart
 CC disease and angina pectoris), vascular disorders (e.g. varicose veins,
 CC Wegeners granulomatosis and wound healing) or cancerous disorders,
 CC multiple sclerosis, Crohn's disease, ulcers, asthma, allergy, infection,
 CC kidney disease (glomerulonephritis), idiopathic thrombocytopenic purpura,
 CC hepatitis, tuberculosis, human immunodeficiency virus, Alzheimer's and
 CC Parkinson's. The 33410 polynucleotide and polypeptide are useful for
 CC diagnosis of a predisposition to a disorder, for evaluating the efficacy
 CC of a therapeutic or prophylactic disorder, for chromosome mapping, as
 CC immunogens, for drug screening, for the detection of mutations in the
 CC gene and for tissue typing. The present sequence represents the coding
 CC sequence of the human carboxylesterase family member, 33410.
 XX
 SQ Sequence 2508 BP; 425 A; 906 C; 751 G; 426 T; 0 other;

Query Match 100.0%; Score 2508; DB 24; Length 2508;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TTCCCGGG 180
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QY 241 GCGGG 300
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QY 301 ACCCTGCGGG 360
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 QY 1921 CGCGGCGCCCGCGCGTGGCACCTGCTGCGGAGCGGAGCGGAGCGCGGCGGCGGAG 1980
 DB 2340 CGCGGCGCCCGCGCGTGGCACCTGCTGCGGAGCGGAGCGGAGCGGCGGCGGAG 2399
 QY 1981 GCCTATGACCGCTTCCCGGGGACTCAGGGAGTACTCAGGAGCTGAGGCTCACCGTG 2040
 DB 2400 GCCTATGACCGCTTCCCGGGGACTCAGGGAGTACTCAGGAGCTGAGGCTCACCGTG 2459
 QY 2041 GCGGTGGGTGCT 2100
 DB 2460 GCGGTGGGTGCT 2519
 QY 2101 CCGGACCGGCGCAGAGCTGGGTGAGGCGGTAGCCACCTGGCGGCTCAGGCTCT 2160
 DB 2520 CCGGACCGGCGCAGAGCTGGGTGAGGCGGTAGCCACCTGGCGGCTCAGGCTCT 2579
 QY 2161 GCGGTGCTGTGGGGGCGCGCTGCTCCCGCGCGCGCGCTGAGCTGCCACAGAGAG 2220
 DB 2580 GCGGTGCTGTGGGGGCGCGCTGCTCCCGCGCGCGCGCTGAGCTGCCACAGAGAG 2639
 QY 2221 GAGCTGGTGTCTACCTGAGCGGGTGGTGGCTGGGCGGAGCCCTGCGGAGCT 2280
 DB 2640 GAGCTGGTGTCTACCTGAGCGGGTGGTGGCTGGGCGGAGCCCTGCGGAGCT 2699
 QY 2281 CTGCGCGCTGCTGCGCGCGCGCTTACACCTTGGCGCTGCGCGCGGAGCCCGAGATGTG 2340

Db 2700 CTGGCGCTCCCTGCGCGCCCGGACTACACCTGGCCCTGCGCGGACCGGACGATGTG 2759
 QY 2341 CCTCTCTTGGCCCGCGGGCCCTGACCTGCTGCCAGTGGCTGGGGCCACCGCCACCC 2400
 Db 2760 CCTCTCTTGGCCCGCGGGCCCTGACCTGCTGCCAGTGGCTGGGGCCACCGCCACCC 2819
 QY 2401 CACCGCGCCCTCCCTTCTATCCCTTGGGCGCTTCCCGCGCCCTCCACCGCCACC 2460
 Db 2820 CACCGCGCCCTCCCTTCTATCCCTTGGGCGCTTCCCGCGCCCTCCACCGCCACC 2879
 QY 2461 AGCCACAAACAGCTACCCACCCCGCCACTCCACCACTCGGATAG 2508
 Db 2880 AGCCACAAACAGCTACCCACCCCGCCACTCCACCACTCGGATAG 2927

RESULT 3
 ID AEN59628
 AC AEN59628 standard; cDNA; 4622 BP.
 XX AEN59628;
 DT 28-JUN-2002 (first entry)
 XX Novel human coding sequence SEQ ID NO: 39.
 DE Human; antianaemic; vulnary; antinflammatory; immunomodulator;
 XX antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
 XX neuroprotective; antiparkinsonian; protein therapy; EST;
 XX expressed sequence tag; gene; ss.
 OS Homo sapiens.
 XX WO200222660-A2.
 XX 21-MAR-2002.
 XX 10-SEP-2001; 2001WO-US26015.
 XX 11-SEP-2000; 2000US-0659671.
 XX (HYSB-) HYSEQ INC.
 XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Yue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX WPI: 2002-292408/33.
 DR P-PSDE; AB97215.
 XX An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis -
 XX Claim 1; SEQ ID NO 39; 509pp; English.

CC The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
 CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
 CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a coding sequence of the
 CC invention.

XX Sequence 4622 BP; 850 A; 1540 C; 1344 G; 888 T; 0 other;
 SQ
 Query Match 99.9%; Score 2506.4; DB 24; Length 4622;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGTGGCTCTGGCGCTGCTGCTGGGGCTGGCGGGCTCAACGGGGAGGGGGT 60

41 ATGTGGCTCTGGCGCTGCTGCTGGGGCTGGCGGGCTCAACGGGGAGGGGGT 100
 QY 61 CCGGGCGCGCGCCCGCGGGCGCCCGCGCTGGGGCTCGGACGCTCGGGAGAGCGC 120
 Db 101 CCGGGCGCGCGCCCGCGGGCGCCCGCGCTGGGGCTCGGACGCTCGGGAGAGCGC 160
 QY 121 TTCCCGGTGTGAACACGGGCTACGGGCGAGTGGCGCGTGTGGCGCGAGCTCAACAAC 180
 Db 161 TTCCCGGTGTGAACACGGGCTACGGGCGAGTGGCGCGTGTGGCGCGAGCTCAACAAC 220
 QY 181 GAGATCTTGGGCGCGCGCTGCTGGGGCTGGCGCTACGCCAGCGCGCGCTGGGC 240
 Db 221 GAGATCTTGGGCGCGCGCTGCTGGGGCTGGCGCTACGCCAGCGCGCGCTGGGC 280
 QY 241 GCCCGCGCTTTCCAGCGCGCTGAGGCGCGCGCTGCTGGCGCGGCTGCGCAACGCCACC 300
 Db 281 GCCCGCGCTTTCCAGCGCGCTGAGGCGCGCGCTGCTGGCGCGGCTGCGCAACGCCACC 340
 QY 301 ACCCTGCGCGCGCTGCGCGCGAGAACCTGACGGGGCGCTGCCCGCANTCATGCTGCT 360
 Db 341 ACCCTGCGCGCGCTGCGCGCGAGAACCTGACGGGGCGCTGCCCGCANTCATGCTGCT 400
 QY 361 GTGTGGTTTCAACCGACAATTTGGAGGGCGCGCCACTACGTGCAGAACACGAGCGAGC 420
 Db 401 GTGTGGTTTCAACCGACAATTTGGAGGGCGCGCCACTACGTGCAGAACACGAGCGAGC 460
 QY 421 TGCCTGTACCTCAACCTTACGTGCGCCACCGAGGAGCGTCCGCTCAAAAAAAGCTGAC 480
 Db 461 TGCCTGTACCTCAACCTTACGTGCGCCACCGAGGAGCGTCCGCTCAAAAAAAGCTGAC 520
 QY 481 GAGCGACGCTCAATCGCGCAGACACAGATATCGTGACCGCTGGGAGAGCGCTGTGATG 540
 Db 521 GAGCGACGCTCAATCGCGCAGACACAGATATCGTGACCGCTGGGAGAGCGCTGTGATG 580
 QY 541 CTGTTTCTCCATGCGCGCTCTACATGGAGGGGACCGGAAACATGTTTCGATGGCTCAGTC 600
 Db 581 CTGTTTCTCCATGCGCGCTCTCTACATGGAGGGGACCGGAAACATGTTTCGATGGCTCAGTC 640
 QY 601 CTGGCTGCTATGGCAACGTCATGTAGCCACGCTCAACTACCGTCTTGGGGTGGCTCGGT 660
 Db 641 CTGGCTGCTATGGCAACGTCATGTAGCCACGCTCAACTACCGTCTTGGGGTGGCTCGGT 700
 QY 661 TTTCTCAGACCGGGGACCGAGGCTGCAAAAGGCAACTATGGGCTCTTGGACACGATCCAG 720
 Db 701 TTTCTCAGACCGGGGACCGAGGCTGCAAAAGGCAACTATGGGCTCTTGGACACGATCCAG 760
 QY 721 GCGCTGCGTGGCTCAGTGAATAATCGCCCACTTTGGGGGCGAACCCCGAGCGTATCAC 780
 Db 761 GCGCTGCGTGGCTCAGTGAATAATCGCCCACTTTGGGGGCGAACCCCGAGCGTATCAC 820
 QY 781 ATCTTTGGTTCCGGGCGAGGGGCTCTCTGCTCAACCTTCTGATCTCTCCCAACCATTC 840
 Db 821 ATCTTTGGTTCCGGGCGAGGGGCTCTCTGCTCAACCTTCTGATCTCTCCCAACCATTC 880
 QY 841 GAAGGGCTGTTCAGAAAGCCATTCGCCAGAGTGGCAACGCCCATTTCCAGCTGGTGTGTC 900
 Db 881 GAAGGGCTGTTCAGAAAGCCATTCGCCAGAGTGGCAACGCCCATTTCCAGCTGGTGTGTC 940
 QY 901 AACTACACCGCTCAAGTACACCGCGCTGTCGGCAGCAAGGTGGCTGTGACCCAGAG 960
 Db 941 AACTACACCGCTCAAGTACACCGCGCTGTCGGCAGCAAGGTGGCTGTGACCCAGAG 1000
 QY 961 GACAGTGTGAAGCTGTGGAGTGTCTGCGCCCGGAAGCCCTCCCGGAGCTGGTGGACAG 1020
 Db 1001 GACAGTGTGAAGCTGTGGAGTGTCTGCGCCCGGAAGCCCTCCCGGAGCTGGTGGACAG 1060
 QY 1021 GAGTGTGAGCTGCGCTACCACTACGCTTTGGGCGCGTGGTGGATGGCGACGTTGTC 1080
 Db 1061 GAGTGTGAGCTGCGCTACCACTACGCTTTGGGCGCGTGGTGGATGGCGACGTTGTC 1120
 QY 1081 CCCGATGACCTGAGATCTCTATGACGAGGAGGAAATTCCTCAACTACGACATGCTCATC 1140
 Db 1121 CCCGATGACCTGAGATCTCTATGACGAGGAGGAAATTCCTCAACTACGACATGCTCATC 1180

QY	1141	GGCGTCAACGAGGAGAGGGGCTCAAGTTCTGGAGGACTCTGAGAGACGCGAGCGGT	1200
DB	1181	GGCGTCAACGAGGAGAGGGGCTCAAGTTCTGGAGGACTCTGAGAGACGCGAGCGGT	1240
QY	1201	GTGTCTGCACGGCTTTGACTTCACTGTCTTCCAACCTTTGTGGACAACCTGTATGGGTAC	1260
DB	1241	GTGTCTGCACGGCTTTGACTTCACTGTCTTCCAACCTTTGTGGACAACCTGTATGGGTAC	1300
QY	1261	CCGGAAGCAAGATGTGCTTTGGGAGACCAATCAAGTTTATGTATACAGACTGGGCGCAC	1320
DB	1301	CCGGAAGCAAGATGTGCTTTGGGAGACCAATCAAGTTTATGTATACAGACTGGGCGCAC	1360
QY	1321	CGGACAAATGCGAAATGCGCGCGCAAAACCTCTGTGGGCTCTTTTACTGACCACCAATGG	1380
DB	1361	CGGACAAATGCGAAATGCGCGCGCAAAACCTCTGTGGGCTCTTTTACTGACCACCAATGG	1420
QY	1381	GTGCACCAAGTGTGGCCACTGCCAAGCTGCACGCCGACTACCAAGTCTCCCGTCTACTTTT	1440
DB	1421	GTGCACCAAGTGTGGCCACTGCCAAGCTGCACGCCGACTACCAAGTCTCCCGTCTACTTTT	1480
QY	1441	TACACCTTCTACCAACCACTGCCAGCGGAGGGCGCGCTGAGTGGGAGATGGGCGCAC	1500
DB	1481	TACACCTTCTACCAACCACTGCCAGCGGAGGGCGCGCTGAGTGGGAGATGGGCGCAC	1540
QY	1501	GGGATGAACCTGCCCTATGTCTTTGGGCTGCCCATGGTGGGTGCCACCGACCTCTTCCCC	1560
DB	1541	GGGATGAACCTGCCCTATGTCTTTGGGCTGCCCATGGTGGGTGCCACCGACCTCTTCCCC	1600
QY	1561	TGTAACCTTCCAAGATGAGCTCATGCTCAGTGCCTGGTTCATGACCTACTGGAACCAAC	1620
DB	1601	TGTAACCTTCCAAGATGAGCTCATGCTCAGTGCCTGGTTCATGACCTACTGGAACCAAC	1660
QY	1621	TTCCGCCAAGACTGGGGACCCCAACACGCGGTGCCGAGGATACCAAGTTCATCCACAC	1680
DB	1661	TTCCGCCAAGACTGGGGACCCCAACACGCGGTGCCGAGGATACCAAGTTCATCCACAC	1720
QY	1681	AAGCCCAATCGCTTCGAGGAGGTGGTGTGGAGCAAAATTCACAGCAAGGAGAAGCAAT	1740
DB	1721	AAGCCCAATCGCTTCGAGGAGGTGGTGTGGAGCAAAATTCACAGCAAGGAGAAGCAAT	1780
QY	1741	CTGCACATAGGCTTGAGCCACGCTGCGGTGACAACTACCGGCCACAGGTGGCCTTC	1800
DB	1781	CTGCACATAGGCTTGAGCCACGCTGCGGTGACAACTACCGGCCACAGGTGGCCTTC	1840
QY	1801	TGGCTGGAGTCTGTGCCCCACTGCACAACTGCAACAGGAGTCTTTCACCAACCAACAG	1860
DB	1841	TGGCTGGAGTCTGTGCCCCACTGCACAACTGCAACAGGAGTCTTTCACCAACCAACAG	1900
QY	1861	CGCTTGCTCTCTAGGCCACGCGGTGCGGCTCGTCCCCCGTGGCGCCCGGGGACAC	1920
DB	1901	CGCTTGCTCTCTAGGCCACGCGGTGCGGCTCGTCCCCCGTGGCGCCCGGGGACAC	1960
QY	1921	CGCGGGCCCCGCGCTGCGACCTGCCCTCCGAGCCGAGCCGAGCCGCGCCCAAGG	1980
DB	1961	CGCGGGCCCCGCGCTGCGACCTGCCCTCCGAGCCGAGCCGAGCCGCGCCCAAGG	2020
QY	1981	GCCTATGACCGCTTCCCGGGGACTCAGGAGTACTCCAAGAGCTGAGCGTCAACGCTG	2040
DB	2021	GCCTATGACCGCTTCCCGGGGACTCAGGAGTACTCCAAGAGCTGAGCGTCAACGCTG	2080
QY	2041	GCGGTGGTGCCTCCCTCTCTCAACATCTGGCCTTTGCTGCCCTCTACTACAAG	2100
DB	2081	GCGGTGGTGCCTCCCTCTCTCAACATCTGGCCTTTGCTGCCCTCTACTACAAG	2140
QY	2101	CGGACCGGGGACAGGAGCTGCGGTGAGGCGGCTTAGCCCACTCGGCGCTCAGGCTCT	2160
DB	2141	CGGACCGGGGACAGGAGCTGCGGTGAGGCGGCTTAGCCCACTCGGCGCTCAGGCTCT	2200
QY	2161	GGCGTGCTGGTGGGGGCCCCCTGCTCCCGCGCGCGCGCGTGAAGTCCACAGAGGAG	2220
DB	2201	GGCGTGCTGGTGGGGGCCCCCTGCTCCCGCGCGCGCGCGTGAAGTCCACAGAGGAG	2260

Qy	2221	GAGCTGTGTCACCTGCAGCTGAAGCGGGGTGTGGCGTCCGGGCGGACCCTGCCGAGGCT	2286
Db	2261	GAGCTGTGTCACTTGAGCTGAAGCGGGGTGTGGCGTCCGGGCGGACCCTGCCGAGGCT	2320
Qy	2281	CTGGCGCCTGCCTGCGCGCGCCGACTACACCTTGCGCCCTGCGCGCGCACCGGACGATGTG	2340
Db	2321	CTGGCGCCTGCCTGCGCGCGCCGACTACACCTTGCGCCCTGCGCGCGCACCGGACGATGTG	2380
Qy	2341	CCTCTCTTTGCCCCCGGGGCGCTTGCACCTCTCTCCAGTAGGCTTGGGGCCACCGCCACCC	2400
Db	2381	CCTCTCTTTGGGCGCGCGGGCGCTTGCACCTCTCTCCAGTAGGCTTGGGGCCACCGCCACCC	2440
Qy	2401	CCACCGCCCCCTCCCTTCATCCCTTGGGCGCCCTTCCCCCGCGCCCTCCACCGCGCAC	2460
Db	2441	CCACCGCCCCCTCCCTTTCATCCCTTGGGCGCCCTTCCCCCGCGCCCTCCACCGCTACC	2500
Qy	2461	AGCCACAACACACGCTTACCCACCCGCCACTCCACCACTCGGGTATAG	2508
Db	2501	AGCCACAACACACGCTTACCCACCCGCCACTCCACCACTCGGGTATAG	2548
 RESULT 4 AAD40569 ID AAD40569 standard; cDNA; 4763 BP.			
XX	AC	AAD40569;	
XX	AC		
XX	AC		
Dt	30-OCT-2002	(first entry)	
DE	Human drug metabolising enzyme	(DME-5) cDNA.	
XX	Human; drug metabolising enzyme; autoimmune; inflammatory disorder;		
KW	acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;		
KW	proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;		
KW	asthma; neurological disorder; Alzheimer's disease; Huntington's disease;		
KW	dementia; Parkinson's disease; developmental disorder; anaemia; adenoma;		
KW	drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;		
KW	renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;		
KW	anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;		
KW	goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant;		
KW	anticonvulsant; nootropic; enzyme; DME-5; gene; ss.		
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
CDS	/177..2684		
FT	/tag= a	"Human DME-5"	
FT	/product=		
FT	/177..218		
sig_peptide	/tag= b		
mat_peptide	/tag= c		
FT	/product= "Mature human DME-5"		
FT	/177..224		
FT	/tag= d		
FT	/225..2681		
mat_peptide	/tag= e		
FT	/product= "Mature human DME-5"		
XX			
PN	WO200246426-A2.		
XX			
PD	13-JUN-2002.		
PF	04-DEC-2001; 2001WO-US47429.		
PR	08-DEC-2000; 2000US-254308P.		
PR	15-DEC-2000; 2000US-256189P.		
PR	21-DEC-2000; 2000US-257113P.		
PR	13-JAN-2001; 2001US-462706P.		
PR	02-FEB-2001; 2001US-266020P.		
XX	(INCY-) INCYTE GENOMICS INC.		
XX			

PI Sanjanwala MM, Yao MG, Au-young J, Baughn MR, Arvizu C, Ring HZ;
PI Lee EA, Ding L, Rafalia AJA, Tang YT, Yue H, Tribouley CM;
PI Lu DAM, Lal PG, Warren BA, Yang J, Walia NK, Nguyen DB;
PI Gandhi AR, Lu Y, Ison CH;
XX WPI: 2002-519668/55.
DR P-PSDB; AAE25020.
DR
XX
XX Novel human drug metabolizing polypeptide, useful in diagnosis,
PT prevention or treatment of autoimmune/inflammatory, cell proliferative,
PT neurological, developmental, endocrine, metabolic and gastrointestinal
PT disorders -
XX
PS Claim 73; Page 162-164; 169pp; English.
XX
CC The invention relates to an isolated human drug metabolising enzyme (DME)
CC and its nucleotide. DME is useful for diagnosing, treating or preventing
CC disorders associated with aberrant expression of DME, where the disorders
CC are selected from autoimmune/inflammatory disorder such as acquired
CC immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,
CC uveitis; a cell proliferative disorder such as arteriosclerosis,
CC cirrhosis, hepatitis, and cancer; a neurological disorder such as
CC Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
CC a developmental disorder such as renal tubular acidosis, epilepsy,
CC anaemia; an endocrine disorder such as adenoma, thrombosis and
CC infections; an eye disorder such as conjunctivitis, glaucoma, cataract;
CC metabolic disorder such as cystic fibrosis, diabetes and goitre; a
CC gastrointestinal disorder such as anorexia, peptic ulcer; and liver
CC disorders. DME is useful in a number of drug screening techniques and to
CC analyse the proteome of a tissue or cell type. The invention is useful
CC for creating knock-in humanised animals or transgenic animals to model
CC human diseases, in somatic or germline gene therapy, to generate a
CC transcript image of a tissue or cell type, for detecting differences in
CC the chromosomal location due to translocation, inversion, etc. among
CC normal, carrier or affected individuals, and as hybridisation probes for
CC mapping naturally occurring genomic sequences. The present sequence is
CC human DME-5 cDNA.
XX
SQ Sequence 4763 BP; 871 A; 1601 C; 1364 G; 927 T; 0 other;

Query Match 99.7%; Score 2500; DB 24; Length 4763;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2503; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTGGCTCTCGCGCTGTGTCTGTGGGGCTGGGGGGCTCAACGGGGGGAGGGGT 60
DB 177 ATGTGGCTCTCGCGCTGTGTCTGTGGGGCTGGGGGGCTCAACGGGGGGAGGGGT 236
QY 61 CCCGG 120
DB 237 CCCGG 296
QY 121 TTCCCGGTGTGAACACGGCTACGGGGGAGTGGGGGGTGGGGGGGGGGGGGGGGGG 180
DB 297 TTCCCGGTGTGAACACGGCTACGGGGGAGTGGGGGGTGGGGGGGGGGGGGGGGGG 356
QY 181 GAGATCCTGG 240
DB 357 GAGATCCTGG 416
QY 241 GCCCGGG 300
DB 417 GCCCGGG 476
QY 301 ACCCTGCGCGGG 360
DB 477 ACCCTGCGCGGG 536
QY 361 GTGTGGTTTACCGAACCTTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
DB 537 GTGTGGTTTACCGAACCTTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 596
QY 421 TGCCTGTACCTCAACCTCTACGTGCGCCACCGAGGAGCGGTCCCTCACAACAAAAACGTGAC 480

DB 597 TSCGTGTACCTCAACCTCTACGTGCCACCGAGGACGGTCCGCTCACAACAAAAACGGTAC 656
QY 481 GAGCGAGCGCTCAATCCGCCAGACACAGATATCCGTGACCCCTGGGAAGAGCCCTGTGATG 540
DB 657 GAGCGAGCGCTCAATCCGCCAGACACAGATATCCGTGACCCCTGGGAAGAGCCCTGTGATG 716
QY 541 CTGTTTCTCCATCGCGCTCTTACATGAGGGGACCGGAAACATGTTTCGATGGCTCAGTC 600
DB 717 CTGTTTCTCCATCGCGCTCTTACATGAGGGGACCGGAAACATGTTTCGATGGCTCAGTC 776
QY 601 CTGCGCTCGCTATGCAACGCTCAATGTAGCCACGCTCAACTACGCTCTTGGGGTCTCGGT 660
DB 777 CTGCGCTCGCTATGCAACGCTCAATGTAGCCACGCTCAACTACGCTCTTGGGGTCTCGGT 836
QY 661 TTTCTCAGCACCGGGGACCGAGGCTGCAAAAGGCAACTATGGGCTCTTGGACCAAGTCCAG 720
DB 837 TTTCTCAGCACCGGGGACCGAGGCTGCAAAAGGCAACTATGGGCTCTTGGACCAAGTCCAG 896
QY 721 GCCCTGCGCTGGCTCAGTGAAGCAATCGCCACTTTTGGGGGGGACCCCGAGCGTATCAC 780
DB 997 GCCCTGCGCTGGCTCAGTGAAGCAATCGCCACTTTTGGGGGGGACCCCGAGCGTATCAC 956
QY 781 ATCTTTGGTTCCGGGGCAGGGGCTCTCTGCGTCAACCTTCTGATCTCTCCCACTTCA 840
DB 957 ATCTTTGGTTCCGGGGCAGGGGCTCTCTGCGTCAACCTTCTGATCTCTCCCACTTCA 1016
QY 841 GAAGGGCTGTTTCCAGAGGCGATCGCCCAAGTGGCAACCCCAATTTCCAGCTGGTCTGTC 900
DB 1017 GAAGGGCTGTTTCCAGAGGCGATCGCCCAAGTGGCAACCCCAATTTCCAGCTGGTCTGTC 1076
QY 901 AACTTACACAGCGCTCAAGTACACGGGCTCTCGGACCAAGGTGGGCTGTGACCGAGAG 960
DB 1077 AACTTACACAGCGCTCAAGTACACGGGCTCTCGGACCAAGGTGGGCTGTGACCGAGAG 1136
QY 961 GACAGTCTGAAGCTGTGGAGTGTCTGCGCGGAAGCCCTCCCGGGAGCTGGTGGACAG 1020
DB 1137 GACAGTCTGAAGCTGTGGAGTGTCTGCGCGGAAGCCCTCCCGGGAGCTGGTGGACAG 1196
QY 1021 GACGTGACGCTGCGGCTACCAATCGCTTTGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1080
DB 1197 GACGTGACGCTGCGGCTACCAATCGCTTTGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1256
QY 1081 CCCGATCACCTCGAGATCTCTATGACAGGAGGAGATTCCTCAACTACGACATGCTCATC 1140
DB 1257 CCCGATCACCTCGAGATCTCTATGACAGGAGGAGATTCCTCAACTACGACATGCTCATC 1316
QY 1141 GGCGTCAACAGGAGAGGGGCTCAAGTTCGTGGAGGACTCTCGAGAGAGGAGGAGCGGT 1200
DB 1317 GGCGTCAACAGGAGAGGGGCTCAAGTTCGTGGAGGAGGAGGAGGAGGAGGAGCGGT 1376
QY 1201 GTGTCTCCAGCGCTTTGACTTTTCACTGCTCCAACTTTTGGGACCACTGTATGGCTAC 1260
DB 1377 GTGTCTCCAGCGCTTTGACTTTTCACTGCTCCAACTTTTGGGACCACTGTATGGCTAC 1436
QY 1261 CCGAAGGCAAGGATGTGCTTCCGGGAGACCATCAAGTTTATGTACAGACTGGGCGGAC 1320
DB 1437 CCGAAGGCAAGGATGTGCTTCCGGGAGACCATCAAGTTTATGTACAGACTGGGCGGAC 1496
QY 1321 CCGGACAAATCGGAATGCGCCGCAAAACCTGCTGGCGCTCTTACTGACCAACCAATGG 1380
DB 1497 CCGGACAAATCGGAATGCGCCGCAAAACCTGCTGGCGCTCTTACTGACCAACCAATGG 1556
QY 1381 GTGGCACAGCTGTGGCCTACTGCCAAGCTGACGCGGACTTACCAAGTCTCCCGTCTACTTT 1440
DB 1557 GTGGCACAGCTGTGGCCTACTGCCAAGCTGACGCGGACTTACCAAGTCTCCCGTCTACTTT 1616
QY 1441 TACACCTTCTACCACTGCGAGGCGGAGGGCGGCTGAGTGGGAGAGTGGGGCGAC 1500
DB 1617 TACACCTTCTACCACTGCGAGGCGGAGGGCGGCTGAGTGGGAGAGTGGGGCGAC 1676
QY 1501 GGGGATGAATGCGCTTATGCTTTGGCGTGGCGCTGATGGTGGGCTGCCACCGGACCTCTTCCCC 1560

Db 1677 GGGGATCAACTGCCCTATGCTTTGGCGTGCCTATGGTGGTGCCACCGACCTCTTCCCC 1736
QY 1561 TGTAACTTCTCCAGATGACGTCATGCTCAGTGCCTGGTGTATGACCTACTTGGACCAAC 1620
Db 1737 TGTAACTTCTCCAGATGACGTCATGCTCAGTGCCTGGTGTATGACCTACTTGGACCAAC 1796
QY 1621 TTCCGCAAGATGGGGACCCCAACACGCGGTGCGCCAGGATACCAAGTTCAACACACC 1680
Db 1797 TTCCGCAAGATGGGGACCCCAACACGCGGTGCGCCAGGATACCAAGTTCAACACACC 1856
QY 1681 AAGCCCAATGCTTCCAGAGGTGCTGGAGGAAATTCACAGCAAGAGAGAGAT 1740
Db 1857 AAGCCCAATGCTTCCAGAGGTGCTGGAGGAAATTCACAGCAAGAGAGAGAT 1916
QY 1741 CTGCATATAGGCTGAAGCCACGCGTGCCTGACAACTACCGGCCCAACAAAGTGCCTTC 1800
Db 1917 CTGCATATAGGCTGAAGCCACGCGTGCCTGACAACTACCGGCCCAACAAAGTGCCTTC 1976
QY 1801 TGGCTGGAGCTGTGCCCCACCTGCAACCTGCAACGAGCTTTCAACACACCAACAG 1860
Db 1977 TGGCTGGAGCTGTGCCCCACCTGCAACCTGCAACGAGCTTTCAACACACCAACAG 2036
QY 1861 CGCTGCTCCCTTACGCCACGCGTGGCGGCTGCTGCCCCCGCTGGCGCCCGGACAC 1920
Db 2037 CGCTGCTCCCTTACGCCACGCGTGGCGGCTGCTGCCCCCGCTGGCGCCCGGACAC 2096
QY 1921 CGCGGCCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 2097 CGCGGCCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2156
QY 1981 GCTATGACGCTTCCCGGGGACTCAGGGAGTACTCAGGAGCTGAGGTACCGGT 2040
Db 2157 GCTATGACGCTTCCCGGGGACTCAGGGAGTACTCAGGAGCTGAGGTACCGGT 2216
QY 2041 GCGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db 2217 GCGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2276
QY 2101 CGGACCGCGGAGGAGTGGGTGCGAGGGCTTACCCACCTGGCGGTGAGGTCT 2160
Db 2277 CGGACCGCGGAGGAGTGGGTGCGAGGGCTTACCCACCTGGCGGTGAGGTCT 2336
QY 2161 GCGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Db 2337 GCGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2396
QY 2221 GAGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Db 2397 GAGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2456
QY 2281 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Db 2457 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2516
QY 2341 CTTCTTTGGGCCCCCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
Db 2517 CTTCTTTGGGCCCCCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2576
QY 2401 CCACGCGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Db 2577 CCACGCGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2636
QY 2461 AGCCACACACACGCTATCCACCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCT 2508
Db 2637 AGCCACACACACGCTATCCACCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCT 2684

RESULT 5
ID AAF82996
XX AAF82996 standard; cDNA; 2523 BP.
AC AAF82996;
XX

DT 29-JUN-2001 (first entry)
XX Human MBSP4 polypeptide encoding cDNA (clone 21417374.0.9).
DE MBSPX; cancer; preclampsia; immune system; neurological; cytostatic;
KW synecological; antinflammatory; neuroprotective; inotropic; relaxant;
KW cardiant; dermatological; gene therapy; human; MBSP4; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
CDS 1..2514
FT /*tag= a
FT /product= "MBSP4"
XX MO20012727-A2.
XX 19-APR-2001.
PD 13-OCT-2000; 2000MO-US28480.
PF 12-OCT-1999; 99US-0159231.
PR 12-JAN-2000; 2000US-0175670.
PR 12-OCT-2000; 2000US-0159231.
XX (CURA-) CURAGEN CORP.
XX Shimketa RA, Lichenstein H, Boldog FL;
PI WPI; 2001-282030/29.
DR P-PSDB; AAB62400.
DR Novel human polynucleotide sequences and the membrane bound or secreted
PT polypeptides encoded by these sequences, designated MBSPX -
PS Claim 9; Page 26-29; 157pp; English.
XX The invention relates to novel polypeptides, termed MBSPX and
CC polynucleotides encoding the MBSPX polypeptides. The MBSPX polypeptide,
CC nucleic acid and an MBSPX antibody are useful for treating or preventing
CC a pathology associated with the protein especially in humans. The MBSPX
CC nucleic acid can be used to express MBSPX protein (e.g. via a recombinant
CC expression vector in a host cell in gene therapy applications), an to
CC detect MBSPX mRNA in a biological sample or a genetic lesion in a MBSPX
CC gene. Disorders associated with insufficient or excessive production of
CC MBSPX protein include cancer, preclampsia, immune system disorders and
CC inflammation, neurological disorders, cardiovascular disorders; and skin
CC and muscle abnormalities. The anti-MBSPX antibodies can be used to detect
CC and isolate MBSPX proteins and modulate MBSPX activity. The present
CC sequence represents the nucleotide sequence of MBSP4, a human neurologin
CC 2 homologues.
XX

Sequence 2523 BP; 426 A; 901 C; 768 G; 428 T; 0 other;
Query Match 97.4%; Score 2443.6; DB 22; Length 2523;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2484; Conservative 0; Mismatches 24; Indels 6; Gaps 2;
QY 1 ATGTGGCTCTGGCGCTGTGTCTGTGGGGCTGGGGGGCTCAACGGGGGGAGGGGT 60
Db 1 ATGTGGCTCTGGCGCTGTGTCTGTGGGGCTGGGGGGCTCAACGGGGGGAGGGGT 60
QY 61 CCGCGGG 120
Db 61 CCGCGGG 120
QY 121 TTCCCGGTGGTGAACACACGGCCCTACGGGGGAGTGCCTGGTGTGGCGGGAGTCAACAC 180
Db 121 TTCCCGGTGGTGAACACACGGCCCTACGGGGGAGTGCCTGGTGTGGCGGGAGTCAACAC 180
QY 181 GAGATCTGG 240
Db 181 GAGATCTGG 240

QY 241 GCCCGCGCTTCAGCGCGCTGAGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 300
Db 241 GCCCGCGCTTCAGCGCGCTGAGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 300
QY 301 ACCCTGCGCGCGCTTCAGCGCGCTGAGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 360
Db 301 ACCCTGCGCGCGCTTCAGCGCGCTGAGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 360
QY 361 GTGTGTTTACCGACAACTTGGAGGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 420
Db 361 GTGTGTTTACCGACAACTTGGAGGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 420
QY 421 TGCGCTGCTACCTCAACCTTACGTCGCGCGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 480
Db 421 TGCGCTGCTACCTCAACCTTACGTCGCGCGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 480
QY 481 GAGCGACGCTCAATCCGCGCAGACACAGATATCCGCTGAGCCCTGGGAGAGCGCTGTGATG 540
Db 481 GAGCGACGCTCAATCCGCGCAGACACAGATATCCGCTGAGCCCTGGGAGAGCGCTGTGATG 540
QY 541 CTGTTTCTCGATGCGCGCTCTACATGAGGAGGACCGGAAACATGTTGATGGCTCAGTC 600
Db 541 CTGTTTCTCGATGCGCGCTCTACATGAGGAGGACCGGAAACATGTTGATGGCTCAGTC 600
QY 601 CTGGCTGCTATGGCAACGCTATTGTAGCCAGCTCAACTACCGCTTGGGGTGTCTCGGT 660
Db 601 CTGGCTGCTATGGCAACGCTATTGTAGCCAGCTCAACTACCGCTTGGGGTGTCTCGGT 660
QY 661 TTTCTCAGCACCGGAGCAGGCTGCAAAAGCAACTATGGGCTCTTGACCCAGATCCAG 720
Db 661 TTTCTCAGCACCGGAGCAGGCTGCAAAAGCAACTATGGGCTCTTGACCCAGATCCAG 720
QY 721 GCCCTGCTGCTCAGTCAAAACATCGCCACTTGGGGGAGCGCGCGCTGATCAC 780
Db 721 GCCCTGCTGCTCAGTCAAAACATCGCCACTTGGGGGAGCGCGCGCTGATCAC 780
QY 781 ATCTTTGGTTCCGGGACAGGCGCTCTGCTGCTCAACCTTGTATCTCTCCACCAATCA 840
Db 781 ATCTTTGGTTCCGGGACAGGCGCTCTGCTGCTCAACCTTGTATCTCTCCACCAATCA 840
QY 841 GAAGGCTGTTCCAGAGGCGCTGCGCCAGAGTGCGACCGCGCAATTCAGTGTGCTC 900
Db 841 GAAGGCTGTTCCAGAGGCGCTGCGCCAGAGTGCGACCGCGCAATTCAGTGTGCTC 900
QY 901 AACTACACCGCTCAAGTACACGGGCTGCTGCGCAGCCAGGCTGGCTGTGACCGGAG 960
Db 901 AACTACACCGCTCAAGTACACGGGCTGCTGCGCAGCCAGGCTGGCTGTGACCGGAG 960
QY 961 GACAGTGTGAAGCTGTGAGTGTCTGCGCGGAGAGCGCTCCCGGAGCTGTTGAGCCAG 1020
Db 961 GACAGTGTGAAGCTGTGAGTGTCTGCGCGGAGAGCGCTCCCGGAGCTGTTGAGCCAG 1020
QY 1021 GACGTGACGCTGCGCTTACACATCGCTTGGCGCGCGCTGTTGGATGGCGAGTGTGTC 1080
Db 1021 GACGTGACGCTGCGCTTACACATCGCTTGGCGCGCGCTGTTGGATGGCGAGTGTGTC 1080
QY 1081 CCGATGACCTTGATCTCTATGACAGGAGAAATTCCTCAACTACGATCTCATC 1140
Db 1081 CCGATGACCTTGATCTCTATGACAGGAGAAATTCCTCAACTACGATCTCATC 1140
QY 1141 GCGCTCAACAGGAGAGGCGCTCAAGTTCGTGGAGACTCTGACAGAGGAGGAGCGGT 1200
Db 1141 GCGCTCAACAGGAGAGGCGCTCAAGTTCGTGGAGACTCTGACAGAGGAGGAGCGGT 1200
QY 1201 GTGTGCGCGCGCTTGTACTTCACTGTCTCAACTTGTGGAGCAACTGTATGGCTAC 1260
Db 1201 GTGTGCGCGCGCTTGTACTTCACTGTCTCAACTTGTGGAGCAACTGTATGGCTAC 1260
QY 1261 CCGGAGGAGAGGATGTGCTTGGGAGACCATCAAGTTTATGACAGACTGGGCGGAC 1320
Db 1261 CCGGAGGAGAGGATGTGCTTGGGAGACCATCAAGTTTATGACAGACTGGGCGGAC 1320

QY 1321 CGGACAAATGCGGAAATGCGCGCAAAACCTGCTGGCGCTCTTTACTGACCAACAATGG 1380
Db 1321 CGGACAAATGCGGAAATGCGCGCAAAACCTGCTGGCGCTCTTTACTGACCAACAATGG 1380
QY 1381 GTGACACAGCTGTGGGCACTGCCAAGCTGACCGCGACTACCAAGTCTCCGCTCTACTTT 1440
Db 1381 GTGACACAGCTGTGGGCACTGCCAAGCTGACCGCGACTACCAAGTCTCCGCTCTACTTT 1440
QY 1441 TACACCTTCTTACCACTGCTGCGGAGGCGCGCTGAGTGGGAGATGCGGCGCAC 1500
Db 1441 TACACCTTCTTACCACTGCTGCGGAGGCGCGCTGAGTGGGAGATGCGGCGCAC 1500
QY 1501 GGGATGAATGCGCTTATGCTTTGGCGTCCCATGCTGGTGGTGCACCGACCTCTTCCC 1560
Db 1501 GGGATGAATGCGCTTATGCTTTGGCGTCCCATGCTGGTGGTGCACCGACCTCTTCCC 1560
QY 1561 TGTAACTTCTTCAAGATGACGCTCATGCTCAGTGGCGTGTGATGACTTACGACCAAC 1620
Db 1561 TGTAACTTCTTCAAGATGACGCTCATGCTCAGTGGCGTGTGATGACTTACGACCAAC 1620
QY 1621 TTGCGCAAGACTGGGACCCCAACAGCGCTGCGCAGGATACCAAGTTTATCCACACC 1680
Db 1621 TTGCGCAAGACTGGGACCCCAACAGCGCTGCGCAGGATACCAAGTTTATCCACACC 1680
QY 1681 AAGCCCAATGCTTCCAGGAGGCTGTGAGCAAAATTCACAGCAGGAGAGAGTAT 1740
Db 1681 AAGCCCAATGCTTCCAGGAGGCTGTGAGCAAAATTCACAGCAGGAGAGAGTAT 1740
QY 1741 CTGCACATAGGCTTGAAGCCACGCTGCTGACAACTTACCGCGCCCAACAGGTTGCTTC 1800
Db 1741 CTGCACATAGGCTTGAAGCCACGCTGCTGACAACTTACCGCGCCCAACAGGTTGCTTC 1800
QY 1801 TGGTGGAGCTGTGCGGCACTGCAACCTGCAACAGGAGCTTTCACCAACACAG 1860
Db 1801 TGGTGGAGCTGTGCGGCACTGCAACCTGCAACAGGAGCTTTCACCAACACAG 1860
QY 1861 CGCTGCTTCCCTACGCAACGCTGCGCGCTGCTGCTCCCC---CGCTGCGCGCGCGG 1917
Db 1861 CGCTGCTTCCCTACGCAACGCTGCGCGCTGCTGCTCCCCCGCGCGCTGCGCGCGG 1920
QY 1918 ACAGCGCGCGCGCGCGCTGCGCAACCTGCTTCCAGAGCCGAGCCGAGCGCGCGCA 1977
Db 1921 ACAGCGCGCGCGCGCGCTGCGCAACCTGCTTCCAGAGCCGAGCCGAGCGCGCGCA 1980
QY 1978 AGGCGCTATGACCGCTTCCCGGGAGCTCAGCGGACTTCTCCAGGAGTGTGAGCTCAC 2037
Db 1981 AGGCGCTATGACCGCTTCCCGGGAGCTCAGCGGACTTCTCCAGGAGTGTGAGCTCAC 2040
QY 2038 GTGCGCTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2097
Db 2041 GTGCGCTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
QY 2098 AAGCGGACCGGCGGAGAGCTGCGGTGCGAGGCGCTTAGCCCACTTGGCGCTCAGGC 2157
Db 2101 AAGCGGACCGGCGGAGAGCTGCGGTGCGAGGCGCTTAGCCCACTTGGCGCTCAGGC 2160
QY 2158 TCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2217
Db 2161 TCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
QY 2218 GAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Db 2221 GAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
QY 2278 GCTTCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2337
Db 2281 GCTTCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
QY 2338 GTGCTCTTCTTGGCGCGCGCGCTTGAACCTTGTGCGCAGTGTGGCTTGGGCGCACCG 2397
Db 2341 GTGCTCTTCTTGGCGCGCGCGCGCTTGAACCTTGTGCGCAGTGTGGCTTGGGCGCACCG 2400
QY 2398 CCGGACCGCGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2454

Db 2401 CCCCCCGGCCCCCTCCCTGCTGCAGATCTTGGGCGCTTCCCGCGCCCTCCACC 2460
 Qy 2455 GCCACGAGCACACACAGCGTATCCCGACCCCGCTCCACCACTCGGTATAG 2508
 Db 2461 GCCACGAGCACACACAGCGTATCCCGACCCCGCTCCACCACTCGGTATAG 2514

RESULT 6

ID ABA94727 standard; cDNA; 2663 BP.
 AC ABA94727;
 XX ABA94727;

XX 23-APR-2002 (first entry)

DE Human drug metabolizing enzyme (DME) cDNA (ID: 7473975CB1).

XX Drug metabolizing enzyme; DME; antiallergic; antianemic; antiasthmatic;
 KW osteopathic; antirheumatic; antiarthritic; dermatological; nephrotropic;
 KW antiinflammatory; vulnerary; antibacterial; virucide; antiparasitic;
 KW protozoacide; fungicide; antihelminthic; cytostatic; ophthalmological;
 KW antiarteriosclerotic; hepatotropic; antidiabetic; anorectic; human;
 KW thrombolytic; metabolic; anticoagulant; antithyroid; gynecological;
 KW antianginal; antitumor; antidiarrhoeic; laxative; enzyme; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 CDS 177..2582
 FT /*tag= a
 FT /product= "DME"
 FT /transl_except= "(pos: 475..477, aa: Xaa)"
 FT /note= "Xaa = unknown"

XX WO200204612-A2.

XX 17-JAN-2002.

XX 05-JUL-2001; 2001WO-US21324.

XX 07-JUL-2000; 2000US-216804P.

XX 14-JUL-2000; 2000US-218948P.

XX 21-JUL-2000; 2000US-220037P.

XX 28-JUL-2000; 2000US-221837P.

XX (INCYTE GENOMICS INC.

XX Baughn MR, Bruns CM, Das D, Ding L, Elliott VS, Gandhi AR;
 PI Hafalia AJA, Kearney L, Khan PA, Lal P, Lee EA, Lu DAM, Lu Y;
 PI Nguyen DB, Patterson C, Ramkumar J, Ring HZ, Sanjanwala MS;
 PI Tang YT, Thangavelu K, Thornton M, Tribouley CM, Wallia NK, Xu Y;
 PI Yang J, Yao MG, Yue H;

XX WPI; 2002-164641/21.

DR P-PSDB; ABB07524.

XX Novel drug metabolizing enzymes and polynucleotides encoding the
 PT enzymes, useful for treating, diagnosing or preventing
 PT autoimmune/inflammatory, cell proliferative, developmental and
 PT endocrine disorders

XX Claim 5; Page 163-164; 167pp; English.

XX The invention provides human drug metabolizing enzyme (DME) polypeptides
 CC and polynucleotides. DMEs can be expressed by standard recombinant
 CC methodology. The DME polypeptides, polynucleotides, modulators and
 CC antibodies are useful for diagnosing, treating and preventing autoimmune
 CC /inflammatory (e.g. allergies, anemia, asthma, osteoporosis, rheumatoid
 CC arthritis, atopic dermatitis, glomerulonephritis and irritable bowel
 CC syndrome, trauma, and bacterial, viral, parasitic, protozoal, fungal or
 CC helminthic infections), cell proliferative (e.g. cancer, atherosclerosis,
 CC and hepatitis), developmental (e.g. cerebral palsy and cataract).

CC endocrine (e.g. thrombosis, goiter, hyperplasia, amenorrhea and
 CC gynaecomastia), eye (e.g. iritis and glaucoma, metabolic (e.g. Addison's
 CC disease, diabetes and obesity), and gastrointestinal disorders (e.g.
 CC anorexia, nausea, abdominal angina, ulcerative colitis, diarrhoea and
 CC constipation). The DME polypeptides are useful in drug screening
 CC techniques, and to analyse the proteome of a tissue or cell type. The DME
 CC polynucleotides are useful for creating knock-in humanized animals or
 CC transgenic animals to model human diseases, and in somatic or germline
 CC gene therapy. The present sequence represents a human DME polynucleotide
 CC sequence.

XX Sequence 2663 BP; 471 A; 916 C; 782 G; 494 T; 0 other;

XX Query Match 90.3%; Score 2265.4; DB 24; Length 2663;
 XX Best Local Similarity 99.7%; Pred. No. 0;
 XX Matches 2269; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGTGGTCTCTGGCGCTGTCTGTGGTGGCGGTGCGGGGGCTCAACCGGGGGGGGGT 60
 Db 177 ATGTGGTCTCTGGCGTGTGTCTGTGGTGGCGGTGCGGGGGCTCAACCGGGGGGGT 236
 Qy 61 CCG 120
 Db 237 CCG 296
 Qy 121 TTCCCGGTGTGTAACACGCGCTACGCGCGAGTGTGCGGGTGTGCGGCGCGAGCTCAAC 180
 Db 297 TTCCCGGTGTGTAACACGCGCTACGCGCGAGTGTGCGGGTGTGCGGCGCGAGCTCAAC 356
 Qy 181 GAGATCTTGGCG 240
 Db 357 GAGATCTTGGCG 416
 Qy 241 GCCCGCGCTTCCAGCGCGCTGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 Db 417 GCCCGCGCTTCCAGCGCGCTGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 476
 Qy 301 ACCCTGCT 360
 Db 477 ACCCTGCT 536
 Qy 361 GTGTGGTTTACCGACAACTTGGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 Db 537 GTGTGGTTTACCGACAACTTGGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 596
 Qy 421 TGCTGTGTACCTCAACCTTACGTGCGCGACGAGCGTCCGCTCAACAAAAAAGCTGAC 480
 Db 597 TGCTGTGTACCTCAACCTTACGTGCGCGACGAGCGTCCGCTCAACAAAAAAGCTGAC 556
 Qy 481 GAGCGAGCGCTCAATCCGCGACAGACAGATATCCGTGACCCCTGGGAAGAGCTGTGATG 540
 Db 657 GAGCGAGCGCTCAATCCGCGACAGACAGATATCCGTGACCCCTGGGAAGAGCTGTGATG 716
 Qy 541 CTGTTTCTCCATGGCGGCTCTTACATGAGGGGACCGGAAACATGTTCGATGGCTCAGTC 600
 Db 717 CTGTTTCTCCATGGCGGCTCTTACATGAGGGGACCGGAAACATGTTCGATGGCTCAGTC 776
 Qy 601 CTGGCTGCCTATGGCAACCTCATTTGTAGCACGCTCAACTACCGTCTTGGGGTGTCTGGT 660
 Db 777 CTGGCTGCCTATGGCAACCTCATTTGTAGCACGCTCAACTACCGTCTTGGGGTGTCTGGT 836
 Qy 661 TTTTCTCAGCACCGGGGACCGAGCTCGAAGAGGAACTATGGGCTCTCTGGACCGAGTCCAG 720
 Db 837 TTTTCTCAGCACCGGGGACCGAGCTCGAAGAGGAACTATGGGCTCTCTGGACCGAGTCCAG 896
 Qy 721 GCCCTGCGTGGCTCAGTGAAGAACTCGCCCACTTTGGGGGCGACCCCGAGCGTATCACC 780
 Db 897 GCCCTGCGTGGCTCAGTGAAGAACTCGCCCACTTTGGGGGCGACCCCGAGCGTATCACC 956
 Qy 781 ATCTTTGTTTCCGGGGGAGGGGCGCTCTCTGCGTCAACCTTCTGATCTCTCCACCATCA 840
 Db 957 ATCTTTGTTTCCGGGGGAGGGGCGCTCTCTGCGTCAACCTTCTGATCTCTCCACCATCA 1016

QY 841 CAAGGGCTGTTCCAGAGGGCCATCGCCAGAGTGGCACCCGCAATTTCCAGCTGGTCTGTC 900
DB 1017 GAAGGGCTGTTCCAGAGGGCCATCGCCAGAGTGGCACCCGCAATTTCCAGCTGGTCTGTC 1076
QY 901 AACTACAGCGCGCTCAAGTACACCGCGTCTGTCAGCAGCAAGTGGGCTGTGACCGAGAG 960
DB 1077 AACTACAGCGCGCTCAAGTACACCGCGTCTGTCAGCAGCAAGTGGGCTGTGACCGAGAG 1136
QY 961 GACAGTCTGAAGCTGTGGAGTGTCTGGCGCGGAGCGCTCCCGGAGCTGTGTGGACCG 1020
DB 1137 GACAGTCTGAAGCTGTGGAGTGTCTGGCGCGGAGCGCTCCCGGAGCTGTGTGGACCG 1196
QY 1021 GACGTGAGCGCTGCCCTACCAATCGCTTTTGGGCGCGTGTGGATGGCGACGTGGTC 1080
DB 1197 GACGTGAGCGCTGCCCTACCAATCGCTTTTGGGCGCGTGTGGATGGCGACGTGGTC 1256
QY 1081 CCGATGACCTTGAGTCTCATGACAGGAGGAAATTCCTCAATACGACATGCTCATC 1140
DB 1257 CCGATGACCTTGAGTCTCATGACAGGAGGAAATTCCTCAATACGACATGCTCATC 1316
QY 1141 GCGCTCAACAGGAGAGGGCCCTCAAGTTCGTGGAGGACTCTCGAGAGCGAGGACGT 1200
DB 1317 GGTGTCAACAGGAGAGGGCCCTCAAGTTCGTGGAGGACTCTCGAGAGCGAGGACGT 1376
QY 1201 GTGTCTCCAGCGCTTTGACTTCACTGTCTCCAACTTTGTGACAACTGTATGCTATC 1260
DB 1377 GTGTCTCCAGCGCTTTGACTTCACTGTCTCCAACTTTGTGACAACTGTATGCTATC 1436
QY 1261 CCGGAGGCAAGATGTCTTCGGGAGACCATCAAGTTTATGTACACAGCTGGGCGAC 1320
DB 1437 CCGGAGGCAAGATGTCTTCGGGAGACCATCAAGTTTATGTACACAGCTGGGCGAC 1496
QY 1321 CCGGACAATGGGAAATGGCGCCAAACCTCTGGCGCTTTTACTGACCAACCAATGG 1380
DB 1497 CCGGACAATGGGAAATGGCGCCAAACCTCTGGCGCTTTTACTGACCAACCAATGG 1556
QY 1381 GTGSCACAGCTGTGCACTGCAAGCTGACCGCGACTACAGTCTCCGCTCTACTTT 1440
DB 1557 GTGSCACAGCTGTGCACTGCAAGCTGACCGCGACTACAGTCTCCGCTCTACTTT 1616
QY 1441 TACACCTTTTACCACTGSCAGGCGGAGGGCGGCGCTGAGTGGCGAGATCGGCGAC 1500
DB 1617 TACACCTTTTACCACTGSCAGGCGGAGGGCGGCGCTGAGTGGCGAGATCGGCGAC 1676
QY 1501 GGGGATGAAGTCCCTTATGTTTGGCGTGCCTATGTTGGTGGTGCACCGAAGCTCTTCC 1560
DB 1677 GGGGATGAAGTCCCTTATGTTTGGCGTGCCTATGTTGGTGGTGCACCGAAGCTCTTCC 1736
QY 1561 TGTAACTTCTCCAAAGATGACGTGCTAGTGGCGTGGTCTGATGACCTTCTGGACCAAC 1620
DB 1737 TGTAACTTCTCCAAAGATGACGTGCTAGTGGCGTGGTCTGATGACCTTCTGGACCAAC 1796
QY 1621 TTGCGCAAGACTGGGACCCCAACAGCGGTGCGCAGGATACCAAGTTCTATCCACACC 1680
DB 1797 TTGCGCAAGACTGGGACCCCAACAGCGGTGCGCAGGATACCAAGTTCTATCCACACC 1856
QY 1681 AAGCCCAATCGCTTCAGAGAGTGTGTGAGCAATTCACAGCAAGAGAGAGATAT 1740
DB 1857 AAGCCCAATCGCTTCAGAGAGTGTGTGAGCAATTCACAGCAAGAGAGAGATAT 1916
QY 1741 CTCACATAGGCTGAAGCCAGCGTGGTGGTGAACAATACCGCGCCAAACAAGTGGCGCTTC 1800
DB 1917 CTCACATAGGCTGAAGCCAGCGTGGTGGTGAACAATACCGCGCCAAACAAGTGGCGCTTC 1976
QY 1801 TGGCTGAGCTGTGCGCCCACTGCAACCTGCAACAGGACTCTTCAACCAACAG 1860
DB 1977 TGGCTGAGCTGTGCGCCCACTGCAACCTGCAACAGGACTCTTCAACCAACAG 2036
QY 1861 CGCTCGCTCCCTTACGCCACGCGTGGCGCTCGTCCCGCGCTGGCGCGCCCGGSCACA 1920
DB 2037 CGCTCGCTCCCTTACGCCACGCGTGGCGCTCGTCCCGCGCTGGCGCGCCCGGSCACA 2096
QY 1921 CGCGCGCCCGCGCTGCGCACTGCGCTTCCCGAGCGCGAGCCCGGCGCCCAAGG 1980

DB 2097 CGCCGGCCCCCGCCCGCTGCCACCTTGCTCCCGAGCCCGAGCCCGGCCCAAGG 2156
QY 1981 GCGTATGACCGCTTCCCGGGGACTCACGGGACTACTCCAGGACTGAGGCTGACCGTG 2040
DB 2157 GCGTATGACCGCTTCCCGGGGACTCACGGGACTACTCCAGGACTGAGGCTGACCGTG 2216
QY 2041 GCGTGGGTGCTTCCCTCTCTTCTCAACATCTCTGCTGGCTTGTGCTTCTTACTACAAG 2100
DB 2217 GCGTGGGTGCTTCCCTCTCTTCTCAACATCTCTGCTGGCTTGTGCTTCTTACTACAAG 2276
QY 2101 CGGGACCGCGCGAGAGCTGCGGTGCGAGGCGGCTTAGCCACCTGGCGGCTCAGGCTCT 2160
DB 2277 CGGGACCGCGCGAGAGCTGCGGTGCGAGGCGGCTTAGCCACCTGGCGGCTCAGGCTCT 2336
QY 2161 GCGTGGCTGTGGGGGGCCCCCTGCTCCCGCGCGCGCTGAGCTGCCACCGAGGAG 2220
DB 2337 GCGTGGCTGTGGGGGGCCCCCTGCTCCCGCGCGCGCTGAGCTGCCACCGAGGAG 2396
QY 2221 GAGCTGGTGTCACTGCACTGAGCGGGGTGCTGGCGTGGGGCGGACCTTCCG 2275
DB 2397 GAGCTGGTGTCACTGCACTGAGCGGGGTGCTGGCGTGGGGCGGACCTTCCG 2451

RESULT 7

ABQ61047

ID ABQ61047 standard; cDNA; 2865 BP.

XX AC ABQ61047;

XX DT 26-FEB-2003 (first entry)

XX DE 3 isoform protein encoding sequence.

XX KW Neuroprotective; immunomodulator; cancer; chromosome Xq13.1;

XX KW cytosolic; anti-inflammatory; gene therapy; nutritional supplement;

XX KW wound; burn; ulcer; Alzheimer's disease; Huntington's disease;

XX KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;

XX KW vulnery; gene; ss.

XX OS Homo sapiens.

XX PN WO200231111-A2.

XX PD 18-APR-2002.

XX PF 11-OCT-2001; 2001WO-US27760.

XX PR 12-OCT-2000; 2000US-0687527.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

XX PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX XX WPI; 2002-426278/45.

XX DR N-PSDB; ABP43803.

XX PT New polypeptides and their encoded proteins, useful as nutritional

XX PT sources or supplements, or in gene therapy, particularly for treating

XX PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or

XX PT inflammation

XX PS Claim 1; SEQ ID # 260; 357pp + sequence listing; English.

XX CC The invention relates to 446 newly isolated polynucleotide sequences.

XX CC The activity of polynucleotides of the invention may be described as,

XX CC vulnery, neuroprotective, immunomodulator, cytosolic and

XX CC anti-inflammatory. Compositions comprising nucleic acids of the invention

XX CC are useful for treating a mammalian subject, or as nutritional sources or

XX CC supplements. These are useful in gene therapy, particularly for treating

XX CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,

XX CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or

QY 899 TCAACTACACCGCCTCAAGTACACGCGGCTGTGGCAGCCAAAGTGGGCTGTGACGAG 958
 Db 1314 TGAACCTACCAACAGTGAAGTACACAGCCTGTGGCAGACAAAGTGGGCTGTATGTGC 1373
 QY 959 AGGACGTGTGAAGTGTGGAGTGTGTGGCCGGAGCCCTCCCGGAGCTGTGGAC 1018
 Db 1374 TGGACACCGTGGATATGTGGAGTGTGTCTTGGGAAAGAGTGCACAAAGGAGCTGGTAGAGC 1433
 QY 1019 AGGACGTGTGAAGTGTGGCCTGTACACATCGCCTTTGGGCGGCTGTGGATGCGCAGCTGG 1078
 Db 1434 AGGACATCCAGCAGCCGCTTACACAGTGGCTTTGGCCCTGTGTATGTATGTATGTCA 1493
 QY 1079 TCCCGGATGACCTGTGATCTCATGTGACAGCAGGAGAAATTCCTCAACTACGACATGCTCA 1138
 Db 1494 TTCCTGATGACCTGTGATCTCATGTGAGCAGGCGAGTTCCTCAACTATGACATCATGCG 1553
 QY 1139 TCGCGCTCAACAGGAGAGGGGCTCAAGTTTCGTGGAGGACTGTGAGAGAGCGAGGAGC 1198
 Db 1554 TAGGTGTCAACAGGCGAGGGTCTCAAGTTTGTGAAGGGGTGTGGACCTGTGAGGATG 1613
 QY 1199 GTGTGTCTGGCAGCGCTTTGACCTTCACTGTCTTCAACTTGTGGACACCTGTATGGCT 1258
 Db 1614 GTGTCTCTGGCAGCTGATTTGACATTTCCGTCTTCCAAATTTTGGGCAATCTGTATGGCT 1673
 QY 1259 ACCGGAAGGCAAGATGTCTTTCGGAGACCACTCAAGTTTATGTATACAGACTGGGCG 1318
 Db 1674 ATCTGTAGGGTATGAGACACCTTCGAGAGACCACTCAAGTTTATGTATACAGACTGGGCG 1733
 QY 1319 ACCGGGACATGGGGAATGGCGGCAACCTGTGCTTCAACTTGTGGACACCTGTATGGCT 1378
 Db 1734 ACCGTGACACCTGTGAGCAGCGCGCTTAAACATGTGTGGACCTTCTTCACTGACCACTG 1793
 QY 1379 GGGTGGACCAAGCTGTGGCCACTGCGAAGTGTGACGCGGACTACCAAGTCTCCCGCTACT 1438
 Db 1794 GGGTGGAGCCTCAGTGTGACAGCGCATCTGCATGCCGCTACGGCTCGCCTACTACT 1853
 QY 1439 TTTACACTTCTACCACTGACAGCGGAGCGGCGGCTGAGTGGGAGATGGGCGC 1498
 Db 1854 TCTACGCTTCTATCATCATCTGACAGAGCCTCATGAGCCTGCTTGTGATGAGATGAGCTC 1913
 QY 1499 ACGGGGATGAACCTGCCCTATGTCTTTGGCGTGCCTATGTGGGTGCGACCGACCTCTTCC 1558
 Db 1914 ATGGGATGAAGTACCTATGTCTTTGGGGTTCCTATGTAGTGGCCCACTGACCTTTTCC 1973
 QY 1559 CCTGTACTTCTCAAGAAAGTGTATGTCTGAGTGGCTGTGATGCTGATGCTGATGCTGATG 1618
 Db 1974 CTTGCAACTTCTCAAGAAAGTGTATGTCTGAGTGGCTGTGATGCTGATGCTGATGCTGATG 2033
 QY 1619 ACTTGGCAAGACTGGGAGCCCAACAGCGGCTGCGCAGGATACCAAGTTTCACTCCACA 1678
 Db 2034 ACTTGGCAAGACTGGGAGTCCCAACAGCGGCTGCGCAGGATACCAAGTTTCACTCCACA 2093
 QY 1679 CCAGCCCAATCGCTTGGAGAGGTGTGTGGAGCAANTTCAACAGAGGAGGAGCT 1738
 Db 2094 CCAAGGCCAATCGCTTGGAGAGGTGTGTGGAGCAANTTCAACAGAGGAGGAGCT 2153
 QY 1739 ATCTGCAATAGGCTTGAAGCAGCGCTGTGCTGACCAACTACCGCGCCCAACAAAGTGGCT 1798
 Db 2154 ACTTTCATCGGCTGAACCAAGGCTTCCAGATCATTTACCGGCGCACTAAGTGGCT 2213
 QY 1799 TCTGGTGGAGCTGTGCTGCGCAGCTGTGACCAACTGTGACAGGAGCTC-----TTCA 1849
 Db 2214 TTTGGAACACTGTGTGCTGCGCAGCTGTGACCAACTGTGACAGGAGCTC-----TTCA 2273
 QY 1850 CCACACCAACGCGCTGCTCTTACCCAGCGGCTGCGGCTGTGCTGCTGCTGCTGCTGCTGCTG 1909
 Db 2274 CCACACCAAGTGTGCTGCGCAGCTGTGACCAACTGTGACAGGAGCTC-----TTCA 2333
 QY 1910 CCGCGGCAACGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1959
 Db 2334 ATGGCAAGACTGTGAGCAGCAAGCGGCGAGCTTCTCACTGCTACAGCAAGAGATG 2393
 QY 1960 -----GAGCGCGAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2010

Db 2394 CCCAGGGTCTTGGAAACGGGAGCCAGGATCCAGGGCCACTCTCTGTGGAGAACCTCGT 2453
 QY 2011 GACTACTCCACGGAGTGAAGCTCACCCTGGGCGGTGGTGCCTCCTCTCTTCTTCAAC 2070
 Db 2454 GACTACTCCACCTGAATTAAGTGTCACTTCGCGGTGGGAGCTCCTCTCTTCTTCAAC 2513
 QY 2071 ATCTGGCTTTGTGCTCCTCTACTACAGCGGAGCCGGCGCAGGAGCTGGGCTGACAG 2130
 Db 2514 GTTCTGGCTTGTGCTCCTCTACTACCGTAAAGGACAAACGGCGCAGGAGCCCTTGGCG 2573
 QY 2131 CGGCTTAGCCACCTGGCGGCTCAGGCTCTGCGCTGCTGTGGGGGCGCCCTGTCTCC 2190
 Db 2574 CAGCTAGC-----CCTCAGCGGAGCGGCGGCGCG 2606
 QY 2191 GCCGCGGCGGTGAGTGTGCCACAGAGAGGAGTGTGTCTACTGACACTGAAGCGGGT 2250
 Db 2607 GAGTTGGAGCTGCTCCAGAGGAGGAGTGTGAGCATTAACAACCTGGGCGCCACCCAC 2666
 QY 2251 GGTGGCTGTGGGCGGAGCCTGCCAGGCTGTGCCCTGTGCCCTGCCCGCGGAGCTACAC 2310
 Db 2667 GAGTGTGAGGCGGCTGCCCGCCCATGACAGCTGTGCCCTCACTGCTTGGCGGAGCTACAC 2726
 QY 2311 CTGGCCTGTGGCGGCGGAGCAGGAGTGTGTCTTGTGGCGCGCGGCGGCTGACCGCTG 2370
 Db 2727 CTGACCTGTGGCGGCTTCCCGGATGACATCCCACTCATGACCCCAACACCATCATG 2786
 QY 2371 CTGCCAGTGGCTGG 2386
 Db 2787 ATCCCACTCCCTGG 2802

RESULT 9
 AAS74457
 ID AAS74457 standard; cDNA; 4975 BP.

XX AC AAS74457;
 XX DT 13-FEB-2002 (first entry)
 XX DNA encoding novel human diagnostic protein #10261.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.

XX WO200175067-A2.
 XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.
 XX P-PSDB; ABG10270.

XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity -

XX Claim 1; SEQ ID NO 10261; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS4197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 4975 BP; 1159 A; 1618 C; 1170 G; 1024 T; 4 other;

Query Match 37.1%; Score 930.4; DB 23; Length 4975;
 Best Local Similarity 91.5%; Pred. No. 1.9e-148;
 Matches 1071; Conservative 0; Mismatches 22; Indels 78; Gaps 5;

QY 1006 GAGCTGGTGACAGGACGTGACGCTGCCC---GCTACACATCGCCTTGGGCCCGTG 1062
 DB 298 GGGGTGCTCGCGGTACTACAGCCTGGCTGAGCTACACATCGCCTTGGGCCCGTG 357
 QY 1063 GTGATGGCGAGTGTGTCCTGAGTACCTGAGTCTCATGACAGGAGAAATTCCTC 1122
 DB 358 GTGATGGCGAGTGTGTCCTGAGTACCTGAGTCTCATGACAGGAGAAATTCCTC 417
 QY 1123 AACTAGACATGCTCATCGCGCTCACACAGGAGAGGCTCAAGTTCGTGAGGACTCT 1182
 DB 418 AACTAGACATGCTCATCGCGCTCACACAGGAGAGGCTCAAGTTCGTGAGGACTCT 477
 QY 1183 GCAGAGAGCAGGACGCTGTGCTGCGAGCGCTTGTGACTCTCACTCTCCAACTTTG 1242
 DB 478 GCAGAGAGCAGGACGCTGTGCTGCGAGCGCTTGTGACTCTCACTCTCCAACTTTG 537
 QY 1243 GACACCTGTATGGTACCGGAGGACAGGATGTGCTTCGGGAGACCAATCAAGTTATG 1302
 DB 538 GACACCTGTATGGTACCGGAGGACAGGATGTGCTTCGGGAGGACCAATCAAGTTATG 570
 QY 1303 TACACAGACTGGGCGCCGACCGGACCAATGGCGAATGCGCGCAAAA-CCCTGCTGCGCT 1361
 DB 571 -----ACTGGCGCCGACCGGACCAATGGCGAATGCGCGCAAAAACCCCTGCTGCGCT 623
 QY 1362 CTTTACTGACCAACCAATGGTGGCCACAGCTGTGGCCACTGCCAAGCTGCACGCCGACTA 1421
 DB 624 CTTTACTGACCAACCAATGGTGGCCACAGCTGTGGCCACTGCCAAGCTGCACGCCGACTA 683
 QY 1422 CCAGTCTCCGCTCTACTTTTACACCTTCTACACCACTGCCAGGAGGCGCGCCTGA 1481
 DB 684 CCAGTCTCCGCTCTACTTTTACACCTTCTACACCACTGCCAGGAGGCGCGCCTGA 743
 QY 1482 GTGGGACAGTGGCGGCGACCGGAGTGAATGCGCCTATGCTTTGGCGTCCCATGCTGGG 1541
 DB 744 GTGGGACAGTGGCGGCGACCGGAGTGAATGCGCCTATGCTTTGGCGTCCCAT----- 797
 QY 1542 TGCCACCGGACCTTTCCTCTGTAACTTCTCCAGAAATGACGTCACTGCTCAGTGGCGTGT 1601
 DB 798 -----GAATGACGTCACTGCTCAGTGGCGTGT 824
 QY 1602 CATGACCTACTGGACCAACTTCCGCAAGACTGGGACCCCAACACGCGGTGCCGACGA 1661
 DB 825 CATGACCTACTGGACCAACTTCCGCAAGACTGGGACCCCAACACGCGGTGCCGACGA 884
 QY 1662 T-ACCAAGTTTCACCAACCAAGCCCAATGGCTTTCAGAGAGGTGTGGAGCAAAATTC 1720
 DB 885 TAACCAAGTTTCACCAACCAAGCCCAATGGCTTTCAGAGAGGTGTGGAGCAAAATTC 944

QY 1721 ACAGCAAGGAGAGCAGTATCTGCATAGGCTTGAGCCACGCGTGGTGCACAACTACC 1780
 DB 945 ACAGCAAGGAGAGCAGTATCTGCATAGGCTTGAGCCACGCGTGGTGCACAACTACC 1004
 QY 1781 GCGCCAAAGGTGGCCTTCTGGCTGGAGCTGCTGCCCCACCTGACAACTGCACAGG 1840
 DB 1005 GCGCCAAAGGTGGCCTTCTGGCTGGAGCTGCTGCCCCACCTGACAACTGCACAGG 1064
 QY 1841 AGCTCTTTCACCAACCAACCAAGGCGCTGCTCCTAGCCACGCGTGGCGGCTCGTCCC 1900
 DB 1065 AGCTCTTTCACCAACCAACCAAGGCGCTGCTCCTAGCCACGCGTGGCGGCTCGTCCC 1124
 QY 1901 CGCTGGCGCCCGGCGCACACGCGCGCCCCCGCGCTGCCCACCTGCTCCGAGCCCG 1960
 DB 1125 CCGCTGGCGCCCGGCGCACAAACGCGCGCCCCCGCGCTGCCCACCTGCTCCGAGCCCG 1184
 QY 1961 AGCCCGAGCCCGGCGCCAAAGGCGCTATGACGCTTCCCGGGGAGTTCACGGGACTCTCA 2020
 DB 1185 AGCCCGAGCCCGGCGCCAAAGGCGCTATGACGCTTCCCGGGGAGTTCACGGGACTCTCA 1244
 QY 2021 CGGAGCTGAGCGTCAACGCTGCGCGCTGGGTGCTCCTCTCTCTCAACATCTCTGGCCT 2080
 DB 1245 CGGAGCTGAGCGTCAACGCTGCGCGCTGGGTGCTCCTCTCTCTCAACATCTCTGGCCT 1304
 QY 2081 TTGCTGCGCTCTACTACAGCGGACCGCGCGGAGGAGCTGCGGTGACGCGGCTTAGCC 2140
 DB 1305 TTGCTGCGCTCTACTACAGCGGACCGCGCGGAGGAGCTGCGGTGACGCGGCTTAGCC 1364
 QY 2141 CACCTGGCGGCTCAGGCTCTGCGCTGCTGG 2171
 DB 1365 CACCTGGCGGCTCAGGCTCTGCGCTGCTGG 1395

RESULT 10
 AAC74943
 ID AAC74943 standard; cDNA; 924 BP.
 XX AC AAC74943;
 XX DT 08-FEB-2001 (first entry)
 XX DE Human ORF498 polynucleotide sequence SEQ ID NO:995.
 KW Human; open reading frame; ORF; detection; cytotstatic; hepatotropic;
 KW vulnary; antipariatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW neurodegenerative disorder; osteoarthritis; proliferative disorder; hypertension;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.
 XX Homo sapiens.
 XX OS
 XX WO200058473-A2.
 XX PD 05-OCT-2000.
 XX PF 31-MAR-2000; 2000WO-US08621.
 XX PR 31-MAR-1999; 99US-0127607.
 XX PR 02-APR-1999; 99US-0127636.
 XX PR 05-APR-1999; 99US-0127728.
 XX PR 30-MAR-2000; 2000US-0540763.
 XX PA (CURA-) CURAGEN CORP.

PI Shimketa RA, Leach M;
 XX WPI: 2000-602362/57.
 DR P-PSDB; AAB40734.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 5; Page 969-970; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
 CC osteoprotective; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 924 BP; 189 A; 306 C; 261 G; 168 T; 0 other;

Query Match 36.8%; Score 924; DB 21; Length 924;
 Best Local Similarity 100.0%; Pred. No. 2.2e-147;
 Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 CGGAGCTGTGGACAGGAGCTGACGCTGCGCGTACACATCGCTTGGGCGCGTG 1062
 DB 1 CGGAGCTGTGGACAGGAGCTGACGCTGCGCGTACACATCGCTTGGGCGCGTG 60
 QY 1063 GTGATGCGGACGTGTGTCGCGGACCTGAGATCTCATGACAGGAGGAAATCTCTC 1122
 DB 61 GTGATGCGGACGTGTGTCGCGGACCTGAGATCTCATGACAGGAGGAAATCTCTC 120
 QY 1123 AACTACGACATGCTCATCGGCTCAACGAGGAGAGGCGCTCAAGTTCGTGAGACTCT 1182
 DB 121 AACTACGACATGCTCATCGGCTCAACGAGGAGAGGCGCTCAAGTTCGTGAGACTCT 180
 QY 1183 GCAGAGAGGAGGAGGCTGTGTCGCGGACCTTGTGACTTCACTCTCCAACTTTTG 1242
 DB 181 GCAGAGAGGAGGAGGCTGTGTCGCGGACCTTGTGACTTCACTCTCCAACTTTTG 240
 QY 1243 GACAACTGTATGCTACCGGAGAGGCAAGATGTGCTTCGGAGACCATCAAGTTTATG 1302
 DB 241 GACAACTGTATGCTACCGGAGAGGCAAGATGTGCTTCGGAGACCATCAAGTTTATG 300
 QY 1303 TACACAGACTGGCGGACCGGACCAATGGGAAATGCGGCAAAACCTGCTGGCGCTC 1362
 DB 301 TACACAGACTGGCGGACCGGACCAATGGGAAATGCGGCAAAACCTGCTGGCGCTC 360
 QY 1363 TTTACTGACCAACCAATGGGTGGACCAAGTGTGGCACTGCCAAGTGCACGCCCACTAC 1422
 DB 361 TTTACTGACCAACCAATGGGTGGACCAAGTGTGGCACTGCCAAGTGCACGCCCACTAC 420
 QY 1423 CAGTCTCCGCTACTTTTACACCTTCTACCACTTGCAGCGGAGGCGGCGCTGAG 1482
 DB 421 CAGTCTCCGCTACTTTTACACCTTCTACCACTTGCAGCGGAGGCGGCGCTGAG 480
 QY 1483 TGGGACAGATGCGGCGACCGGGATGAATCGCTTATGTCTTTGGCGTGCCTATGGTGGT 1542

DB 481 TGGGACAGATGCGGCGACCGGGATGAATCGCTTATGTCTTTGGCGTGCCTATGGTGGT 540
 QY 1543 GCCACGACCTCTTCCCTGTAACTTCTCCAAAGATGAGTCACTCAGTGCCTGTGTC 1602
 DB 541 GCCACGACCTCTTCCCTGTAACTTCTCCAAAGATGAGTCACTCAGTGCCTGTGTC 600
 QY 1603 ATGACCTACTTGGACCAACTTCCCAAGACTGGGGACCCCAACACCGCGTGCAGGAT 1662
 DB 601 ATGACCTACTTGGACCAACTTCCCAAGACTGGGGACCCCAACACCGCGTGCAGGAT 660
 QY 1663 ACCAAGTTTCATCCACACCAAGCCCAATCGCTTCGAGGAGTGGTGTGGAGCAAAATTCAC 1722
 DB 661 ACCAAGTTTCATCCACACCAAGCCCAATCGCTTCGAGGAGTGGTGTGGAGCAAAATTCAC 720
 QY 1723 AGCAAGAGAGAGCAGTATCTGACATATAGCCCTTGAAGCCACGCGTGGTGAACCTACCGC 1782
 DB 721 AGCAAGAGAGAGCAGTATCTGACATATAGCCCTTGAAGCCACGCGTGGTGAACCTACCGC 780
 QY 1783 GCCAACAAGGTGCGCTTCTTGGCTGGAGCTGTCGCCCTTGCACCACTGCACACGAG 1842
 DB 781 GCCAACAAGGTGCGCTTCTTGGCTGGAGCTGTCGCCCTTGCACCACTGCACACGAG 840
 QY 1843 CTCTTCCACCAACCAACGCGCTGCTTCCCTAGCCACGCGTGGCGCTGCTGCTCCCCC 1902
 DB 841 CTCTTCCACCAACCAACGCGCTGCTTCCCTAGCCACGCGTGGCGCTGCTGCTCCCCC 900
 QY 1903 GCTGGGCGCGCGCGGACACGCGG 1926
 DB 901 GCTGGGCGCGCGCGGACACGCGG 924

RESULT 11
 AAC58592
 ID AAC58592 standard; cDNA; 3112 BP.
 AC AAC58592;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO701 protein UNQ365 encoding cDNA SEQ ID NO:66.
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatologic; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neurotropic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antiproliferative; antiallergic;
 KW antiinflammatory; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease; ss.
 XX Homo sapiens.
 OS
 XX
 FN WO200053758-A2.
 PD 14-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US05841.
 PF
 XX 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99US-0123618.
 PR 12-MAR-1999; 99US-0123957.
 PR 13-MAR-1999; 99US-0125775.
 PR 12-APR-1999; 99US-0128849.
 PR 20-APR-1999; 99WO-US08615.
 PR 28-APR-1999; 99US-0131445.
 PR 04-MAY-1999; 99US-0132371.
 PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1998; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.

PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX

DR WPI: 2000-572271/53.

XX P-FSD; AAB33427.

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

XX Claim 23; Fig 27; 309pp; English.

CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central,
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

XX Sequence 3112 BP; 853 A; 867 C; 712 G; 680 T; 0 other;

Query Match 36.4%; Score 912.2; DB 21; Length 3112;

Best Local Similarity 64.7%; Pred. No. 2,3e-145;

Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGCGAGGAGCGCTTCCCGTGGTGAACACGCGCTACCGGCGAGTGCCTGTCGCGG 167

Db	112	CAGCCAAAGCAGAGTATCCAGTTGTCAACACAAATATGSCAAATCCGGGCGCTAAGAAC	171
QY	168	CGAGCTCAACACAGAGATCCCTGGGCCCCGCTGCTGAGTTCTTGGGCGTGCCTACGCCAC	227
Db	172	ACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCTC	231
QY	228	GGCGCCCTTGGGCGCCCGCTTCCAGCCGCTGAGCGCCCGCGCTCGTGCGCGCGGT	287
Db	232	ACCCCCCACTGGAGAGCGGTTTACGCCCCAGAACCCCGTCTCTCTGACTGGCAT	291
QY	288	GGCAACGCCACCAACCCCTGCCCGCCGCTGCCCGAGAACCTGACG---GGGCGCTGCC	344
Db	292	CGGAATACTACTCAGTTTGTGTGTGTGTCGCCAGCAGCCTGGATGAGAGATCCTTACT	351
QY	345	CGCCATCATGTGCTGTGTGTGTTCACCGAACATTTGGAGCGCGCCCACTACGTGCA	404
Db	352	GCATGACATGTGCCCATCTGTTTACCGCCAAATTTGGATACTTTTGATGACTATGTTC	411
QY	405	GAAACAGAGCGAGGACTGCTGTGCTCACTCACTGTCGCCACCGAGGAGCGTCCGCT	464
Db	412	AGATCAAAATGAAGACTGCTTACTTTAAACATCTAGTGTCCACGGAAGATGAGGCAA	471
QY	465	CACAAAAAAGCTGACGAGGCG-----ACGCTCAATCCGCCAGACACAGATATCCG	515
Db	472	CACAAAGAAAAACGAGATGATATAACGAGTAATGACCGTGTGAAGACGAGATATTC	531
QY	516	TGACCCCTG---GGAAGAGCCTGTGATGCTGTTTCTCCATGCGCGCTCTTACATGAGGG	572
Db	532	TGATCAGAACAGTAAGAACCGCTCATGGTCTATATCCATGGGGGATCTTACATGAGGG	591
QY	573	CACCGGAAACATGTTTCAGTGGCTCAGTCTGGCTGCTATGGCAACGTCATTTGAGGCC	632
Db	592	CACCGGCAACATGATTGACGCGACATTTGGCAAGCTACGAAACGTCATCGTGATCAC	651
QY	633	GCTCACTACCGTCTTGGGCTGCTGCTTCTCAGCACCGGGGACGAGCTGCAAAAGG	692
Db	652	CATTAACTACCGTCTGGGAATACTAGGGTTTTTAAAGTACCGGTGACCCAGCAGCAAAAGG	711
QY	693	CAACTATGGGCTCTGACACGAGTCCAGGCGCTGCGCTGCTCAGTGAACACATCGCCCA	752
Db	712	CAACTATGGGCTCTGATGAGATTAAGCACTGCGGTGATTTGAGGAGATTTGGGAGC	771
QY	753	CTTTGGGGGCGACCCCGAGCGTATCACCATCTTTTGGTTCCGGGGGACGGGCGCTCTCGCT	812
Db	772	CTTTGGGGGCGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGCTGGGGCGCTCTGTGT	831
QY	813	CAACTTCTGATCTCTCCCAACATTCAGAGGGCTGTTCCAGAGGCCATCGCCACAG	872
Db	832	CAGCTTTGACCGCTGTCCTACTACTAGAAAGTCTCTTCCAGAGGCCATCATTTAGAG	891
QY	873	TGGCACCGCCATTTCCAGCTGGTCTGTCACTACAGCGCGCTCAAGTACACGCGGTGCT	932
Db	892	CGGCACCGCCCTGTCAGCTGGGAGTGAATACAGCGCGGCCCAAGTACACTCGGATATT	951
QY	933	GGCAGCCAAAGTGGCTGTGACCGAGAGGACAGTGTGTAAGCTGTGGAGTGTCTGGCGCG	992
Db	952	GGCAGACAAAGTGGCTGCAACATGCTGGACACCAAGGATGAGTGAATGCTTGGCGAA	1011
QY	993	GAAGCCCTCCCGGAGCTGTGACCGAGGAGCGTGCAGCGCTGCCCGCTACACATCGCCTT	1052
Db	1012	CAAGAACTACAAGAGGCTCATCAGAGACCATCACCCCGGCCACCTACACATAGCCTT	1071
QY	1053	TGGGCGCGTGGTGGAGTGGGAGCGTGTGCCCGAGTACCTTGAGATCCTCATGACAGGG	1112
Db	1072	CGGCGCGGTGATCGACGGGACGTCATCCAGACGACCCCGAGATCCTGATGGAGCAAG	1131
QY	1113	AGATTTCTCACTAGACATGCTCATCGGCTGACAGGAGGAGGCGCTCAAGTCTGT	1172
Db	1132	CGAGTTCTCTCACTAGACATCATGCTGGCGGTCAACCAAGGGGAGGCGCTGAAGTCTGT	1191
QY	1173	GGAGGACTCTGCAGAGAGGAGGACGCTGTGCTGCCAGCGCTTTTGAATTTCACTTCTCTC	1232

1192 GAGCGGATCGTGATAACGAGGAGCGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTC 1251
1233 CAACCTTTGTGGCAACCTGTATGGCTACCGGAAAGCAAGATGTGCTTTGGGAGACCAT 1292
1252 CAACCTTCGTGGCAACCTTTACGGCTACCGTGAAGGAAAGACACTTTTGGGGAGACTAT 1311
1293 CAAGTTTATATACACAGACTGGGCCGACCGGGAATGCGAAATGCGCGGCAAAACCTT 1352
1312 CAAGTTTATATACACAGACTGGGCCGACCGGGAATGCGGGAATGCGGCGGAAACCTT 1371
1353 GCTGGGCTCTTTACTGACACCAATGGGTGGCAACAGCTGTGGCACTGCCAAGTGA 1412
1372 GGTGGCTCTTTACTGACCAACAGTGGGTGGGCCCGCGCGTGGCC---GCCGACTGCA 1428
1413 CGCGGACTACAGCTCTCCGCTCTACTTTTACACTTCTACCACTGCTCCAGCGCGGAGG 1472
1429 CGCGGACTAGGCTCCCGCACTTCTTATGCTTCTATCATCTGCTCAAGCGAAT 1488
1473 CGCGCTGAGTGGGAGATGCGGCGACCGGGATGAATGCCCTATGTTTGGCGTGCC 1532
1489 GAAGCCAGCTGGGAGATTCGGCCCATGCTGATAGGTCCCTATGTTCTCGGCATCC 1548
1533 CATGTGGGTGCCACGACTCTTCCCTGTAACTTCTCAGAAATGAGTCACTCTCAG 1592
1549 CATGATCGTCCACCGAGCTCTTCACTGTAACTTTTCCAAAGACGAGCTCATGCTCAG 1608
1593 TGGCGGTGATGACTACTGACCACTTCCCAAGACTGGGGACCCCAACCGCCGCT 1652
1609 CGCGGTGATCATGACTTCTGACGAACTTCCGCAAACTGCTGATCCAAATCAACCACT 1668
1653 GCGCGAGGATACCAAGTTCATCCACCAAGCGCAATGCTTCGAGGAGGTGGTGGAG 1712
1669 TCGTCAAGATCAAGTTCATCCACCAAAACCGCTTTGAAGAGTGGCGTGTGTC 1728
1713 CAATTCACAGCAGGAGAGCAGTATCTGCACATAGCCTGAAGCCACGCGTGCCTGA 1772
1729 CAAGTATAATCCAAAGACAGCTCTATCTGCAATTTGCTTGAAACCCAGAGTGAGGA 1788
1773 CAATACCGGCGCAACAGGTGGCTTCTGGTGGAGTCTGGTCCCGCCACCTGCAACCT 1832
1789 TCACACCGGCGCAACAGAGTGGCTTCTGGTGGAGTCTGGTCTCTCATTTGCAACCT 1848
1833 GCA-----CAGCGAGCTCTTCAACCAACAGCGCTGCTCTCCCTACGCGCAGCG 1893
1849 GAACGAGATATTCAGTATGTTTCAACCAACCAAGGTTCTTCAACGAGATGATC 1908
1884 CTGGCGGCTGTGCTCCCGCGTGGCGCCCGCGGCAACGCGCGCCCGCGCTGCGAC 1943
1909 ATTCCCTATGCGACCCGCGGATCTCCCGCCCAAGATATGGCAACCAACGCGCGAGC 1968
1944 CTGCTCTCCGAGCCGAGCGCGAGC-----CCGCGCCCAAGGC 1982
1969 AATCACTCTGCGCAACATCCCAACACTTAAGGACCTTCAAAAACAGGGCGCTGAGGA 2028
1983 CTATGACGCTTCCCGGGGACTCAAGGACTACTTCCAGGAGTGGAGCTGACCGTGGC 2042
2029 CACAAGTCTCTTCAATGAACCAACAGAGATTTATCCACGAAATTAAGTGTACCAATGC 2088
2043 GGTGGGTGCTCCCTCTCTTCTCAACATCTGCTGCTTCTGCTGCTCTTACTACAGCG 2102
2089 GGTGGGGGCTGCTCTCTCTCTTCTCAACATCTTACTGCTTTTGGCGGCTGCTACTACAAA 2148
2103 GGACGGCGGAGGAGTGTGGGTGAGCGGCTTAGCCCACTGCGGCTCAGGCTCTGG 2162
2149 GGACAGAGGCGCATGAGACTCAGAGGCGCCCGAGTCCCGAGAGAAACACCAATGA 2208
2163 GTGCTGTGGGGGCGGCTGCTCCCGCGCGGGCGGTGAGTGGCAACAGAGGAGGA 2222
2209 TATGCTCATATCCAGAACGAGAGATCATGTTCTCTGAGATGAAGCAGCTGGAACAGCA 2268
2223 GCTGTGTCACTGAGTGAAGCGGGTGGTGGCGGCGGAGCCTCGCGAGGCTCT 2282
2269 TCAGAGTGTGAGTGTGTCAG-----GCACACGACACACT 2304

QY 2283 GCGCCCTGCTGCGCCGCCGACTACACCTTGGCCCTGCGCGGCGCACCGGACGATGTGCC 2342
Db 2305 GAGGCTCACTGCGCCGCCGAGACTACACCTTCAAGTGGCGGCTGCGCGGAGATGACATCCC 2364
QY 2343 TCTTTTGGCGCCCGGGGCTGAGCCCTGCTGCTGCGGAGTGGCGCTG 2385
Db 2365 ACTTATGACGCCAAACACCATCATCATGATTCCAAACACACTG 2407

RESULT 12

AAZ34209
ID AAZ34209 standard; cDNA; 3113 BP.

XX AAZ34209;

XX 07-DEC-1999 (first entry)

XX Human PRO701 nucleotide sequence.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein; ss.

XX Homo sapiens.

XX WO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1998; 98US-0077450.

XX 11-MAR-1998; 98US-0077632.

XX 11-MAR-1998; 98US-0077841.

XX 11-MAR-1998; 98US-0077849.

XX 12-MAR-1998; 98US-0077791.

XX 13-MAR-1998; 98US-0078004.

XX 17-MAR-1998; 98US-0040220.

XX 20-MAR-1998; 98US-0078886.

XX 20-MAR-1998; 98US-0078910.

XX 20-MAR-1998; 98US-0078936.

XX 20-MAR-1998; 98US-0078939.

XX 25-MAR-1998; 98US-0079294.

XX 26-MAR-1998; 98US-0079656.

XX 27-MAR-1998; 98US-0079663.

XX 27-MAR-1998; 98US-0079664.

XX 27-MAR-1998; 98US-0079689.

XX 27-MAR-1998; 98US-0079728.

XX 27-MAR-1998; 98US-0079786.

XX 30-MAR-1998; 98US-0079920.

XX 31-MAR-1998; 98US-0079923.

XX 31-MAR-1998; 98US-0080105.

XX 31-MAR-1998; 98US-0080165.

XX 31-MAR-1998; 98US-0080194.

XX 01-APR-1998; 98US-0080327.

XX 01-APR-1998; 98US-0080328.

XX 01-APR-1998; 98US-0080333.

XX 01-APR-1998; 98US-0080334.

XX 08-APR-1998; 98US-0081049.

XX 08-APR-1998; 98US-0081070.

XX 08-APR-1998; 98US-0081071.

XX 09-APR-1998; 98US-0081195.

XX 09-APR-1998; 98US-0081203.

XX 09-APR-1998; 98US-0081229.

XX 15-APR-1998; 98US-0081817.

XX 15-APR-1998; 98US-0081838.

XX 15-APR-1998; 98US-0081952.

XX 15-APR-1998; 98US-0081955.

XX 21-APR-1998; 98US-0082568.

XX 21-APR-1998; 98US-0082569.

XX 22-APR-1998; 98US-0082700.

PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083332.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083436.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 30-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 07-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX (GETH) GENENTECH INC.

PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
PI WPI; 1999-551358/46.
XX P-PSDB; AA41740.

XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -

XX Claim 2; Fig 150; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AA433891 to
XX AA434338, and AA41685 to AA41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.

SQL	Sequence	3113 BP; 853 A; 867 C; 712 G; 681 T; 0 other;
	Query Match	36.4%; Score 912.2; DB 20; Length 3113;
	Best Local Similarity	64.7%; Pred. No. 2.3e-145;
	Matches 1503; Conservative	0; Mismatches 748; Indels 72; Gaps 7;
QY	108	CGCGAGGAGCGCTTCCCGGTGGTGAACACCGCCCTACGGGCGAGTGC
DB	112	CAGCCAAAGCAGATATCCAGTTGTCAACACAAATTTATGGCAAAATCCGGGGCTAAGAAC
QY	168	CGAGCTCAACACGAGATCCTGGGCGCGCTGTGTCAGTCTTGGGCTGCGCTACGCCAC
DB	172	ACCGTTACCCATGAGATCTTGGGTCCAGTGGAGAGTACTAGGGGTCCCTCTATGCCTC
QY	228	GCAGCCCTGGGCGCGCGCTTCCAGCCGCTTCCAGCGCGCTGAGGCGCGCTGTCGGCGCGGT
DB	232	ACCCCCCACTGGAGAGAGCGGTTTTCAGSCCCCAAGAACCCCGCTCTCTCGACTGGCAT
QY	288	GGGCAACGCCACCCCTGCGCGCGCTGCGCGAGAACCTTGCAGC---GGGCGCTGCC
DB	292	CCGAAATATCTACTCAGTTTGTCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
QY	345	CGCCATCATGCTGCTGTGTGCTTACCGCAACTTTGGAGCGCGCGCCACCTACGTGCA
DB	352	GCATGACATGCTGCCATCTGCTTACCGCAATTTGGATCTTTGATGACCTATGTTCA
QY	405	GAACGAGGAGGAGTGCCTGTACCTCAACTTACGTGCGCCACCGAGGAGCGTCCGCT
DB	412	AGATCAAAATGAAGACTGCTTAAACATCTAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT
QY	465	CACAAAAACGTCACGAGGCG-----ACGCTCAATCCCGCCACACACAGATATCG
DB	472	CACAAAGAAACGACATGATATACGAGTAATGACCGTGTGAAGACGAGATATTC
QY	516	TGACCTTG---GGAAGAGCGCTGTGATGCTGTTTCTCCATGGCGGCTCTTACATGAGGG
DB	532	TGATCAGAAACAGTAAAGAGCGCTGCTGCTATATCCATGGGGGATCTTACATGAGGG
QY	573	GACCGAAACATGTTCCATGGCTCAGTCTTGGTGCCTATGGAACCTCATTTAGTACAC
DB	592	CACCGCAACATGATGACCGGACATTTTGGCAAGCTACGGAACCTCATCGTGAATCAC
QY	633	GCTCACTACCGTCTTGGGGTGTCTCGGTTTCTCAGCACCGGAGCCAGCGTCAAAAGG
DB	652	CATTAACCTACCGTCTGGAATCTAGGGTTTAAAGTACCGTGCACGACGACGACGAGG
QY	693	CACTATGGCTCTGACACGATCCAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
DB	712	CACTATGGCTCTGCTGATCAGATTCAAGCACTGCGTGTGATGAGGAGATGTGGAGC
QY	753	CTTTGGGCGGACCCCGAGCGTATCACCATCTTTTGGTTCCGGGCGAGGCGCTCTCGCT
DB	772	CTTTGGGCGGACCCCGAGAGTGAACCTCTTTGGCTCGGGGCTTGGGCGCTCTCTGTGT
QY	813	CACTTTCTGATCTCTCCACCATTCAGAGGCTGTTCCAGAGGCTATCCAGGCTATCCCGCAG
DB	832	CAGCTCTTGACCTGTCCCACTACTCAGAAAGTCTCTTCCAGAGGCTATCATTTAGAG
QY	873	TGSCACCGCATTTCCAGCTGCTGTCACTACGAGCGCTCAAGTACACGCGGTGCT
DB	892	CGGACCGCGCTTCTCAGCTGGGCGAGTGAACCTACCGCGCGGCGGACGATACACTCGGATAT
QY	933	GGCAGCAAGGTGGCTGTGACCGAGAGGACAGTGTGAGCTGTGAGTGTCTGGCGCG
DB	952	GGCAGCAAGGTGGCTGTGACCATGCTGGACACCAACGACATGTTAGATGCTTGGCGAA
QY	993	GAAGCCCTCCGGAGCTGTGACAGGAGCTGAGCTGCGGCTGCGGCTACCATCGCTT
DB	1012	CAAGAACTACAGGAGCTCATCAGCAGACCATCACCCCGGCGACCTACCATACAGCTT
QY	1053	TGGGCGCGGTGGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
DB	1072	CGGCGCGGTGATCGAGCGGAGCTCATCCAGAGGACCCCGAGATCTCTGATGGAGAGG

1113 AGAATTCCTCACTAGCATCTCTATCGCGCTCAACAGGAGAGAGGCTCAAGTTGCT 1172
 1132 CGAGTTCTCTCACTAGCATCTATGCTGGGCTCAACAGGAGAGGCTCAAGTTGCT 1191
 1173 GGAGGACTCTGACAGAGGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
 1192 GGACGGGATCTGATTAACAGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1251
 1233 CAACTTTGAGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1292
 1252 CAACTTTGAGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311
 1293 CAACTTTGAGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1352
 1312 CAACTTTGAGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1371
 1353 GCTGGGCTCTTACTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1412
 1372 GGTGGCTCTCTTACTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
 1413 CGCGACTACAGTCTCCGCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 1472
 1429 CGCGAGTACAGTCTCCGCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 1488
 1473 CGCGCTGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAG 1532
 1489 GAAGCCAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAG 1548
 1533 CATGGTGGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAG 1592
 1549 CATGGTGGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAG 1608
 1593 TGCGGTGCTCATGCTTACTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1652
 1609 CGCGGTGCTCATGCTTACTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1668
 1653 GCAGGAGTACCAAGTCTCATGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1712
 1669 TCCTCAGGATACCAAGTCTCATGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728
 1713 CAAATTCACAGAGAGAGAGAGAGTCTGACATAGGCTGAGAGAGAGAGAGAGAGAGAG 1772
 1729 CAAATTCACAGAGAGAGAGAGTCTGACATAGGCTGAGAGAGAGAGAGAGAGAGAG 1788
 1773 CAAATTCACAGAGAGAGAGTCTGACATAGGCTGAGAGAGAGAGAGAGAGAGAG 1832
 1789 TCCTCAGGATACCAAGTCTCATGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1848
 1833 GCA-----CACGAGTCTTCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1893
 1849 GAAAGAGATATTCAAGTCTTCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1908
 1884 CTGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1943
 1909 ATTTCCTATGAGACCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1968
 1944 CTGCTCTCCGAGCGGAGCGCGAGC-----CGGCGCAAGGCG 1982
 1969 AATCACTCTCTGCAACAATCTTCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2028
 1983 CTATGACCGTCTCCGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2042
 2029 CAACTTGTCTCTTATTGAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2088
 2043 CGTGGGTGCT 2102
 2089 CGTGGGTGCT 2148
 2103 GGACCGGCGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2162
 2149 GGACAGAGGCGGCTGAGACTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2208

2163 CGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2222
 2209 TATGCTTACATCCAGAACGAGAGATCATGCTCTGAGATGAGAGCTGAGACAGCA 2268
 2223 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2282
 2269 TCACGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2304
 2283 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2342
 2305 GAGGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2364
 2343 TCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2385
 2365 ACTTATGAGCGCAACACACCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2407

RESULT 13

AAC78552
 ID AAC78552 standard; cDNA; 3113 BP.
 XX AAC78552;
 AC AC
 XX XX
 DT 08-FEB-2001 (first entry)
 XX XX
 DE Human PRO701 (UNQ365) nucleotide sequence SEQ ID NO:374.
 XX XX
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 XX XX expressed sequence tag; detection; cancer; ss.
 OS Homo sapiens.
 XX XX
 PN WO200053756-A2.
 XX XX
 PD 14-SEP-2000.
 XX XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood W;
 XX WPI; 2000-611443/58.
 DR P-PSDB; AAB44296.
 DR P-PSDB; AAB44296.

XX Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX Claim 2; Fig 150; 636pp; English.
 PS

CC AAC7458 to AAC7459 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC7460 to AAC7498 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SQ Sequence 3113 BP; 853 A; 867 C; 712 G; 681 T; 0 other;
 Query Match 36.4%; Score 912.2; DB 21; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.3e-145;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
 QY 108 CGGCGAGGAGCGCTTCCCGTGGTGAACACGGCTACGGCGAGTGGCGGTGGCGGCG 167
 DB 112 CAGCCAGCAGTATCCAGTGTCTACACAAATATGGCAAAATCCGGGCGCTAAGAAC 171
 QY 168 CGAGCTCAACACAGAGATCTCGGCGCCGCTGTCGACAGTCTTGGGCGTGCCTTACGCCAC 227
 DB 172 ACCGTTACCCAAATGAGATCTTGGGTCCAGTGGAGAGTACTTAAAGGGTCCCTATGCCTC 231
 QY 228 GCGCGCCCTGGGCGCCGCGCTTCCAGCGCTGAGGCGCGCGCTCGTGGCGCGGCGT 287
 DB 232 ACCCCCACTGGAGAGAGGCGGTTTCCAGCGCCCGAGAACCCCGCTCTCTGGACTGGCAT 291
 QY 288 GCGCAACGCGCACACCTTGGCGCCGCTGCGCGCAGAACCTTGCACG---GGGCGGTGCC 344
 DB 292 CCGAAATACTACTCAGTTTCTGCTGTGTGCGCCCGACACCTGGATGAGAGATCTTACT 351
 QY 345 CGCCATCATGCTCCTGTGTGTGTACACGAACTTGGAGGGCGGCCACCACTACGTGCA 404
 DB 352 GCATGACATGCTCCCATCTGGTTTACCAGCAATTTGGATATTTGATGACCTATGTTCA 411
 QY 405 GAACACGAGCGAGACTGCTGTACCTCAACCTCTACGTGCGCCACCGAGGAGCGTCCGCT 464
 DB 412 AGATCAAAATGAGACTGCTGCTTACTTAAACATCTACGTGCGCCACGGAAGATGGAGCMA 471
 QY 465 CACAAAAAAGTGACGAGCGG-----ACGCTCAATCCGCGCAGACACAGATATCCG 515
 DB 472 CACAAAAAAGACGAGATGATATACGAGTAAATGACCGTGTGAAGACGAGATATTTCA 531
 QY 516 TGACCCCTG---GGAAGAACCTGTGATGCTGTCTTCCATGCGCGCTCTACATGGAGG 572
 DB 532 TGATGAAACAGTAAGAGCCCGTATGGTCTATATCCATGGGGGATCTTACATGGAGGG 591
 QY 573 GACCGAAACATGTTTGATGGCTCAGTCTGCTGCTGCTATGCAACAGTCAATGTAGCCAC 632
 DB 592 CACCGCAACATGATGACCGCAGCATTTTGGCAAGCTACGGAACGTCATCGTGATCAC 651
 QY 633 GCTCACTACCTCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
 DB 652 CATTAACCTCTGCGGAATACTAGGGTTTAAAGTACCGGTGACCGAGGAGCAAAAGG 711
 QY 693 CAACATGAGGCTCTGGGACAGATCCAGCCCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 752
 DB 712 CAACATGAGGCTCTGGGACAGATCCAGCACTGCGGTGGATGAGGAGATGCGGAGC 771
 QY 753 CTTTGGGGGCGACCCGAGCGATCACCATCTTTGGTTCGCGGGGAGGGGCTCTCTGCT 812
 DB 772 CTTTGGGGGCGACCCCAAGAGAGTACCATCTTTGGCTCGGGGGGCTGGGGGCTCTGCT 831
 QY 813 CAACCTTCTGATCTCTCCCACTTCCAGAGGGGCTGTTCCAGAGGCCATCGGCCAGAG 872
 DB 832 CAGCGTGTGACCTGTCCCACTACTCAGAGAGTCTTCCAGAGGCCATCATTTAGAG 891
 QY 873 TGGCACCGCATTTCCAGTGTGTGTCAACTACAGCGCTCAAGTACACGCGGCTGCT 932

DB 892 CGGACACCGCCCTGTCCAGCTGGGAGTGAACTACCCAGCGCGCAAGTACACTCGATATT 951
 QY 933 GGACGCCAGGTGGGCTGTGACCGAGAGAGACAGTGTCTGAAGCTGTGGAGTGTCTGGCGG 992
 DB 952 GGACACAGGTGGGCTGTGCAACATGCTGGACACCAACCGACATGTGTAGATGCTCTCGGAA 1011
 QY 993 GAAGCCCTCCCGGGAGCTGGTGGACAGGAGCTGCGAGCTGCGCCCTACCACTGCCTT 1052
 DB 1012 CAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCCGGCCCTTACCATATACCTT 1071
 QY 1053 TGGGCGCGT 1112
 DB 1072 CGGCGCGGT 1131
 QY 1113 AGAATTCCTCAACTACGACATGCTCATCGCGCTCAACACGAGGAGAGGAGGCTCAAGTTCGT 1172
 DB 1132 CGAGTTCCTCAACTACGACATGCTGTGGGCTCAACACGAGGAGAGGAGGCTTGAAGTTCGT 1191
 QY 1173 GGAGACTCTGACAGAGAGCGAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1232
 DB 1192 GGACGGCATCTGT 1251
 QY 1233 CAACCTTCTGTGACAACTGT 1292
 DB 1252 CAACCTTCTGTGACAACTGT 1311
 QY 1293 CAAGTTATGTACACAGACTGGGCGGACCGGGAACAATGGGGAATGCGCGCAAAACCT 1352
 DB 1312 CAAGTTATGTACACAGACTGGGCGGATAGGAAACCCCGAGAGCGCGCGGAAACCT 1371
 QY 1353 GCTGGCGCTCTTACTGACACCAATGGGTGGACACAGCTGTGGCCACTGTGCCAAGCTGCA 1412
 DB 1372 GGTGGCTCTCTTACTGACCAACAGTGGGTGGGCGCGCGCGCTGTGCC---GCCGACCTGCA 1428
 QY 1413 CGCGCAGTACCGCTCTCCCGTCTACTTTTACACCTTCTACACACCTGCGAGGCGGAGG 1472
 DB 1429 CGCGCAGTACCGCTCTCCCGTCTACTTTTACACCTTCTATGCTCTATCATCTGCAACAGCGAAT 1488
 QY 1473 CGCGCCTGAGTGGGAGATGCGGGCGACGGGGATGAACCTGCTTATGCTTGTGTGGCGTCC 1532
 DB 1489 GAAGCCCGAGTGGGAGATTCGGGCCCATGGTGTGAGGTGCTTGTCTTGTGGCATCC 1548
 QY 1533 CATGGTGGTGGCCACCGACCTCTTCCCGTCTTAACTTCTCCAAAGATGACGCTCATGCTCAG 1592
 DB 1549 CATGATCGTCCCGACCGAGCTCTTCACTGTGTAATCTTTCAGAAACGACGCTCATGCTCAG 1608
 QY 1593 TGGCGTGTGATGACCTTCTGACCAACTTTCGCAAGACTGGGGACCCCAACCCAGCGGT 1652
 DB 1609 CGCGGTGGTCAATGACCTTCTGACGAACTTGGCAAACTGGTGTATCCAAATCAACAGT 1668
 QY 1653 GCGCAGGATACCAAGTTCATCCACACCGACCCATCGCTTCGAGAGGTTGTGTGGAG 1712
 DB 1669 TCTCAGATACCAAGTTCATCCACAAACCCAAACCCCTTTGAAGAGTGGCGCTGGTC 1728
 QY 1713 CAATATCAACAGACAGAGAGAGAGTATCTGCAATAGGCTGAAAGCCAGCGGTGCGTGA 1772
 DB 1729 CAAGTATAATCCCAAGACAGCTCTATCTGCATATTTGGCTTGAACCCAGAGTGAAGA 1788
 QY 1773 CAACTACCGGCCCAACAGGTGGCTTCTGCTGAGGCTGTGCGCCCACTGCAACCT 1832
 DB 1789 TCACTACCGGGCAACCAAGTGGCTTCTGCTGGAACCTGCTTCTCATTTTGCACAACTT 1848
 QY 1833 GCA-----CACGGAGCTCTTCAACACCAACCGCGCTGCTTCCCTACGCCACCGG 1883
 DB 1849 GAACGAGATATTCAGTATGTTTCAACACCAACCAAGGTTCTTCCACACAGATGACATC 1908
 QY 1884 CTGGCGCGCTCTGCTCCCGCGCTGGCGCGCGCGCGGACACCGCGCGCGCGCGCGCTGCGCAC 1943
 DB 1909 ATTCTCCTATGCAACCGCGGCTCTTCCCGCAAGATATGGCCCAACCAACCAACCGCGCAC 1968
 QY 1944 CTGCGCTCCCGAGCGCGCGCGCGGAG-----CGGCGCGCGCGCGCGCGCGCGCGCG 1982
 DB 1969 AATCACTCTCTGCCAACATCCCAACACTCTAAGGACCTCTCAAAACAGGCGCTTGAGGA 2028

PA

XX PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertschen ME;
 PI Goddard A, Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kijavini J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI: 2003-298163/28.
 DR P-PSDB; ABU61126.
 XX
 XX
 PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies
 XX
 XX Claim 2; Fig 150; 459pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists. The
 CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
 CC apoptosis or death of the cell. The PRO polypeptides are useful for
 CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
 CC cardiac insufficiency, nervous system disorders, kidney disorders,
 CC bone and cartilage disorders or arthritis, tumours, and wound healing.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, and in gene therapy.
 CC analysis of individuals with genetic disorders, and in gene therapy.
 CC The present sequence encodes a human PRO polypeptide of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipdsIDEntry.html.
 XX
 SQ Sequence 3113 BP; 853 A; 867 C; 712 G; 681 T; 0 other;

Query Match 36.4%; Score 912.2; DB 25; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2,3e-145;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

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 QY 345 CGCCATCATGCTGCTGT 404
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 Db 1796 TACTGACCAAGTGGGCGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1855
 QY 1425 GTCTCCGCTTACTTTTACACCTTTACACCACTGCGGAGGCGGCGGCGGCGGCGG 1484
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 QY 1485 GGCAGATGGGCGGACAGGAGTGAATGCGCTATGCTTTGGCGTGCCCATGTTGGTGC 1544
 Db 1916 GGCAGATGGGCGGACATGGTATGAGTCCCTATGCTTTCGGCATCCCCATGATCGGTC 1975
 QY 1545 CACCGACTCTTCCCTGTAACTTCTCAGAGATGAGTCACTGCTCAGTGGCGGTGCTAT 1604
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 Job time : 613.415 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 16:16:41 ; Search time 8928.48 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	2508	100.0	2508	6	AX469738	AX469738 Sequence
2	2508	100.0	4667	6	AX469736	AX469736 Sequence
3	2506.4	99.9	2793	9	AF376802	AF376802 Homo sapi
4	2506.4	99.9	4622	6	AX405624	AX405624 Sequence
5	2500	99.7	4763	6	AX477706	AX477706 Sequence
6	2443.6	97.4	2523	6	AX179306	AX179306 Sequence
7	2265.4	90.3	2663	6	AX380442	AX380442 Sequence
8	2173.4	86.7	3993	10	RNU41662	U41662 Rattus norv
9	1651.8	65.9	3716	9	AB037787	AB037787 Homo sapi
10	1011.4	40.3	3813	9	AF217411	AF217411 Homo sapi
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C 24	778.4	31.0	5631	10	AK122433	AK122433 Mus muscu
C 25	773.8	30.9	222871	2	AC108094	AC108094 Homo sapi
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36	523	20.9	223877	2	AC098923	AC098923 Rattus no
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C 44	492.8	19.6	315176	2	AC078956	AC078956 Homo sapi
C 45	489.6	19.5	146181	9	AC142316	AC142316 Pan trogl

ALIGNMENTS

RESULT	1	2508 bp	DNA	linear	PAT 16-JUL-2002
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LOCUS	AX469738				
DEFINITION	Sequence 3 from Patent WO0216616.				
ACCESSION	AX469738				
VERSION	AX469738.1	GI:21901866			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Curtis,R.A.				
TITLE	Human carboxylesterase family member and uses thereof				
JOURNAL	Patent: WO 0216616-A 3 28-FEB-2002;				

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BASE COUNT 464 a 1001 c 843 g 485 t

Query Match 99.9%; Score 2506.4; DB 9; Length 2793;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	614	CTGTCTTCTCATGGGCTTCTACATGAGGGGACCGGAAACATGTTTGGAGGCTCAGTC	673
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DB	974	AACATACGAGCGCTCAAGTACACGGGCTGTGCGACGCCAAGTGGGTGTGACGAGAG	1033
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RESULT 5

AX477706
LOCUS
DEFINITION
Sequence 18 from Patent WO0246426.
ACCESSION
AX477706
VERSION
AX477706.1 GI:22216861

AX477706 4763 bp DNA linear PAT 12-AUG-2002

KEYWORDS
Homo sapiens (human)

SOURCE
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

1
Sanjanwala, M.M., Yao, M.G., Au-Young, J., Baughn, M.R., Arvizu, C.,

Ring, H.Z., Lee, E.A., Ding, L., Hafalia, A.J., Tang, Y.T., Yue, H.,

Tribouley, C.M., Lu, D.A., Lai, P.G., Warren, B.A., Yang, J.,

Walia, N.K., Nguyen, D.B., Gandhi, A.R. and Ison, C.H.

Drug metabolizing enzymes

Patent: WO 0246426-A 18 13-JUN-2002;

Incyte Genomics, Inc. (US)

Location/Qualifiers

FEATURES

source

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2503; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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LOCUS 2523 bp DNA linear PAT 03-JUL-2001

DEFINITION Sequence 7 from Patent WO0127277.

ACCESSION AXI179306

VERSION AXI179306.1 GI:14598977

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Shimketa,R.A., Lichenstein,H. and Boldog,F.L.

TITLE Proteins and polynucleotides encoded thereby

JOURNAL Patent: WO 0127277-A 7 19-APR-2001;

Curagen Corporation (US)

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QY	2038	GTGGCGTGGGTGCTCCCTCCTCTTCCTCAACATCTCGGCCTTTGTGTCCTCTACTAC	2097
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LOCUS	AX380442	Sequence 30 from Patent WO204612.	PAT 18-MAR-2002
DEFINITION	AX380442		
ACCESSION	AX380442.1	GI:19575351	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Baughn,M.R., Bruns,C.M., Das,D., Ding,L., Elliott,V.S.,	
		Gandhi,A.R., Rafalia,A.J., Kearney,L., Khan,F.A., Lai,P., Lee,E.A.,	
		Lu,D.A., Lu,Y., Nguyen,D.B., Patterson,C., Ramkumar,J., Ring,H.Z.,	
		Sanjanwala,M.S., Tang,Y.T., Thornton,M. and Tribouley,C.M.	
TITLE		Drug metabolizing enzymes	
JOURNAL		Patent: WO 0204612-A 30 17-JAN-2002;	
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Best Local Similarity		99.7%;	Fred. No. 3.1e-292;
Matches 2669; Conservative		0; Mismatches	6; Indels 0; Gaps 0;
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RESULT 8

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DEFINITION
ACCESSION         U41662
VERSION           U41662.1 GI:1145788
KEYWORDS
SOURCE            Rattus norvegicus (Norway rat)
ORGANISM          Rattus norvegicus
REFERENCE
AUTHORS           Ichchenko, K., Nguyen, T. and Sudhof, T.C.
TITLE            Structures, alternative splicing, and neuroligin binding of multiple
                neuroligins
JOURNAL           J. Biol. Chem. 271 (5), 2676-2682 (1996)
MEDLINE           96162010
PUBMED            8576240
REFERENCE
AUTHORS           Ichchenko, K., Nguyen, T. and Sudhof, T.C.
TITLE            Direct Submission
JOURNAL           Submitted (01-DEC-1995) Konstantin Ichchenko, Molecular Genetics,
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RESULT 10

AF217411 3813 bp mRNA linear PRI 21-MAY-2000
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DEFINITION alternatively spliced.
ACCESSION AF217411
VERSION AF217411.1 GI:7960130
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3813)
AUTHORS Philibert,R.A., Winfield,S.L., Sandhu,H.K., Martin,B.M. and
Ginns,E.I.
TITLE The structure and expression of the human neurotrophin-3 gene
JOURNAL Gene 246 (1-2), 303-310 (2000)
MEDLINE 20231756
PubMed 10767552
REFERENCE 2 (bases 1 to 3813)
AUTHORS Philibert,R.A., Winfield,S.L. and Sandhu,H.K.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1999) Psychiatry, University of Iowa, 500 Newton,
Iowa City, IA 52242, USA

FEATURES

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JOURNAL
Submitted (01-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer

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BC034018
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VERSION
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SOURCE
ORGANISM

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BC034018
MGC.
BC034018.1 GI:21706446
Homo sapiens (human)

REFERENCE
AUTHORS

Strausberg, R.L., Feilgold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D.,
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Fahey, J., Helton, S., Kettelman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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Generation and initial analysis of more than 15,000 full-length
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257

TITLE
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MEDLINE
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2 (bases 1 to 4115)
Strausberg, R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-3590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

REMARK
COMMENT

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 AUTHORS Nagase,T., Ishikawa,K., Kikuno,R., Hirose,M., Nomura,N. and Chara,O.
 TITLE Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
 JOURNAL DNA Res. 6 (5), 337-345 (1999)
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 PUBMED 10574462
 REFERENCE
 AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
 TITLE Direct Submission
 JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ohara@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,

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source

Nat. Genet. 34 (1), 27-29 (2003)
22608338
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2 (bases 1 to 5454)
Jamin, S., Quach, H., Fellous, M. and Bourgeron, T.
Evolution and expression of the human neurotrophin family, including
two primate specific members on the X and Y chromosomes
Unpublished
3 (bases 1 to 5454)
Jamin, S., Quach, H., Fellous, M. and Bourgeron, T.
Direct Submission
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Query Match 35.3%; Score 886.2; DB 9; Length 5454;
Best Local Similarity 64.0%; Pred No. 7.5e-103;
Matches 1478; Conservative 0; Mismatches 728; Indels 105; Gaps 5;

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Pred. No. is the number of results predicted by chance to have a

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7	2587.8	55.4	184349	9	AC113189 Homo sapi
8	2586.2	55.4	113187	2	AC007732 Homo sapi
9	2508	53.7	2508	6	AX469738 Sequence
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REFERENCE
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AUTHORS Curtis, R.A.
TITLE Human carboxylesterase family member and uses thereof
JOURNAL Patent: WO 0216616 A 1 28-FEB-2002

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 Sanjanwala, M.M., Yao, M.G., Au-Young, J., Baughn, M.R., Arvizu, C.,
 Ring, H.Z., Lee, E.A., Ding, L., Hafalia, A.J., Tang, Y.T., Yue, H.,
 Triboley, C.M., Lu, D.A., Lal, P.G., Warren, B.A., Yang, J.,
 Walla, N.K., Nguyen, D.B., Gandhi, A.R. and Ison, C.H.
 Drug metabolizing enzymes
 Patent: WO 0246426-A 18 13-JUN-2002;
 Incyte Genomics, Inc. (US)

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Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F.,										
Xue, A.J., Yang, Y., Wehrman, T. and Brmanac, R.T.										
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REFERENCE
AUTHORS Nagase,T., Kikuno,R., Ishikawa,K.I., Hirose,M. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro
JOURNAL DNA Res. 7 (1), 55-73 (2000)
MEDLINE 20181126
PUBMED 10718198

REFERENCE
AUTHORS Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:++81-438-52-3913, Fax:++81-438-52-3914)

FEATURES

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AF376802

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VERSION	AF376802.1	GI:21309946			
KEYWORDS					
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ORGANISM	Homo sapiens				
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DB	1321	CCTGTATGGCTACCCGGGAAGCAAGATGCTGCTTCGGGAGACCATCAAGTTTATGTACAC	1380
QY	1727	AGACTGGGCGGACCGGGACAATGGCGAAATGCGCGCAAAACCTGTGTGGCGCTCTTTAC	1786
DB	1381	AGACTGGGCGGACCGGGACAATGGCGAAATGCGCGCAAAACCTGTGTGGCGCTCTTTAC	1440
QY	1787	TCACCACCAATGGGTGGCACACAGCTGGCCACTGCCAAGCTGCACGCCGACTACAGTC	1846
DB	1441	TCACCACCAATGGGTGGCACACAGCTGGCCACTGCCAAGCTGCACGCCGACTACAGTC	1500
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DB	1501	TCCCTCTACTTTTACACCTTCTACCACTGCCAGCGGAGCGCGCGCTCGAGTGGCG	1560
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DB	1561	AGATCGCGGACCGGGATGAAGTGCCTATGTCTTTGGCGTGCCCATGTGGGTGCCAC	1620
QY	1967	CGACTCTTCCCTGTAACTTCTTCCAAAGATGAGCTCATGCTCAGTGCCTTGGTCATGAC	2026
DB	1621	CGACTCTTCCCTGTAACTTCTTCCAAAGATGAGCTCATGCTCAGTGCCTTGGTCATGAC	1680
QY	2027	CTACTGGACCAACTTCGCCAAGACTGGGACCCCAACAGCCGGTGCCGAGGATACCAA	2086
DB	1681	CTACTGGACCAACTTCGCCAAGACTGGGACCCCAACAGCCGGTGCCGAGGATACCAA	1740
QY	2087	GTTTCATCCACCAAGGCCAAATCGCTTCGAGGAGGTGGTGTGGAGCAAAATCAACAGCAA	2146
DB	1741	GTTTCATCCACCAAGGCCAAATCGCTTCGAGGAGGTGGTGTGGAGCAAAATCAACAGCAA	1800
QY	2147	GGAGAGCAGTATCTGCACATAGCCCTGAAGCCACAGCGTGCGGTGAACATACCGGCCAA	2206
DB	1801	GGAGAGCAGTATCTGCACATAGCCCTGAAGCCACAGCGTGCGGTGAACATACCGGCCAA	1860
QY	2207	CAAGTGGCCCTTCTGGGTGGAGCTGCTGCCCAACTCTGCACAACTGCACACGAGAGCTCTT	2266
DB	1861	CAAGTGGCCCTTCTGGGTGGAGCTGCTGCCCAACTCTGCACAACTGCACACGAGAGCTCTT	1920
QY	2267	CACACACACAGGCGCTGCTTCCTACGCCACAGCGTGCGCGCTCGTCCCGCGCTGG	2326
DB	1921	CACACACACAGGCGCTGCTTCCTACGCCACAGCGTGCGCGCTCGTCCCGCGCTGG	1980
QY	2327	CGCCCCGGGCACACCGCGGCCCGCGCGCTGCACACCTGCCTCCGAGCCCGAGCCCGA	2386
DB	1981	CGCCCCGGGCACACCGCGGCCCGCGCGCTGCACACCTGCCTCCGAGCCCGAGCCCGA	2040
QY	2387	GCCCGGCCAAGGCGCTATGACCGCTTCCCGGGGACTACCGGAGCTACTCCACGGAGCT	2446
DB	2041	GCCCGGCCAAGGCGCTATGACCGCTTCCCGGGGACTACCGGAGCTACTCCACGGAGCT	2100
QY	2447	GAGCGTCACCGTGGCGGTGGTGCCTCCCTCCCTTCCTCAACATCTCGGCTTGTCTGC	2506
DB	2101	GAGCGTCACCGTGGCGGTGGTGCCTCCCTCCCTTCCTCAACATCTCGGCTTGTCTGC	2160
QY	2507	CTCTACTACAAGCGGACCGGCGGAGGAGCTGCGGTGCAGCGCGCTTAGCCCACTGG	2566
DB	2161	CTCTACTACAAGCGGACCGGCGGAGGAGCTGCGGTGCAGCGCGCTTAGCCCACTGG	2220
QY	2567	CGGCTCAGGCTCTGGGTGCTGGTGGGGGCCCGCTGCTCCCGCGCGGGCGGTGAGCT	2626
DB	2221	CGGCTCAGGCTCTGGGTGCTGGTGGGGGCCCGCTGCTCCCGCGCGGGCGGTGAGCT	2280
QY	2627	GCCACAGAGGAGGAGCTGGTGTCACTGCAAGCTGAAGCGGGGTGGTGGCGTGGGGCGGA	2686
DB	2281	GCCACAGAGGAGGAGCTGGTGTCACTGCAAGCTGAAGCGGGGTGGTGGCGTGGGGCGGA	2340
QY	2687	CCCTGCGGAGGCTCTGGGCGCTGCTGCTCCCGCGCGGACTACACCTGCGCGCGGGC	2746
DB	2341	CCCTGCGGAGGCTCTGGGCGCTGCTGCTCCCGCGCGGACTACACCTGCGCGCGGGC	2400

QY	2747	ACCGGACGATGCTCTCTTGGCCCGGGGCCCTGACCTCTGTCACCACTCGGCTGGG	2806
Db	2401	ACCGGACGATGCTCTCTTGGCCCGGGGCCCTGACCTCTGTCACCACTCGGCTGGG	2460
QY	2807	GCACCGGCACCCACGCGCCCTCTCTTCACTCCCTTGGGGCCCTTCCCGCGGCCCC	2866
Db	2461	GCACCGGCACCCACGCGCCCTCTCTTCACTCCCTTGGGGCCCTTCCCGCGGCCCC	2520
QY	2867	TCCACCGCCACACGCGCCACCAACACGCTACCCACCCCACTCCACCACTCGGCTATA	2926
Db	2521	TCCACCGCCACACGCGCCACCAACACGCTACCCACCCCACTCCACCACTCGGCTATA	2580
QY	2927	GCGGGTGGGTGGGAGCGCTCTCTCCCGCGCCCTCTGCGCGCGCTTCCCGCGGCCCG	2986
Db	2581	GCGGGTGGGTGGGAGCGCTCTCTCCCGCGCCCTCTGCGCGCGCTTCCCGCGGCCCG	2640
QY	2987	GGAGGAGGACTTGGCAACTGGCTTTTCTCTGTGGAGTGGTCAACGCGCATCCAGCAGCG	3046
Db	2641	GGAGGAGGACTTGGCAACTGGCTTTTCTCTGTGGAGTGGTCAACGCGCATCCAGCAGCG	2700
QY	3047	CTAAGTGGGACATGGGATTCCTCTCCGCGATGGCTCTTCCACGCGAGAGGCCCA	3106
Db	2701	CTAAGTGGGACATGGGATTCCTCTCCGCGATGGCTCTTCCACGCGAGAGGCCCA	2759
QY	3107	GTCTCTTCTCTGGACTTGGGCTTTTGAACAATG	3140
Db	2760	GTCTCTTCTCTGGACTTGGGCTTTTGAACAATG	2793
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LOCUS	RNU41662	3993 bp mRNA linear	ROD 25-APR-1996
DEFINITION	Rattus norvegicus neuroligin 2 mRNA, complete cds.		
ACCESSION	U41662		
VERSION	U41662.1	GI:1145788	
KEYWORDS			
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
AUTHORS	1. (bases 1 to 3993)		
TITLE	Ichchenko, K., Nguyen, T. and Sudhof, T. C.		
JOURNAL	Structures, alternative splicing, and neuroligin binding of multiple neuroligins		
MEDLINE	J. Biol. Chem. 271 (5), 2676-2682 (1996)		
PUBMED	96162010		
AUTHORS	8576240		
TITLE	2 (bases 1 to 3993)		
JOURNAL	Ichchenko, K., Nguyen, T. and Sudhof, T. C.		
MEDLINE	Direct Submission		
PUBMED	Submitted (01-DEC-1995) Konstantin Ichchenko, Molecular Genetics, UTSWMC@Dallas, 5323 Harry Hines Blvd., Dallas, TX 75235, USA		
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QY		173	CAGTCTGGGCGTCGCCTTCACTTTCTCCACTTCCTTCCCCTTCCCCACACCCGTGCCCCCT	232
Db		310	CAGTCTGGGCGCTCCGAGCATCTTTCTTCTACCTTTCTTCCCTTTCCCCACACCCCTTACCCCT	369
QY		233	CCATGGAGAGAAACAGACCCTCTCTGTGTCAGTCTAAACCCAGTGTCCTCCCCAAACCCCC	292
Db		370	CCATGGAGAGAAATAGACTCCTCTTCTGTGCCCTTCTAACCCAGAGTCCCTACCCGTACCCC	429
QY		293	TCTCCCTCTCTTCCCGCGCGCTCTCTCCCTCTGTGGGCGAGGGGGGCGTCTCCTCCCTC	352
Db		430	TCTCTCTTCTTTCCTCCAC - CCCCCTCTCTCTCTGTGGGCGAGGGGGGCGTCTCCTCCCTC	488
QY		353	TCCCCCTCTCTCTCTCTCTCCAGAGGGGGGGGTCCAGGGAGGGAGGGGGGTCTCCCC	412
Db		489	TCCCCCTCTCTCTCTCTC-----CGAGGGGGGGGTACGGGAGGGAGGGGGGTCTCCCC	543
QY		413	GATCAGCATGTGGCTCTGTGGCGTGTGTCTGTGTGGGCTGTGGGGGGCTCAAACCGGGGG	472
Db		544	AATCAGCATGTGGCTCTGTGGCTGTGTCTGTGTGGGCTGTGGCTTAACCGGGAGG	603
QY		473	AGGGGTCCCAGCGCGCGCGCCCGCGCGCTCGGCGTCTGGAGCTCTGGCGA	532
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QY		533	GGAGGGCTTCCCGGTGTGAACAACGCGCTACCGGGGAGTGGCGGTGTGGGGCGCAGCT	592
Db		664	GGAGGGCTTCCCGGTGTGAACAACGCGCTACCGGGGAGTGGCGGTGTGGGGCGCAGCT	723
QY		593	CAACAAAGATCTGTGGGCGCGCTGTGCAGATTCTTGGGCGTGCCTACGCCACCGCGCC	652
Db		724	CAACAAAGATCTGTGGGCGCGTGTGTGCAGTTCTTGGGCGTGCCTACGCCACCGCGCC	783
QY		653	CTGGGCGCGCGCGCTTCCAGCGCGCTGAGGCGCGCGCTCTGTGGCGCGCGGTGGCGAA	712
Db		784	CTTGGCGCGCGCGCTTCCAGCGCGCTGAGGCGCTGTGCTCTGTGGCGCGCGCA	843
QY		713	CGCACACACCTTGGCGCGCGCTTGGCGCGCGCTTGGCGCGCGGTGGCGCGCATCAT	772
Db		844	CGCACACACCTTGGCGCGCGCTTGGCGCGCGCTTGGCGCGCGGTGGCGCGCATCAT	903
QY		773	GTCGCTGTGTGTACCGACAACTTGGAGCGCGCGCACCTACGTGCAGAACACAGAG	832
Db		904	GTCGCTGTGTGTACCGACAACTTGGAGCGCGCGCACCTACGTGCAGAACACAGAG	963
QY		833	CGAGGACTGCTGTACCTGAACCTTACGTGCCACCGAGGACGCTCGCTTCAAAAAA	892
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RESULT 7							PRI 04-OCT-2002
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DEFINITION	Homo sapiens chromosome 17, clone RP11-104H15,						complete sequence.
ACCESSION	AC113189						
VERSION	AC113189.11	GI:23499591					
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SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 183439)						
AUTHORS	Birren,B., Nusbaum,C. and Lander,E.						
TITLE	Homo sapiens chromosome 17, clone Rp11-104H15						
JOURNAL	Unpublished						
REFERENCE	2 (bases 1 to 183439)						
AUTHORS	Birren,B., Lincoln,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckgatter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazarro,B., Choepel,X., Collangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Gilde,S., Gord S., Govettte,M., Graham,L., Grand-pierre,N., Hagos,B., Horton,L., Hulme W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karas,C., Kells,C., Larocque,K., Lamazares,R., Landers,T., Lehoczyk,J., Levine,R., Lit,G., Maclean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Mereus,L., Mihova.C., Mlenga,V., Murphy,T., Naylor J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor T., O'Donnell,P., O'Neill,D., Oliver.J.,						

Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
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 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,W.

Direct Submission

Submitted (26-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 184349)

JOURNAL
REFERENCE
AUTHORS

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
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 Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
 McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,W.

Direct Submission

Submitted (18-SEP-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 184349)

JOURNAL
REFERENCE
AUTHORS

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,W.

Direct Submission

Submitted (04-OCT-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Oct 4, 2002 this sequence version replaced gi:23129328.

COMMENT

All repeats were identified using RepeatMasker:

Snit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L23113

Center clone name: 104_H_15

Location/Qualifiers

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 VERSION
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 KEYWORDS
 HTG; HTGS PHASE2; HTGS_FULLTOP; HTGS_CANCELLED.
 SOURCE
 Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 113187)
 Birren,B., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 17, clone RP5-1030A12
 Unpublished
 2 (bases 1 to 113187)
 Birren,B., Linton,J., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
 Castile,A., Cerny,J., Collangelo,M., Collins,S., Collymore,A.,
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 Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
 Karatas,A., Lehocsky,J., Lieu,C., Locke,K., Macdonald,P.,
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 Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
 Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
 Direct Submission

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Submitted (05-JUN-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 113187)
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
 McCarthy,M., Melchior,J., Meneus,L., Mihova,T., Mlenga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
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 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission

TITLE
 JOURNAL
 COMMENT

Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Sep 12, 2002 this sequence version replaced GI:21700697.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L528
 Center clone name: 1030_A_12

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 38427: contig of 39427 bp in length
 * 39428 39527: gap of 100 bp
 * 39528 113187: contig of 73660 bp in length.
 * Location/Qualifiers
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FEATURES
 source

[illegible]

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VERSION	AX469738.1		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.		
AUTHORS	1		
TITLE	Curtis, R.A.		
JOURNAL	Human carboxylesterase family member and uses thereof		
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VERSION AX179306.1 GI:14598977
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shinkets, R.A., Lichenstein, H. and Boldog, F.I.
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ORIGIN

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Homo sapiens chromosome 17 clone 363G12 map 17, *** SEQUENCING IN

PROGRESS ***, 11 unordered pieces.

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HTG: HTGS_PHASE1.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 146756)

Birren,B., Paman,K., McKernan,K., Munro,C., Nusbaum,C., Richardson,P. and Lander,E.

Homo sapiens chromosome 17, clone 363G12

Unpublished

2 (bases 1 to 146756)

Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W., Fasanan,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P., Barna,N., Chang,A., Cooke,P., Daly,M.J., Devon,K., Dewar,K., Forres,C., Gage,D., Geraghty,K., Guitau,G., Hagos,B., Huang,J., Jacotot,L., Lane,K., Lee,K., Mackenzie,J., Marquis,N., McDermott,J., Molla,M., Moloney,N., Morrow,J., Nachman,A., Naylor,J., O'Connor,T., Olotu,A., Peterson,K., Rollins,G., Spencer,J., Stillewell,J., Stone,C., Strickland,C., Sydney,K., Tang,L., Traish,A., Wilmer,F., Zemtseva,I. and Zody,M.

Direct Submission

Submitted (17-JUN-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Dec 11, 1997 this sequence version replaced gi:2661149.

The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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*	2414	4445: contig of 2032 bp in length
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*	131152	146756: contig of 15605 bp in length.

Location/Qualifiers

1. 146756

/organism="Homo sapiens"

FEATURES

source

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AL603707 234182 bp DNA linear ROD 17-NOV-2001
 Mouse DNA sequence from clone RP23-422L16 on chromosome 11,
 complete sequence.
 AL603707
 VERSION
 AL603707.5 GI:17017790
 HTG
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 234182)
 Pearce, A.
 Direct Submission
 Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Nov 20, 2001 this sequence version replaced gi:16605765.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em., EMBL; Sw.,
 SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/c_elegans/wormpep RP23-422L16 is
 from the RP23-422L16 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see http://www.chori.org/bacpac/home.htm
 VECT03: PBACe3.6
 This sequence is the entire insert of clone RP23-422L16.
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Search completed: February 19, 2004, 00:22:31
Job time : 16627.5 secs

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3	2883.4	51.1	2663	13	US-0-374-694-30	Sequence 30, Appl
4	1618.2	34.7	1969	11	US-09-764-891-7886	Sequence 7886, App
5	1092	23.4	1446	11	US-09-809-391-139	Sequence 139, App
6	1092	23.4	1446	13	US-09-882-171-139	Sequence 139, App
7	912.2	19.5	3113	10	US-09-978-295A-374	Sequence 374, App
8	912.2	19.5	3113	10	US-09-978-697-374	Sequence 374, App
9	912.2	19.5	3113	10	US-09-978-192A-374	Sequence 374, App
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Qy 121 TC

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

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US-09-934-323-3
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; Patent No. US20020150910A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 33410. A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-081001
; CURRENT APPLICATION NUMBER: US/09/934,323
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,774
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2508
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; ORGANISM: Homo sapiens
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[illegible]

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Qy 898 ACAGCGGAGCGCTCAATCGCGCAGACAGATATCCGTGAGCCCTGGGAGAGCGCTGTGA 957
Db 655 ACAGCGGAGCGCTCAATCGCGCAGACAGATATCCGTGAGCCCTGGGAGAGCGCTGTGA 714
Qy 958 TGCTGTTTCTCATGCGCGCTCTACATGAGGAGCGGAGCGGAAACATGTTGATGCTCAG 1017
Db 715 TGCTGTTTCTCATGCGCGCTCTACATGAGGAGCGGAGCGGAAACATGTTGATGCTCAG 774
Qy 1018 TCCTGGCTGCTTATGGCAACGTCATTGTAGCCAGCTCAACTACCGTCTTGGGCTGCTCG 1077
Db 775 TCCTGGCTGCTTATGGCAACGTCATTGTAGCCAGCTCAACTACCGTCTTGGGCTGCTCG 834
Qy 1078 GTTTTCTCAGACCGGGGACGAGCTGCAAAAGGCACTATGGGCTCTGAGCAGATCC 1137
Db 835 GTTTTCTCAGACCGGGGACGAGCTGCAAAAGGCACTATGGGCTCTGAGCAGATCC 894
Qy 1138 AGCCCTCGCTGCTCAGTGAACATCGCCACTTTGGGGGCGACCCCGAGCGTATCA 1197
Db 895 AGCCCTCGCTGCTCAGTGAACATCGCCACTTTGGGGGCGACCCCGAGCGTATCA 954
Qy 1198 CAATCTTTGGTTCGGGGACGAGGCTCTCTCGTCAACCTTCTGATCTCTCCACCAT 1257
Db 955 CAATCTTTGGTTCGGGGACGAGGCTCTCTCGTCAACCTTCTGATCTCTCCACCAT 1014
Qy 1258 CAGAGGCTGCTTTCAGAGGCTTCGCCAGAGTGGCAGCGCCATTTCCAGCTGCTCG 1317
Db 1015 CAGAGGCTGCTTTCAGAGGCTTCGCCAGAGTGGCAGCGCCATTTCCAGCTGCTCG 1074
Qy 1318 TCACTACACGCGCTCAAGTACACGCGCTGCTGGCAGCAAGTGGGCTGTGACCGAG 1377
Db 1075 TCACTACACGCGCTCAAGTACACGCGCTGCTGGCAGCAAGTGGGCTGTGACCGAG 1134
Qy 1378 AGGACAGTCTGAAGCTGTGAGTGTCTGCGCGGAGCGCTCCCGGAGCTGTGAGCC 1437
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Qy 1558 TCGCGCTCAACACGAGGAGAGGCTCAAGTTCTGAGGAGCTCTGACAGAGCGAGGAGC 1617
Db 1315 TCGGTGTCAACACGAGGAGAGGCTCAAGTTCTGAGGAGCTCTGACAGAGCGAGGAGC 1374
Qy 1618 GTGTGTCTGCGAGCGCTTGAATTCATGCTTCCAACTTTGAGCAACCTGTATGGCT 1677
Db 1375 GTGTGTCTGCGAGCGCTTTGACTTCACTGCTTCCAACTTTGAGCAACCTGTATGGCT 1434
Qy 1678 ACCCGAAGGCAAGGATGTCTTCGGGAGACCATCAAGTTTATGACAGACTGGCGC 1737
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Qy 1798 GGGTGGCACAGCTGTGGCCACTGCCAAGTGCACGCCGACTACCAAGTGTCCCGTCTACT 1857
Db 1555 GGGTGGCACAGCTGTGGCCACTGCCAAGTGCACGCCGACTACCAAGTGTCCCGTCTACT 1614
Qy 1858 TTTTACACCTTTTACCAACCACTGCGAGGCGCGCTGAGTGGGAGAGTGCAGCGC 1917
Db 1615 TTTTACACCTTTTACCAACCACTGCGAGGCGCGCTGAGTGGGAGAGTGCAGCGC 1674
Qy 1918 ACSEGAATGAATGCGCCCTATGTCTTTGGCGTGCCTATGAGTGGTGCACACCTCTTCC 1977
Db 1675 ACSEGAATGAATGCGCCCTATGTCTTTGGCGTGCCTATGAGTGGTGCACACCTCTTCC 1734
Qy 1978 CTTGTAACTTCTTCAAGAAATGAGTCACTGCTCAGTGCCTGCTGATGAGTGCAGCA 2037
Db 1735 CTTGTAACTTCTTCAAGAAATGAGTCACTGCTCAGTGCCTGCTGATGAGTGCAGCA 1794
Qy 2038 ACTTCCGCAAGACTGGGAGACCCCAACAGCCGCTGCCAGGATACCAAGTTTCAACCA 2097
Db 1795 ACTTCCGCAAGACTGGGAGACCCCAACAGCCGCTGCCAGGATACCAAGTTTCAACCA 1854
Qy 2098 CCAAGCCCAATCGCTTCGAGGAGGTGCTGAGGAGAAATTCACAGCAGGAGAGAGCT 2157
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Qy 2158 ATCTGCACATAGGCTTGAAGCCACGCTGCTGCTGACAACTTACCGCCCAACAGAGTGGCT 2217
Db 1915 ATCTGCACATAGGCTTGAAGCCACGCTGCTGCTGACAACTTACCGCCCAACAGAGTGGCT 1974
Qy 2218 TCTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Db 1975 TCTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2034
Qy 2278 CCGCGCTGCTTCCCTACGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2337
Db 2035 CCGCGCTGCTTCCCTACGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2094
Qy 2338 CAGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2397
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Db 2155 GGGCTTATGACCGCTTCCCGGGGACTCAGCGGACTTCCAGCGTCAACGAGTCAACG 2214
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Qy 2518 AGCGGAGCGCGCGGAGAGTGGGCTGAGCGGCTTAGCCCACTTGGCGGCTCAGGCT 2577
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Qy 2578 CTGGCTGCTTGGTGGGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2637
Db 2335 CTGGCTGCTTGGTGGGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2394
Qy 2638 AGGAGCTGCTCACTGAGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 2694
Db 2395 AGGAGCTGCTCACTGAGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 2451

RESULT 4

US-09-764-891-7886
; Sequence 7886, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7886
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7886

Query Match      34.7%; Score 1618.2; DB 11; Length 1969;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1642; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 3021 GAGTCGTGTCACAGCCGATCCAGACAGCGCTAAGGTGACATGGGATTCCTCCCTGCGATCGG 3080
Db 1 GAGTCGTGTCACAGCCGATCCAGACAGCGCTAAGGTGACATGGGATTCCTCCCTGCGATCGG 60

QY 3081 TGTCTTTCCACAGAGAGAGCCGAGTCTCTCTCTGATCTGGGCTTTGAACTG 3140
Db 61 TGTCTTTCCACAGAGAGAG-CCAGTCTCTCTCTGATCTGGGCTTTGAACTG 119

QY 3141 GGGGGCGTTTCTCCCGCCCAATGGGACACCAAGTCTTCGGTGTGGAAATGTGGTATTT 3200
Db 120 GGGGGCGTTTCTCCCGCCCAATGGGACACCAAGTCTTCGGTGTGGAAATGTGGTATTT 179

QY 3201 CCGCGTGGAGTGTGCTTTCTCAACCGGGTGTGTTTCCATGTGAGGTGAGGTT 3260
Db 180 CCGCGTGGAGTGTGCTTTCTCAACCGGGTGTGTTTCCATGTGAGGTGAGGTT 239

QY 3261 TTTTGTGCGACCGTGGACACATGTTGGCCCGCTCAAGAAATTTCTGTGGGGATTTGTAC 3320
Db 240 TTTTGTGCGACCGTGGACACATGTTGGCCCGCTCAAGAAATTTCTGTGGGGATTTGTAC 299

QY 3321 CCAGAAATCTGTTCCCGATCCCTTCTCCGACCTCTCCCTCCCTCCCTCCCTGGAGA 3380
Db 300 CCAGAAATCTGTTCCCGATCCCTTCTCCGACCTCTCCCTCCCTCCCTCCCTGGAGA 359

QY 3381 CCCTGGAAGTGTGTGTTCACATACAGTACACCTTGGCCACACAGACACAGAGATGGAG 3440
Db 360 CCCTGGAAGTGTGTGTTCACATACAGTACACCTTGGCCACACAGACACAGAGATGGAG 419

QY 3441 CTTGGGAGAGAGAGAGAAATACAGCCCTTGGCCCTCCCTCCCTCCCTCCCTCCCTG 3500
Db 420 CTTGGGAGAGAGAGAGAAATACAGCCCTTGGCCCTCCCTCCCTCCCTCCCTCCCTG 479

QY 3501 GCGAAGCATTTCCCGCCGACGCCCCCTTGGCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3560
Db 480 GCGAAGCATTTCCCGCCGACGCCCCCTTGGCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 539

QY 3561 GGGAGGCGCTCAGTTCACAGAGAGACAGACAGATTTCTGCTGGGGAGGAGAGT 3620
Db 540 GGGAGGCGCTCAGTTCACAGAGAGACAGACAGATTTCTGCTGGGGAGGAGAGT 599

QY 3621 CCAGCATCTGATGCTGCTGGAAGCTTAATTTCCGTCGAGGAGGCAATTTCTCTGA 3680
Db 600 CCAGCATCTGATGCTGCTGGAAGCTTAATTTCCGTCGAGGAGGCAATTTCTCTGA 659

QY 3681 GTGGAACAGGTTCTTGATGTGGATGTGTGTTCCCGAGGAGAGCGCCCTCTCTCC 3740
Db 660 GTGGAACAGGTTCTTGATGTGGATGTGTGTTCCCGAGGAGAGCGCCCTCTCTCC 719

QY 3741 CAGCATTCCCTCCCTCCCGAGGCTCAGGCGCCAGCACCAGTTCCTCTCAGATGSCA 3800
Db 720 CAGCATTCCCTCCCTCCCGAGGCTCAGGCGCCAGCACCAGTTCCTCTCAGATGSCA 779

QY 3801 GGTGAGACAGACTTCTAGTGTGAGGAGTGAAGGAGTGAAGGAGGAGGAGGAGG 3860
Db 780 GGTGAGACAGACTTCTAGTGTGAGGAGTGAAGGAGTGAAGGAGGAGGAGGAGG 839

QY 3861 CCGGCCCTTCTGCTCCCGAGTGGGGGAGGGGTGTGGCAACGTCGCCCGCCCGCAGAGGCCA 3920

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RESULT 5
US-09-391-139
; Sequence 139, Application US/09/809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens

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QY 3921 CGCATGTTTGACCAAAAGCCCTCATTTGGTCTCGAGGACAGCCCTTTTCCAGGGCTCAGA 3980
Db 900 CGCATGTTTGACCAAAAGCCCTCATTTGGTCTCGAGGACAGCCCTTTTCCAGGGCTCAGA 959
QY 3981 GCATTGCTCATCCGTGCGCAAACTGGGTAGGTGGATTTGAGCGGAAAGACTCCCAAAATGT 4040
Db 960 GCATTGCTCATCCGTGCGCAAACTGGGTAGGTGGATTTGAGCGGAAAGACTCCCAAAATGT 1019
QY 4041 GCGAAGATTTCCAGTCCAGGCGAGGCGAGGGAATAAGGCAAGCAGGATACAGGG 4100
Db 1020 GCGAAGATTTCCAGTCCAGGCGAGGCGAGGGAATAAGGCAAGCAGGATACAGGG 1079
QY 4101 CGAGGAGTGTGCGAGGTGAGGGGCTCCCGCTGTGCGCTTCTCTCTCCTCACCATCTCTCCC 4160
Db 1080 CGAGGAGTGTGCGAGGTGAGGGGCTCCCGCTGTGCGCTTCTCTCTCCTCACCATCTCTCCC 1139
QY 4161 CCACCTGCTCAGTCTCTGCTTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4220
Db 1140 CCACCTGCTCAGTCTCTGCTTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1199
QY 4221 ATCTCAGTGTGAGACAGCCCTTCTCTCTCATCTGACACCCCTCTCTCTCTCTCTCTCTCT 4280
Db 1200 ATCTCAGTGTGAGACAGCCCTTCTCTCTCAGCTGACACCCCTCTCTCTCTCTCTCTCTCT 1259
QY 4281 CTTTCTCTGAAAGAAAGAGCCCTTGAATGTGTGAGGAGGAGTGGGGAGAGAGGTCTCA 4340
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QY 4401 GACAGGCTTGGGCGAGACACAGCAGAGGAAATTTGAAATGTGTGAGGTGAGGTGAGGTGAGGT 4460
Db 1380 GACAGGCTTGGGCGAGACACAGCAGAGGAAATTTGAAATGTGTGAGGTGAGGTGAGGTGAGGT 1439
QY 4461 GGGCCCTTGGGCTTGGGCAATTTGGGAAAGAAATGATGTCTGGAAGGGCTTAAGGAGACAG 4520
Db 1440 GGGCCCTTGGGCTTGGGCAATTTGGGAAAGAAATGATGTCTGGAAGGGCTTAAGGAGACAG 1499
QY 4521 TCGAGAGGGGAGAGTCCCTCATCTGCTGGCATTTTGTGGGTGTGTGCTGCAAACTTGAA 4580
Db 1500 TCGAGAGGGGAGAGTCCCTCATCTGCTGGCATTTTGTGGGTGTGTGCTGCAAACTTGAA 1559
QY 4581 TAGGGGCTGGGGTGTGTCTTCCACTGACACCCAAATCCAGAAATCCCTGTGTGTGAGT-C 4639
Db 1560 TAGGGGCTGGGGTGTGTCTTCCACTGACACCCAAATCCAGAAATCCCTGTGTGTGAGTCC 1619
QY 4640 CCAGAACTTGGCTCTGACCTGCTCCCT 4666
Db 1620 CCAGAACTTGGCTCTGACCTGCTCCCT 1646

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; LOCATION: (1)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-809-391-139

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Best Local Similarity 99.0%; Pred. No. 1.1e-257;
Matches 1133; Conservative 6; Mismatches 1; Indels 4; Gaps 4;

QY 3524 CCCCCTGGCAGCAGTTCAGATGAGCAGCAGTTCCTCCGGGGAGGCGCCCTCACCTTCCAGAGA 3583
DB 3 CCCCCTGGCAGCAGTTCAGATGAGCAGCAGTTCCTCCGGGGAGGCGCCCTCACCTTCCAGAGA 62

QY 3584 GGCAGACACAGATTTCTCTCTGGGGAGGAGAGTCCACGATCTCTGATGCTCCCTGG 3643
DB 63 GGCAGACACAGATTTCTCTCTGGGGAGGAGAGTCCACGATCTCTGATGCTCCCTGG 122

QY 3644 AAGCTTATTTCCCGTGGCCAGGACGATTTCTCTGAGTGGAAACAGGTTCTTGGCATGTG 3703
DB 123 AAGCTTATTTCCCGTGGCCAGGATGATTTCTCTGAGTGGAAACAGGTTCTTGGCATGTG 182

QY 3704 GATGTGTTTCCCGAGCAGACGGCCCTCTCTTCCAGACCTTCCCTGCTCCCTCCAG 3763
DB 183 GATGTGTTTCCCGAGCAGACGGCCCTCTCTTCCAGACCTTCCCTGCTCCCTCCAG 242

QY 3764 GCCTCAGGCCAGCACCCAGTTCCTCTCTCACATGGCAGGTGAGCAGACACTTCTAGTTGG 3823
DB 243 GCCTCAGG-CCAGCACCCAGTTCCTCTCTCACATGGCAGGTGAGCAGACACTTCTAGTTGG 301

QY 3824 CAGGAGCTGAGGAGGTGAAACAAACCCCGAGGAGGCCCGCCCTTGTCTCCGAGTTGGG 3883
DB 302 CAGGAGCTGAGGAGGTGAAACAAACCCCGAGGAGGCCCGCCCTTGTCTCCGAGTTGGG 361

QY 3884 GGGAGGGGGTGTGCAACGTGCCCCCGCAGAGGCCACGATGTTTGACAAAGCCCTCA 3943
DB 362 GGGAGGGGGTGTGCAACGTGCCCCCGCAGAGGCCACGATGTTTGACAAAGCCCTCA 421

QY 3944 TTGTGTCGAGACAGCTTTTCCCGAGGCTCAGAGCATTTGCTCATCTCCGTGCGAAACT 4003
DB 422 TTGTGTCGAGACAGCTTTTCCCGAGGCTCAGAGCATTTGCTCATCTCCGTGCGAAACT 481

QY 4004 GGGTAGTGTGATTTAGCGGAAAGACTCCCAAAATGTGCAAGAAATTTCCAGTCCCAAG 4063
DB 482 GGGTAGTGTGATTTAGCGGAAAGACTCCCAAAATGTGCAAGAAATTTCCAGTCCCAAG 541

QY 4064 CAGGCGAGGAGAACTAAGGCGCAAGCAGGATACAGGCGGAGGAGTGTGCGAGTGGGG 4123
DB 542 CAGGCGAGGAGAACTAAGGCGCAAGCAGGATACAGGCGGAGGAGTGTGCGAGTGGGG 601

QY 4124 GCTCCGCGCTGTGCGCCCTTCTCTCACCATGTCTCCCGCCAGCCTGCTCAGTTCTCCGTT 4183
DB 602 GCTCCGCGCTGTGCGCCCTTCTCTCACCATGTCTCCCGCCAGCCTGCTCAGTTCTCCGTT 661

QY 4184 CCCCCTCATCTCCGTCGCCCTCTTTGAAAGTGTCCCATCTCAGTGTGAGCAAGCCCTTC 4243
DB 662 CCCCCTCATCTCCGTCGCCCTCTTTGAAAGTGTCCCATCTCAGTGTGAGCAAGCCCTTC 721

QY 4244 TCCTCATCTGACACCCCTCTCTGAGCGGCGCCCTCTCTGCTGAAAGAAAGAGGCT 4303
DB 722 TCCTCATCTGACACCCCTCTCTGAGCGGCGCCCTCTCTGCTGAAAGAAAGAGGCT 780

QY 4304 TGAATGTGAGGAGGAGCAGTGGGAGAAAGGTCTCACCGGACAGGTTGGGAGATAGG 4363
DB 781 TGAATGTGAGGAGGAGCAGTGGGAGAAAGGTCTCACCGGAGAGGTTGGGAGATAGG 840

QY 4364 TCACGGTGTCTGGGAGACAGATGAGGGGGCAGTGGGGACAGGGCTTGGGAGACACAG 4423
DB 841 TCACGGTGTCTGGGAGACAGATGAGGGGGCAGTGGGGACAGGGCTTGGGAGACACAG 900

QY 4424 CAGGAATAATTTGAAATGTGTAGGTGACTTCCCGGAGGCGCTTGGGCTTGGGCAATTTGG 4483
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RESULT 6
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; Sequence 139, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
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128 PRIOR APPLICATION NUMBER: 60/056,881
129 PRIOR FILING DATE: 1997-08-22
130 PRIOR APPLICATION NUMBER: 60/056,909
131 PRIOR FILING DATE: 1997-08-22
132 PRIOR APPLICATION NUMBER: 60/056,875
133 PRIOR FILING DATE: 1997-08-22
134 PRIOR APPLICATION NUMBER: 60/056,862
135 PRIOR FILING DATE: 1997-08-22
136 PRIOR APPLICATION NUMBER: 60/056,887
137 PRIOR FILING DATE: 1997-08-22
138 PRIOR APPLICATION NUMBER: 60/056,908
139 PRIOR FILING DATE: 1997-08-22
140 PRIOR APPLICATION NUMBER: 60/048,964
141 PRIOR FILING DATE: 1997-06-06
142 PRIOR APPLICATION NUMBER: 60/057,650
143 PRIOR FILING DATE: 1997-09-05
144 PRIOR APPLICATION NUMBER: 60/056,884
145 PRIOR FILING DATE: 1997-08-22
146 PRIOR APPLICATION NUMBER: 60/057,669

; PRIOR FILING DATE: 1997-09-05

Query Match 23.4%; Score 1092; DB 13; Length 1446;
 Best Local Similarity 99.0%; Pred. No. 1.1e-257;
 Matches 1133; Conservative 6; Mismatches 1; Indels 4; Gaps 4;

QY	3524	CCCCCTTGGCACAAGTCAGATGAAGACAGCTTCTGCGGGAGGAGCCCTCACCTTCCAGAGA	3583
DB	3	CCCCCTTGGCACAAGTCAGATGAAGACAGCTTCTGCGGGAGGAGCCCTCACCTTCCAGAGA	62
QY	3584	GGACACACAGATTTCTGCTGGGGAGGAGGAGTCCACGCATCTCTGATGCTGCCTGG	3643
DB	63	GGACACACAGATTTCTGCTGGGGAGGAGGAGTCCACGCATCTCTGATGCTGCCTGG	122
QY	3644	AAGCTTATTTTCCGCTGGCCAGGACGATTTCTCTGAGTGGAACAGGTTCTTGATGTG	3703
DB	123	AAGCTTATTTTCCGCTGGCCAGGATTTCTCTGAGTGGAACAGGTTCTTGATGTG	182
QY	3704	GATGTGTTTCCAGGAGGAGGAGGAGGAGTCCACGCATCTCTGATGCTGCCTGG	3763
DB	183	GATGTGTTTCCAGGAGGAGGAGGAGGAGTCCACGCATCTCTGATGCTGCCTGG	242
QY	3764	GCTCAGGCCCCAGCAGCAGGAGTCTCTGAGTGGAACAGGTTCTTGATGTG	3823
DB	243	GCTCAGG-CCAGCAGGAGTCTCTGAGTGGAACAGGTTCTTGATGTG	301
QY	3824	CAGGAGCTGAGGAGGAGTGAACAAACCCGAGGAGGAGGAGGAGTCTGCTCCGAGTTGGG	3883
DB	302	CAGGAGCTGAGGAGGAGTGAACAAACCCGAGGAGGAGGAGGAGTCTGCTCCGAGTTGGG	361
QY	3884	GGGAGGGGTGGCAACGCTGCCCCCGGAGGAGGAGGAGGAGTCTGAGTGGAACAGGTTCTG	3943
DB	362	GGGAGGGGTGGCAACGCTGCCCCCGGAGGAGGAGGAGGAGTCTGAGTGGAACAGGTTCTG	421
QY	3944	TTGTGCTCCGAGGAGGAGTCTGCTCCGAGTTGGG	4003
DB	422	TTGTGCTCCGAGGAGGAGTCTGCTCCGAGTTGGG	481
QY	4004	GGGTAGGTGGATTTGAGGAGGAGGAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGGTTCTG	4063
DB	482	GGGTAGGTGGATTTGAGGAGGAGGAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGGTTCTG	541
QY	4064	CAGGAGGAGGAGGAGTGAACAAACCCGAGGAGGAGGAGGAGTCTGAGTGGAACAGGTTCTG	4123
DB	542	CAGGAGGAGGAGGAGTGAACAAACCCGAGGAGGAGGAGGAGTCTGAGTGGAACAGGTTCTG	601
QY	4124	GCTCCGCTGTGCCCCCTTCTCTCACCAGTCTGCTCCGAGTTGGG	4183
DB	602	GCTCCGCTGTGCCCCCTTCTCTCACCAGTCTGCTCCGAGTTGGG	661
QY	4184	CCCCCTTCTCCGCTCCCTCTTGGAGTCTGCTCCGAGTTGGG	4243
DB	662	CCCCCTTCTCCGCTCCCTCTTGGAGTCTGCTCCGAGTTGGG	721
QY	4244	TCCTCATCTGACCCCTCTCTGACGAGCAGGAGGAGGAGTCTGAGTGGAACAGGTTCTG	4303
DB	722	TCCTCATCTGACCCCTCTCTGACGAGCAGGAGGAGGAGTCTGAGTGGAACAGGTTCTG	780
QY	4304	TGAATGTTGGAGGAGGAGTGGGAGGAGGAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGG	4363
DB	781	TGAATGTTGGAGGAGGAGTGGGAGGAGGAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGG	840
QY	4364	TCAGCGTGTCTGGGAGACAGATGAGGAGGAGGAGGAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGG	4423
DB	841	TCAGCGTGTCTGGGAGACAGATGAGGAGGAGGAGGAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGG	900
QY	4424	CAGGAGTATTTGAATGTTGAGTGAAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGGTTCTGAGTGGAACAGG	4483
DB	901	CAGGAGTATTTGAATGTTGAGTGAAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGGTTCTGAGTGGAACAGG	959
QY	4484	GAAGAGATGATGCTGGAAGGAGTGAAGGAGACAGTGAAGGAGGAGGAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGG	4543
DB	960	GAAGAGATGATGCTGGAAGGAGTGAAGGAGACAGTGAAGGAGGAGGAGTCTGAGTGGAACAGGTTCTGAGTGGAACAGG	1019

QY	4544	TGCTGGCATTTTGTGGGTTGTAGTGCCAAACTTGAATAGGGGCTGGGTGCTGCTTCC	4603
DB	1020	TGCTGGCATTTTGTGGGTTGTAGTGCCAAACTTGAATAGGGGCTGGGTGCTGCTTCC	1079
QY	4604	ACTGACACCCAAATCCAGAAATCCCTGCTTGTAGT-CCCAGAACTTTGCTTGTAGTGT	4662
DB	1080	ACTGACACCCAAATCCAGAAATCCCTGCTTGTAGT-CCCAGAACTTTGCTTGTAGTGT	1139
QY	4663	CCCT 4666	
DB	1140	CCCT 1143	

RESULT 7

US-09-978-295A-374
 ; Sequence 374, Application US/09978295A
 ; Patent No. US2002015606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Steward, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
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 ; PRIOR FILING DATE: 1998-03-12
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 ; PRIOR FILING DATE: 1998-03-13

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7 PRIOR APPLICATION NUMBER: 60/078939
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137 PRIOR APPLICATION NUMBER: 60/085580
138 PRIOR FILING DATE: 1998-05-15
139 PRIOR APPLICATION NUMBER: 60/085573
140 PRIOR FILING DATE: 1998-05-15
141 PRIOR APPLICATION NUMBER: 60/085704
142 PRIOR FILING DATE: 1998-05-15
143 PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 10; Length 3113;
Best Local Similarity 64.7%; Pred. No. 1.4e-213;

Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 527 CGGGAGGAGCGCTTCCGGTGTGTAACACGGCCCTACGGGCGAGTCCGGGTGTGGCGG 586
Db 112 CAGCCAGGACAGTATCCAGTGTGTAACCAAAATATGGCAAAATCCGGGGCTAAGAAC 171
QY 587 CGAGCTCAACAAGAGAGATCCTGGGCGCGGTGGTGCAGTTCCTGGGGGTGCCCTACGCCAC 646
Db 172 ACCGTTACCCAAATGAGATCTTGGTCCAGTGGAGCAGTACTTAGGGTCCCTATGCCCTC 231
QY 647 GCGGCCCTGGGGCGCGCGCTTCAGCGGCTGAGGCGCGCGCTCGTGGCCCGCGGT 706
Db 232 ACCCCCACTGGAGAGAGCGGTTTCAGCCGCCAGAACCCCGCTCTCTGACTGGCAT 291
QY 707 GCGCAACGCGCACCCCTCGCGCCCGCTCGCGCAGACCTGCAAG---GGGCGCTGCC 763
Db 292 CGGAATACTACTCAGTTTGTCTGTGTGCCCCCAGACCTCTGGATGAGATCCTTACT 351
QY 764 CGGCATCTGTGCTGTGTGTACCGAACCTTGGAGGGCGCGCCACCTACGTGCA 823
Db 352 GATGACATCTGCTGCTGCTGTGTGCCCCCAGACCTCTGGATGAGATCCTTACT 411
QY 824 GAACAGAGCGAGGACTGCTGTACTCAACCTCTACGTGCCACCGAGGACGTCGCT 883
Db 412 AGATCAAAATGAGACTGCTTACTTAAACATCTACGTGCCACCGAAGATGGAGCCAA 471
QY 884 CACAAAAAAGCGTACGAGCGG-----ACGCTCAATCGCGCAGACACAGATATCCG 934
Db 472 CACAAAGAAAAACGAGATGATATAACGAGTAAAGCGTGTGTAAGAGAAATATCA 531
QY 935 TCACCTCG---GGAAGAGCCTGTGATGCTGTCTTCCATGGCGGCTCCTACATGGAGG 991
Db 532 TGATCAGAACATAGAGAGCGGCTCATGCTCTATATCCATGGGGATCTTACATGGAGG 591
QY 992 GACCGAAACATGTTTCGATGGTCACTGCTGCTGCTATGCAACGTCATTGTAGCCAC 1051
Db 592 CACCGGCAATGATTGACGCGAGCATTTTGGAGCTACGGAAAGCTCATCTGTATCAC 651
QY 1052 GCTCAACTACCTGTGGGTGCTCGGTTTCTCAGCACCGGGACCGAGTGCANAAAG 1111
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QY 1172 CTTGGGGCGACCCGAGCGTATCACCATCTTGGTTCGGGGCAGGGCTCCTCGCT 1231
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QY 1232 CAACCTTCTGATCTCTCCACCATTCAGAGGCTGTTCCAGAGGCCATCGCCAGAG 1291
Db 832 CAGCTGTGTACCTGTCCCACTACTCAGAGGCTCTTTCAGAGGCTCTTTCAGAGGCTCATTCAGAG 891
QY 1292 TGGCAACCGCATTTCCAGTGGTGTGTAACCTACAGCCGCTCAAGTACACGGGCTGCT 1351
Db 892 CGGCACCGCTGTCCAGCTGGGAGTGAATACACCGCGCCAAATACACTCGGATAT 951
QY 1352 GGCAGCCAGCTGGGCTGTGACCGAGGACAGTGTGAGAGCTGTGAGTGTCTGGCGG 1411
Db 952 GGCAGACAGTGGCTGTGCAACATGCTGGACACACCGGACATGGTAGAATGCTGCGGAA 1011
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QY 1472 TGGGCGGTGTGATGGCAGCTGTGTCGCGATGACCTGTAGATCTCTATGAGAGGG 1531
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QY 1532 AGAATTCCTCAACTACGACATGCTCATCGCGCTCAACACGAGGAGGGCTCAAGTTCT 1591
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Db 1429 CGCGAGTACGGCTCCCGACCTTCTATGCTTCTATCATCTGCTGCTGCTGCGCATCC 1488
QY 1892 CGGCGCTGAGTGGGAGATGCGCGGACCGGGATGAATGCTGCTTGTCTTGGCGTGC 1951
Db 1489 GAAGCCCGAGTGGGAGATTCGGCCCATGGTGTAGGTCCCTATGTCTTGGCATCCC 1548
QY 1952 CATGTTGGGTGGCCACGACCTCTTCCCTGTACTTCTCCAGAAATGAGTCACTGCTAG 2011
Db 1549 CATGATCGTCCCGACCGAGCTCTTCACTTGAATCTTTCAGAAAGAGAGCTGATGCTAG 1608
QY 2012 TGCGGTGTCATGACCTACTTGGACCAACTTCGCAAGACTGGGGAGCCCAACAGCGCT 2071
Db 1609 CGCGGTGGTCTATGACCTACTTGGACGAACTTCGCCAAAATCTGGTATCCAAATCAACCACT 1668
QY 2072 GCGCAGGATACCAAGTTCATCCACCAAGCCCATGCTCTCGAGGAGTGTGTGGAG 2131
Db 1669 TCCTCAGGATACCAAGTTCATTCACAAAAACCAACCGCTTGAAGAAAGTGGCTGTCT 1728
QY 2132 CAAATTCACAGCAGGAGGAGCAGTATCTGCACATAGGCTGAAAGCCACGCGTGGTGA 2191
Db 1729 CAAATTAATTCACAAAGACCACTCTATCTGATATGCTTGAACCCAGAGTGAAGA 1788
QY 2192 CAACTACCGCGCACAGGTGGCTCTTGGTGTGAGTCTGTGCGCCACCTGCAACCT 2251
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QY 2252 GCA-----CAGGGAGCTCTTCAACCAACCAACCGCGCTGCTTCCCTACGCCAGCG 2302
Db 1849 GAACGAGATATTCAGTATGTTTCAACCAACCAAGGTTCTCTCCACAGACATGACATC 1908
QY 2303 CTGGCGCGCTCTGCTCCCGCTGGCGCGCCCGGCAACACGCGGCGCCCGCGCTGCGCAC 2362
Db 1909 ATTTCCCTATGGCACCCGCGCATCTCCGCGCAAGATATGGCCAAACCAACAGCGCCAGC 1968
QY 2363 CCGTCTCCCGAGCGCGAGCCGAGC-----CGGCGCCAAAGGCG 2401
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QY 2402 CTATGACCGCTTCCCGGGAGCTCAGGGACTACTTCCACGGAGTGTGAGCTGCGCTGCG 2461
Db 2029 CACAACTGTCTCTATTGAAACCAAAACGAGATATTTCCACCGAAATTAAGTGTCAACCTGC 2088
QY 2462 CGTGGTGCCTCCCTCTCTTCTCAACATCTGCGCTTGTGCTGCTTGTACTACAAGG 2521
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QY 2582 CGTGGCTGTGGGGCGCTGCTCTCCCGCGCGGGCGGTGAGTGTCCACACGAGGAGGA 2641
Db 2209 TATGCTCACAATCCAGAACGAAGAGATCTGTCTCTGAGATGAAGCAGCTGGAACAGA 2268

QY 2642 GCTGCTGTCAGCTGAGCGGGGTGGTGGCTGGGGCGGACCTGCGGAGGCTCT 2701
DB 2649 TCACAGATGTGATCGCTGCAG-----GCACAGACACT 2304
QY 2702 GCGCCCTGCTGCGCGCCGACCTACACCTTGGCCCTGCGCGGGGACCGGACGATGTGCC 2761
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RESULT 8
US-09-978-697-374
; Sequence 374, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavrin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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Query Match 19.5%; Score 912.2; DB 10; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 1.4e-213;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

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 QY 292 CCGAATATCTACAGTTTGTCTGTGCGCGCGCGCTGCGCGCGAGATCCCTTACT 351
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 QY 764 CGCATCATCTGCTGCTGTGTGTTTCAACGACAACTTGGAGGCGCGCGCGCTTACCTGCA 823
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 QY 352 GCATGACATGCTGCCCATCTGGTTTACCGCAATTTGGATCTTTGATGACCTATGTTCA 411
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 QY 824 GAACGAGAGGAGGAGTCTGCTGCTTACCTTAACTTACGTTGCGCGCGCGAGAGCGCTCCGT 883
 DB |||||
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 QY 532 TGATCAGAAACAGTAAGAGCGCGCTCATGCTCTATATCCATGGGGGATCTTACATGAGGG 591
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 DB |||||
 QY 592 CACCGGCAACATGATTGACGGGAGCATTTTGGCAAGCTACGGAACGCTCATCTGATCAC 651
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 QY 652 CATTAACCTACCGTCTGGGAATACTAGGGTTTTTAAGTACCGGTGACCGAGCAAAAGG 711
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Qy	2702	GGCGCCTGCTTGCCTGCGCCGCTACACCTGGCCCTGCGCGGACCGGACGATGTGCC	2761
Db	2305	GAGGCTACCTTGCCTGCGCCGACAGTACACCTCAGCTGCGCGGTGCGCCAGATGACATCCC	2364
Qy	2762	TCTCTTGCCCCCGGGGCCCTGACCCCTGCTGCCAGTGGCGCTG	2804
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RESULT 9

US-09-978-192A-374

; Sequence 374, Application US/09978192A

; Patent No. US20020177553A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tunas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630P1C9

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

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138 PRIOR FILING DATE: 1998-05-15
139 PRIOR APPLICATION NUMBER: 60/085697

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Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

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Query Match 19.5%; Score 912.2; DB 10; Length 3113;

Best Local Similarity 64.7%; Pred. No. 1.4e-213;

Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 527 CGGCGAGGAGCGTCTCCCGTGTGTGAACACGGGCTACGGGCGAGTGGCGGGTGTGCGGCG 586

Db 112 CAGCCAGACAGATATCCAGTTCTCAACAAATATGCAAAATCGGGGCTTANGAAC 171
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Db 232 ACCCCCACTGGAGAGAGGCGGTTTTCAGCCCCCAGAACCCCGTCTCTCTGAGCTGGCAT 291
QY 707 GCGCAACGCCACACCTGCGGCCCCGCTGCGCGAGAGAACTTGCAGC-----GGGCGGTGCC 763
Db 292 CCGAAATACTACTCAGTTTGTCTGTGTGCCCCCAGCACCTGAGAGATCTCTACT 351
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Db 412 AGATCAAAATGAAGACTGCTTTTACTTAAACATCTACGTGCCCAACGAAAGATGGAGCCAA 471
QY 884 CACAAAAAAGCTGACGAGGCG-----ACGCTCAATCCGCGAGACACAGATATCGG 934
Db 472 CACAAAGAAAAACGAGATGATATACGAGTATGACCGTGTGAGAGCAAGATATCA 531
QY 935 TGACCCCTG---GGAAGAGCCTGTGATGCTGTTTCTCCATGCGGCTCTCATGAGGG 991
Db 532 TGATCAAGACAGTAAGAAGCCCGTCACTGTTTATATCCATGGGGGATCTTACATGAGGG 591
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QY 1052 GCTCAACTACCTCTTGGGGTGTCTGCTTTCTAGACCGGGGACGAGCTGCAAAAG 1111
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Db 832 CAGCTTGTGACCTCTCTCCATCTCAGAGGTCTCTTCCAGAGGCGCATCTTCAGAG 891
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QY 1352 GGCAGCCAAAGGTGGGCTGTGACCGAGAGACAGTCTCAAGCTGTGGAGTCTCTGCGCG 1411
Db 952 GGCAGCAAGGTGCGCTGCAACATCTCTGACACGACGACATGTTAGTATGCTTGGGAA 1011
QY 1412 GAAGCCCTCCCGGAGCTGTGGACAGAGCGTGAGCGCTGCGCGCTTACCAATCGGCTT 1471
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Db 1072 CGGGCGGCTGTGAGCGGCGAGCTCATCCAGACGACCCCGGAGATCTTGTAGTGGAGG 1131
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Db 1132 CGAGTTCTCTCACTACGATCATCTGCGGGGTCAACCAAGGGGAGGCGCTTCAAGTTGCT 1191
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%; Pred. No. 1.4e-213;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

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QY 992 GACCGGAAACATGTTGATGGCTGAGTCTGCTGCTATGCAAGCTGATGAGCCAC 1051
Db 592 CACCGGAAACATGATGACCGGAGCATTTTGGCAAGCTACGGAAACGTCATCGTATCAC 651
QY 1052 GCTCAACTACCGTCTTGGGGTGTCTGGTCTTCTCAGCACCGGGGACAGGCTGCAAAAGG 1111
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QY 1832 CGCGGACTACAGCTCTCCGCTCTACTTTTACACTTTTACACTTTTACACTTTTACACTTTTAC 1891
Db 1428 CGCGGAGTACAGCTCTCCGCTCTACTTTTACACTTTTACACTTTTACACTTTTACACTTTTAC 1488
QY 1892 CGGCTGAGTGGGAGAGTGGGCGAGCGGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1951
Db 1489 GAAGCCAGCTGGGAGAGTGGGCGAGTGGGCGAGTGGGCGAGTGGGCGAGTGGGCGAGTGGGCG 1548
QY 1952 CATGGTGGGTCACCGAGCTCTTCCCTGTAACCTTCTCCAGAAATGAGCTGCTGCTGCTGCTGCT 2011
Db 1549 CATGATCGGTCACCGAGCTCTTCACTGTAACCTTCTCCAGAAATGAGCTGCTGCTGCTGCTGCT 1608
QY 2012 TGCCGTGGTCTATGACTTACTGGACCAACTCTGCGCAAGACTGCGGAGCCCAACAGCCGCT 2071

Db 1609 CGCCGTGGTCTATGACCTACTGAGCGAATCTTCCCAAACTGGTATCCAAATCAACCACT 1668
QY 2072 GCGCAGGATACCAAGTTCATCCACCAAGCCCAATCGCTTGGAGAGGAGTGGTGGAG 2131
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QY 2132 CAAATTCACACAGCAGGAGAGCAGTATCTGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCT 2191
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Db 2209 TATGCT 2268
QY 2642 GCT 2701
Db 2269 TCACGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2304
QY 2702 GCGGCT 2761
Db 2305 GAGGCT 2364
QY 2762 TCTTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2804
Db 2365 ACTTATGAGCGCAACACCACTCACCATGATTTCCAAACACACATG 2407

RESULT 14

US-09-978-191A-374
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; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 11; Length 3113;
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 QY 527 CGGCGAGAGCGCTCCCGGTGGTGAACACCGCCTACGGCGAGTGGCGGTGGCGCG 586
 DB 112 CAGCCAGACAGTATCCAGTTGTCAGTGTCAACACAAATATGGCAAAATCCGGGCGCTAAGAAC 171
 QY 587 CGAGCTCAACACGAGATCCCTGGGCGCGCTCGTGCAGTTCTTGGCGGTGCCCTACGCCAC 646
 DB 172 ACCGTTACCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGTCCCTATGCTC 231
 QY 647 GCGGCGCTGGGCGCGCGCTTCAGCGCGCTTGAGCGCGCGCGCGCTCGTGGCGCGCGCT 706
 DB 232 ACCCGCCACTGGAGAGGCGGTTTCAGCGCGCGCGCGCGCGCGCGCTCTCTGGAGTGGCAT 291
 QY 707 GCGCAACGCCACCCCTCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 763
 DB 292 CCGAATATCTACTCAGTTTGT 351
 QY 764 CGCATATGCTGT 823
 DB 352 GCATGATGCTGCGCCATCTGGTTACCGCAATTTGGATATTTGATGACCTATGTTC 411
 QY 824 GAACAGAGCGAGAGTCTGT 883
 DB 412 AGATCAAAATGAGACTGCTTACTTAAACATCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 471
 QY 884 CACAAAAAAGCGTACGAGCGCG-----ACGCTCAATCCCGCGAGACAGATATCCG 934
 DB 472 CACAAAGAAAAACGAGATGATATAACAGGTATGACCGGTGTGTGTGTGTGTGTGTGTGTGT 531
 QY 935 TGACCTGTG---GGAGAGAGCTGT 991

DB 532 TGATCAGAACAGTAAAGCCCGTCATGCTATATCCATGGGAGTCTTACATGGAGG 591
 QY 992 CACCGGAAACATGTTTCATGCTCAGTCTCGCTTATGGCAACGCTTATGTTAGCCAC 1051
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 QY 1232 CAACCTTCTGATCTCTCCCAACATTCAGAGGGCTGTTCCAGAGGCCATTCGCCACAG 1291
 DB 832 CAGCTGTGACCGCTGTCACCTACTCAGAGGTCTCTTCCAGAGGCCATTCATTCAGAG 891
 QY 1292 TGGCACCGCCATTTCCAGCTGGTCTGTCAACTACCACTACAGCGCTCAAGTACACGCGGTGCT 1351
 DB 892 CGGCACCGCCCTGTCAGCTGGGCGTGAATACCACTACAGCGCGCCAGATCACTCGATATT 951
 QY 1352 GGCAGCCAGGTGGCTGTGACCGAGAGACAGTGTGTAAGTGTGGAGTGTCTGCGCGG 1411
 DB 952 GGCAGACAAAGTCTCGCTGCAACATGTGTGACACCAAGAGTGTGTAAGTGTCTGCGGAA 1011
 QY 1412 GAAAGCCCTCCCGGAGCTGGTGGACAGGAGCTGCGCGCTGCGCGCTTACCATCGCTT 1471
 DB 1012 CAGAACTACAGAGCTCATCCAGAGACCATCACCGCGCCACCTACACATAGCCCTT 1071
 QY 1472 TGGGCGCGTGGTGGATGGGAGAGTGTGTCGCCGATGACCTGAGATCTCTCATGACAGGG 1531
 DB 1072 CGGCGCGGTGATCGACGGGAGCTCATCCAGAGACGACCCAGATCTCTGATGGAGCAAG 1131
 QY 1532 AGAATTTCTCACTACAGATGCTCATCGGCGCTCAACAGGAGGAGGGGCTCAAGTTGCT 1591
 DB 1132 CGAGTTCTTCACTACAGATCATGCTGGCGCTCAACAGGAGGAGGGGCTGAGTTGCT 1191
 QY 1592 GGAGGACTCTGACAGAGAGGAGGAGCGGTGTGTCTGCGAGCGCTTTGACTTCACTGTCTC 1651
 DB 1192 GGAAGCGATCTGGATTAACAGAGAGCGGTGTGACGCCACGACTTTGACTTCTCGGTGTC 1251
 QY 1652 CAACCTTGTGGAGAACCTGTATGGCTACCGGAGAGGAGGATGTGCTTGGGAGACCAT 1711
 DB 1252 CAACCTTGTGGAGAACCTTTACGGCTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1311
 QY 1712 CAAGTTTATGTACAGACTGGGCGGACCGGAGCAATGGCGAAATGGCGGCAAAACCT 1771
 DB 1312 CAAGTTTATGTACAGACTGGGCGGATAGGAAACCGGAGAGCGCGGAGGAGGAGGAGGAGT 1371
 QY 1772 GCTGGGCTTCTTATGACACCAATGGGTGGACACAGCTGTGGCCACTGCGCAAGCTGCA 1831
 DB 1372 GGTGGCTCTCTTACTGACCACTGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1428
 QY 1832 CGCGGACTACCACTCTCCGCTCTACTTTTACACCTTCTACACCACTGCGGAGCGGCGGAGG 1891
 DB 1429 CGGCGAGTACGCTCCCGCACTCTTCTGTGCTTCTATCATCTGCGGAGGAGGAGGAGT 1488
 QY 1892 CCGGCTGAGTGGGAGATGCGGCGACCGGAGTGAATGCGGCTATGTCTTTTGGCGTGC 1951
 DB 1489 GAAAGCCAGCTGGGAGATTCGGGCGGATGGTGTGAGGTGCGGCTTCTGCTTCTGCGCATCC 1548
 QY 1952 CATGTGTGGTGGCGGAGCTTCCCGCTTAACTTCTCCAGAGATGACGCTGCTGCTCAG 2011
 DB 1549 CATGATCGGTCCCGGAGCTCTTCAAGTTGTAATTTTCCAGAGACGAGCTGCTGCTCAG 1608
 QY 2012 TGCCGTGTGATGACCTACTTGGACCAACTTCCCAAGACTGGGAGCCCGGAGGAGGAGG 2071

Db 1609 CGCGTGGTCTATGACCTACTGGACGAACTTCGCAAACTGGTGATCCAAATCAACCACT 1668
 QY 2072 GCGCAGGATACCAAGTTCATCCACCAAGCCCAATCGCTTCGAGGAGGTGGTGGAG 2131
 Db 1669 TCCTCAGGATACCAAGTTCATCCACCAAAACCCACCGCTTTGAAGAAGTGGCGTGGC 1728
 QY 2132 CAAATTCACAGAGGAGAGACAGTATCTGCATAGGCTTGAAGCCACGCGTGGTGA 2191
 Db 1729 CAAGTATATCCCAAGACAGCTATCTGCATATGGCTTGAACCCACAGAGTGAAGA 1788
 QY 2192 CAACTACCGCGCAACAAAGTGGCTTCCTGGGTGGAGTCTGGTCCACCTGCACCACT 2251
 Db 1789 TCCTACCGGGCAACGAAGTGGCTTCCTGGGTGGAGTCTGGTCCATTTGGCAACTT 1848
 QY 2252 GCA-----CACGGAGCTTCCACCAACCAACGCGCTGCTCCCTACGCGCAGCG 2302
 Db 1849 GAACGAGATATTCAGTATGTTTCAACAACCAACCAAGGTTCTCCACGAGATGACATC 1908
 QY 2303 CTGGCGGCTGCTCCCGCGTGGCGCGCGCGGACACGCGCGCGCGCGCGCTGGCAC 2362
 Db 1909 ATTTCCTATGACACCGCGGATCTCCCGCGCAAGATATGGCCAAACCAACCGCCAGC 1968
 QY 2363 CTGCTCTCCGAGCGCGCGCGCGGCT-----CCGCGCCCAAGGCG 2401
 Db 1969 ATCACTCTCGCAACATCCCAACACTCTAAGGACCTCACAACAGGCGCTGAGGA 2028
 QY 2402 CTATGACGCTTCCCGGGAGTCAAGGAGTACTCAAGGAGTGAAGTCAACGTTGGC 2461
 Db 2029 CACAACTGCTCTATTGAACCAACCAAGAGATATTCCACCGAATTAAGTGTCACTTGC 2088
 QY 2462 CTGGGTGCT 2521
 Db 2089 CTGGGGGCTGCT 2148
 QY 2522 GACCGCGGAGGAGTGGCGGTGAGCGGCTTAGCCCACTTGGCGGCTCAGGCTCTGG 2581
 Db 2149 GGACAAGAGCGGCTGAGACTCAAGCGCGCGCGCTCCCGAGAGAAACCAACCAATGA 2208
 QY 2582 CTGCTGCTGGTGGGCGCGCT 2641
 Db 2209 TATGCTCAGATCAGAGAGAGATATGCTCTGAGATGAAGCAGTGGGAACAGGA 2268
 QY 2642 GCTGTGTCTGAGTGAAGCGGGGTGGTGGCGTGGCGGACCTCGCGAGGCTCT 2701
 Db 2269 TCAGAGTGTGAGTGGTGCAG-----GCACAGCAGCACT 2304
 QY 2702 GCGCGCTGCTGCGCGCGCGCGCGCTGAGTGGCGTGGCGGCGGCGGCGGCGGCGGCGGCG 2761
 Db 2305 GAGGCTACCTTCTGCGCGCGCGCGCGCGCTGAGTGGCGTGGCGGCGGCGGCGGCGGCGG 2364
 QY 2762 TCTCTTGGCGCGCGCGCGCGCTGAGTGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGG 2804
 Db 2365 ACTTATGAGCGCAACACCATCACCATGATTCDAACACACTG 2407

RESULT 15

US-09-978-403A-374
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 ; Publication No. US20030050240A1
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 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC17
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 ; CURRENT FILING DATE: 2002-03-19
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 ; PRIOR FILING DATE: 2001-07-30
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 11; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 1.4e-213;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

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QY	587	CGAGCTCAACACAGAGATCTCGGCCCGCTCGTGAGTTCTTTGGCGTGCCCTACGCCAC	646
Db	172	ACCGTTACCCAATGAGATCTTGGTCCAGTGGAGCAGTACTTAGGGTCCCTATGCTC	231
QY	647	GCGGCCCTGGGGCGCGCGCTTCCAGCGCTGAGGGCGCGCTGTGGCCCGGGCT	706
Db	232	ACCCCCACTGGAGAGAGCGGTTCAGCCCCCAGACCCCGCTCTCTGAGACTGGCAT	291
QY	707	GCGCAACGCCACCACTGCGCGCGCTGCGCGCAGAACCTGCACG---GGCGCTGCC	763
Db	292	CGAAATACTACTCAGTTTGTGTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACT	351
QY	764	CGCCATCATGCTGCTGTGTGTTCCAGCAACATTTGAGGGCGCGCCACCTACGTGCA	823
Db	352	GCATGACATGTGCCCATCTGGTTTACCGCCAAATTTGGATACTTTTGATGACCTATGTTCA	411
QY	824	GAACGAGAGCGAGGACTGCTGTACTCAACTCTTACGTGCCACCGAGGAGCGGTCCGCT	883
Db	412	AGATCAAAATGAAGACTGCTTTACTTAAACATCTACGTGCCACCGAGATGAGGCCAA	471
QY	884	CACAAAAAAGTGCAGGCGG-----ACGCTCAATCCGCCAGACACAGATATCCG	934
Db	472	CACAAAGAAAAACCGCAGATGATATAACCGTGTGTAAGACGAGATATTCATCA	531
QY	935	TGACCCCTG---GGAAGAGCGCTGTGCTCTTTCTCCATGCGCGCTCTCATATGGAGG	991

Db 532 TGATCAGAACAGTAGAAGCCGTCATGGTCTATATATCATGGGGATCTTACATGGAGGG 591
 Qy 992 GACCGAAACATGTTGATGCTAGTCTCGCTGCTATCGCAACGTCATGTTAGCCAC 1051
 Db 592 CACCGCAACATGATTTGACGAGCATTTTGGCAGCTTACGGAACGTCATCGTGATCAC 651
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 Qy 1112 CAACTATGGGCTCTGGACCAATCAGGCCCTGGGCTGAGTGAACATCGCCCA 1171
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 Qy 1172 CTTTGGGGCGCACCGGAGCTATCACCATCTTTGGTTCCGGGGCAGGGCCCTCTCGT 1231
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 Qy 1292 TGGCACCGCATTTCCAGCTGCTGTCACTACAGCGCTCAAGTACAGCGGCTGCT 1351
 Db 892 CGGCACCGCCCTGTCCAGCTGGGAGTGAACATACAGCGGCCCAAGTACACTCGGATAT 951
 Qy 1352 GGCAGCCAAAGTGGGCTGTGACCGAGAGGACAGTGTGAAGTGTCTGGGCCG 1411
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 Qy 1412 GAAGCCTCCCGAGCTGTGGACCAAGACGTCGACGCTGCCGCTTACCAATGCGCTT 1471
 Db 1012 CAAGAACTACAAAGAGTCTATCCAGCAGACCATCACCCCGGCCACCTTACCACATAGCCT 1071
 Qy 1472 TGGCCCGTGTGATGCGAGCTGTCTCCGATGACCTGAGATCTCTATGACAGAGG 1531
 Db 1072 CGGCGCGTGTGACGCGGAGCTATCCAGACGACCCCAAGTCTCTGATGAGCAAG 1131
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 Db 1132 CGAGTTCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGAGGCGCTGAAGTTCTGT 1191
 Qy 1592 GGAGGACTCTCAGAGAGCGGAGGCTGTCTGCGAGCGCTTGGCTTCACTGCTCTC 1651
 Db 1192 GGAGCGCATCTGTGATAACGAGGAGCGTGTGACGCCCAAGCACTTGTGACTTCTCCGTGTC 1251
 Qy 1652 CAATTTTGTGACAACTGTATGCTTACCGGAGGCAAGGATGTCTTCGGGAGACCAT 1711
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 Qy 1772 GCTGGCGCTCTTTACTGACCAACCAATGGGTGGACACAGCTGTGCCACTGCCAAGCTGCA 1831
 Db 1372 GGTGGCTCTCTTTACTGACCAACAGTGGGTGGGCCCGCCCGCTGGCC---GCCAGCTGCA 1428
 Qy 1832 GGCGACTACAGTCTCCCGTCTACTTTTACACTTCTACCACTTCCAGGCGGAGG 1891
 Db 1429 CGCGCAGTACGGCTCCCGCACTTCTATGCTTCTATCATCATCTGCGCAAGCGAAAT 1488
 Qy 1892 CCGGCTGAGTGGGAGATGGGCGACGGGATGAATGCCCTATGTCTTTGGCGTGC 1951
 Db 1489 GAAGCCAGCTGGGCAATTCGGGCCATGGTGTGAGGTTCCCTATGTCTTGGCATCCC 1548
 Qy 1952 CATGGTGGGTGCCACCGCACTCTTCCCTGTAACCTTCTCCAGAAATGAGTCAATGCTCAG 2011
 Db 1549 CATGATCGGTCCCAACCGAGCTCTTCACTGTACTTTTCCAGAAAGAGCTCATGCTCAG 1608
 Qy 2012 TGGCGGTGATGACCTACTTGACCAACTCTGCGCAAGACTGGGGACCCCAACAGCGGCT 2071
 Db 1609 CGCGTGGTCTATGACCTTACTGGACGAACTTCGCCAAACTGGTGTATCCAAATCAACAGT 1668

Qy 2072 GCGCAGGATACAAAGTTTATCCACCAAGCCCAATCGCTTCGAGGAGTGTGTGGAG 2131
 Db 1669 TCTCAGGATACCAAGTTTCAITTCACAAAAACCAACCGCTTGAAGAAGTGGCTGGTC 1728
 Qy 2132 CAAATTTCAACAGCAGGAGACAGTCTACTGACATAGGCTTGAAGCCACGCGTGGTGA 2191
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 Qy 2252 GCA-----CAGCGAGCTTTCACACACACAGCGCTGCTCTCTAGCCACGG 2302
 Db 1849 GAACGAGATATTTCCAGTATGTTTCAACCAACCAAAAGGTTCTCTCCACGACATGACATC 1908
 Qy 2303 CTGGCGGCTCTCTCTCCCGCTGGGCGCCCGGCAACGCGGCGCCCGCGCTTCCGCAC 2362
 Db 1909 ATTTCCTATGACACCGCGGATCTCCCGGCAAGATATGGCCAAACCAACAGCCGACG 1968
 Qy 2363 CCGTCTCCGAGCGCGAGCCCGAGC-----CGGCGCCAAAGGCG 2401
 Db 1969 AATCACTCTCTGCAACAAATCCCAACACTCTAAGGACCTTCAAAAAACAGGCGCTGAGGA 2028
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 Qy 2462 CCGTGGTGGCTCTCTCTCTCTCAACATCTGGCCTTTGCTGCGCTTCTACTACAAAGC 2521
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 Db 2149 GGACAGAGGCGGCTATGAGACTCAAGGCGCCCGAGTCCCGAGAGAAACACCAAAATGA 2208
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 Qy 2702 GCGCCCTGCTGCGCGCGCGCTGACCTGCGCGCTGCGCGCGCACCGGACGATGTGCC 2761
 Db 2305 GAGGCTCACCTGCGCGCGCAGACTACACCTCACGCTGCGCGCTGCGCAGATGACATCCC 2364
 Qy 2762 TCTCTTGGCGCGCGCGCGCTGACCTGCTGCGCGCGCTGCGCGCGCTGCGCGCTG 2804
 Db 2365 ACTTATGACGCGCAACACCATCAGCATGATTTCCAAACACACTG 2407

Search completed: February 19, 2004, 11:54:03
 Job time : 1528.21 secs

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 17:13:07 ; Search time 9101.14 Seconds
 (without alignments)
 12463.166 Million cell updates/sec

Title: US-09-934-323-1

Perfect score: 4667

Sequence: 1 ggcacaggaacttggtct.....ttgccttgactgcctc 4667

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrt:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991.8	21.3	3853	11 AK039018	AK039018 Mus muscu
2	789.8	16.9	1058	12 BM000364	BM000364 AGENCOURT
3	781.2	16.7	945	12 BI861707	BI861707 60338389
4	756.4	16.2	887	13 BQ437258	BQ437258 AGENCOURT

5	741.2	15.9	1884	11 BC028738	Homo sapi
6	733.6	15.7	1157	12 BM477185	AGENCOURT
7	699.8	15.0	790	14 CA324321	UI-M-FYO
8	682.8	14.6	981	13 BU542698	AGENCOURT
9	676.6	14.5	942	13 BU173291	AGENCOURT
10	674.6	14.5	919	13 BQ891968	AGENCOURT
11	667.6	14.3	766	14 CA749282	UI-M-FYO
12	667.2	14.3	735	10 BF058856	7k3se09-X
13	665.8	14.3	1073	10 BF529926	602042317
14	661.8	14.2	879	13 BQ947939	AGENCOURT
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ALIGNMENTS

RESULT 1
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 DEFINITION
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 Mus musculus adult male hypothalamus cDNA, RIKEN full-length
 enriched library, clone: A230085M13 product: NEUROLOGIN 3 ISOFORM
 HNL3 homolog [Homo sapiens], full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AK039018.1 GI:26332978
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
 1
 CARNINCI, P. and HAYASHIZAKI, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 PUBMED 10349636

AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 CARNINCI, P., SHIBATA, Y., HAYATSU, N., SUGAHARA, Y., SHIBATA, K.,
 ITOH, M., KONNO, H., OKAZAKI, Y., MURAMATSU, M. and HAYASHIZAKI, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 PUBMED 11042159

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 ACCESSION
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 VERSION
 BM800364.1 GI:19117175
 EST.
 Homo sapiens (human)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 1 (bases 1 to 1058)

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VERSION	1	GI:16002454	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgs.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue procurement: DCTD/DTF cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12015 row: b column: 24 High quality sequence stop: 753.		
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BC028738 1884 bp mRNA linear HTC 01-MAY-2002
 DEFINITION Homo sapiens, Similar to neurologin 3, clone IMAGE:5263628, mRNA.
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 VERSION BC028738.1 GI:20380993
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1884)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE Strausberg, R.
 JOURNAL Direct Submission
 Submitted (29-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
 Series: IPAK Plate: 47 Row: h Column: 12
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9506786
 This clone has the following problem: frame shifted.

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BASE COUNT      202 a      341 c      266 g      171 t      1 others
ORIGIN

Query Match      14.6%; Score 682.8; DB 13; Length 981;
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Matches 763; Conservative 0; Mismatches 77; Indels 4; Gaps 3;

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Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 942)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNA3543 row: c column: 09
High quality sequence stop: 482.
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/clone="IMAGE:6172736"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.75 Kb. Library constructed by Life
Technologies."
BASE COUNT      196 a      263 c      289 g      189 t      5 others
ORIGIN

Query Match      14.5%; Score 676.6; DB 13; Length 942;
Best Local Similarity 92.1%; Pred. No. 2.2e-118;
Matches 791; Conservative 0; Mismatches 56; Indels 12; Gaps 7;

QY 3640 CTGGAAGCTTATTTCCCTGGCCAGGACGATTTCTCTAGTGGAAAACAGTTCTTGA 3699
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DB 61 TGTGGATGTGTTCCTCCAGGACGCGCCCTCTCTCTCCAGCACTTCCCTGCTCCC 120
QY 3760 CCAGGCTTCAGGCCCCAGCACCCAGTTCTCTCTCATATGGCAGGTGAGCACACTTCTAG 3819
DB 121 CCAGGCTTCAGGCCCCAGCACCCAGTTCTCTCTCATATGGCAGGTGAGCACACTTCTAG 180
QY 3820 TTGGCAGGAGCTGAGAGGGTGAACAAACCCGAGGAGGCCCGCCCTTGTCTCCGAGT 3879
DB 181 TTGGCAGGAGCTGAGAGGGTGAACAAACCCGAGGAGGCCCGCCCTTGTCTCCGAGT 240
QY 3880 TGGGGGGGGGGGTGTGGCAACGTGCCCCCGCAGAGGCCACGATGTTTGACCAAGCC 3939

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Db      241 TGGGGGAGGGGTGTGCAAGCTGCCCCCGAGAGCCACGATGTTTACCAAGGCC 300
QY      3940 CTCATTGTGTCGAGGACAGCCTTTTCCCGAGGCTCAGAGCATTGCTCATCGTGCCA 3999
Db      301 CTCATTGTGTCGAGGACAGCCTTTTCCCGAGGCTCAGAGCATTGCTCATCGTGCCA 360
QY      4000 AACTGGGTAGGTGGATTGAGCGGAAGACTCCCAATATGTCACCAAGATTTCCAGTCC 4059
Db      361 AACTGGGTAGGTGGATTGAGCGGAAGACTCCCAATATGTCACCAAGATTTCCAGTCC 420
QY      4060 CAGGCGGCGAGGGGAACTAAGGCGAAGCAGAGATACAGGCGGAGGATGTGCA-GGTG 4118
Db      421 CAGGCGGCGAGGGGAACTAAGGCGAAGCAGAGATACAGGCGGAGGATGTGCAANNGTG 480
QY      4119 AGGGGGCTCCCGCTGTGCCCCCTTCTCTCCTCAGCATGTCTCCCCCAGCTCGCTTCT 4178
Db      481 AGGGGGCTCCCGCTGTGCCCCCTTCTCTCCTCAGCATGTCTCCCCCAGCTCGCTTCT 540
QY      4179 CCGTTCCTCTCATCTCCGTCCTCCCTCCTCTTGAAGCTGTCCCATCTCAGTGTGACACCA 4237
Db      541 CCGTTCCTCTCATCTCCGTCCTCCCTCCTTGAAGCTGTCCCATCTCAGTGTGACACCA 600
QY      4238 GCCTTCCTCTCATCTGACCACTCTCTCTGACCGACGCGCCCTCTCTTGTCTGAAAGAAAG 4297
Db      601 GCCTTCCTCTCATCTGACCACTCTCTCTGACCGACGCGCCCTCTCTTGTCTGAAAGAAAG 660
QY      4298 GAGCCTTG-AATGTGTGAGGG--AGGCAGTGGGAGAAAGTCTCACCGGACAGGTT-GG 4353
Db      661 GAGCCTTGAAATGTGTGAGGGAGGAGTGGGAGAAAGTCTCACCGGACAGGTTGGG 720
QY      4354 GAGAAATGAGTGTGAGGGAGGAGTGGGAGAAAGTCTCACCGGACAGGTTGGG 4408
Db      721 GAAAAATGAGTGTGAGGGAGGAGTGGGAGAAAGTCTCACCGGACAGGTTGGG 780
QY      4409 TTGGCGCAGACACCA-GCAGGAATATTTGAATGTGTGAGTCACTCCCCGAGGCGCTT 4467
Db      781 GTAGGCGAGATCTCAGGAGGAATATTTGAATGTGTGAGGCGACTCCCCGGGAAG 840
QY      4468 GGGCTTGGGCAATTGGGAA 4486
Db      841 GCCCTTGGGCTTGGGCA 859

RESULT 10
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LOCUS   AGENCOURT 8695255 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6377489
DEFINITION 5', mRNA sequence.
ACCESSION B0891968
VERSION   B0891968.1 GI:22283982
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1 (bases 1 to 919)
JOURNAL   NTH-MGC http://mgc.nci.nih.gov/.
COMMENT   National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-f@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Rubin Laboratory
          DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Clone distribution: Agencourt Bioscience Corporation
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1CM2561 row: f column: 18
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          High quality sequence stop: 486.
          Location/Qualifiers

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/clone="IMAGE:6377489"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
Note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 187 a 290 c 275 g 167 t
ORIGIN
Query Match 14.5%; Score 674.6; DB 13; Length 919;
Best Local Similarity 98.0%; Pred. No. 5.4e-118;
Matches 683; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 774 CTGCGTGTGTGTTTCCCGACAACTTGGAGGCGCGCCACCTAGCTGCGACGACGAGC 833
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QY 834 GAGGACTGCTGTACTCAACTCTAGTGCCACCGAGGACGGTCCGCTCACAATAAAA 893
Db 61 GAGGACTGCTGTACTCAACTCTAGTGCCACCGAGGACGGTCCGCTCACAATAAAA 120
QY 894 GTGACGAGGCGAGCTCAATCCGCGACACACATATCCGTGACCTGGGAGAGCCT 953
Db 121 COTGACGAGGCGAGCTCAATCCGCGACACACATATCCGTGACCTGGGAGAGCCT 180
QY 954 GTGATGTGTTTCTCCATGGCGGCTCTTACATGAGGGGACCGGAAACATGTTCCATGGC 1013
Db 181 GTGATGTGTTTCTCCATGGCGGCTCTTACATGAGGGGACCGGAAACATGTTCCATGGC 240
QY 1014 TCAGTCTCGGTGCTATGCGAACGTATGTAGCAGCGTCAACTACCGTCTTGGGGTG 1073
Db 241 TCAGTCTCGGTGCTATGCGAACGTATGTAGCAGCGTCAACTACCGTCTTGGGGTG 300
QY 1074 CTCGGTTTTCTCAGCACCGGGGACGAGCTGCAAAAGGCAACTATGGCTCTCTGCCAC 1133
Db 301 CTCGGTTTTCTCAGCACCGGGGACGAGCTGCAAAAGGCAACTATGGCTCTCTGCCAC 360
QY 1134 ATCCAGGCCCTGCGCTGCTCAGTGAATAAATGCCCACTTTGGGGGCGACCCCGAGCGT 1193
Db 361 ATCCAGGCCCTGCGCTGCTCAGTGAATAAATGCCCACTTTGGGGGCGACCCCGAGCGT 420
QY 1194 ATCAACCATCTTTGGTTCGGGGCAGGGGCTCTCTGCGTCAACCTTCTGTATCTCTCCAC 1253
Db 421 ATCAACCATCTTTGGTTCGGGGCAGGGGCTCTCTGCGTCAACCTTCTGTATCTCTCCAC 480
QY 1254 CATTGAGAGGCTGTTTCCAGAGGCGCATCGCCGAGTGCGCACCGCCCAATTTCCAGCTGG 1313
Db 481 CATTGAGAGGCTGTTTCCAGAGGCGCATCGCCGAGTGCGCACCGCCCAATTTCCAGCTGG 540
QY 1314 TCTGTCAACTACGAGCGCTCAAGTACAGCGGCTCTGCGACGCAAGGTGGGCTGTGAC 1373
Db 541 TCTGTCAACTACGAGCGCTCAAGTACAGCGGCTCTGCGACGCAAGGTGGGCTGTGAC 600
QY 1374 CGAGGAGCAGTGTCTGAAGCTGTGGAGTGTCTGCGCGGGAAGCCCTCCCGGGAGCTGGTG 1433
Db 601 CGAGGAGCAGTGTCTGAAGCTGTGGAGTGTCTGCGCGGGAAGCCCTCCCGGGAGCTGGGG 660
QY 1434 GACGAGGAGCTGAGCTGCGCGCTGCTACCATCGCT 1470
Db 661 GACGAGGAGCTGAGCTGCGCGCTGCTACCATCGCT 1470

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RESULT 11	
CA749282	766 bp mRNA linear EST 27-NOV-2002
LOCUS	UI-M-FYO-cdd-g-01-0-UI.r1 NIH.BMAP_FYO Mus musculus cDNA clone
DEFINITION	IMAGE: 6831482 5', mRNA sequence.
ACCESSION	CA749282
VERSION	CA749282.1 GI:25570887
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 766) NIH-MGC http://mgs.nhl.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs@remail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov This clone was contributed by the Brain Molecular Anatomy Project (BMAP).
AUTHORS	The following repetitive elements were found in this cDNA sequence: 62-157 >(GGGA)nSimple_repeat (matched complement) 254-296, >GC-richLow_complexity
TITLE	Seq primer: pYX-5.
JOURNAL	
COMMENT	
FEATURES	
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	/dev_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"
	/lab_host="DH10B (T1 phage resistant)"
	/clone_lib="NIH BMAP FYO"
	/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
	109 a 290 c 236 g 129 t 2 others
BASE COUNT	
ORIGIN	
Query Match 14.3%; Score 667.6; DB 14; Length 766;	
Best Local Similarity 93.4%; Pred. No. 1.1e-116;	
Matches 720; Conservative 0; Mismatches 45; Indels 6; Gaps 2;	
QY	217 CCACCCTGCCCCCTCCAT-GGAGAGAACAGACCCCCTTCCTGTGCCAGTTAAACCCAG 275
Db	
	1 CCACCCCTACCCCTCATNGGAGAGAAATAGACTCCTCTTCTGTGCCCTTCTTAACCCAG 60
QY	276 GTCCCTCCCAACCCCTCTCTCCCTCTTCCCGCCGCTCTCTCCCTCTCTGGGGCGAG 335
Db	
	61 GTCCCTTCCGTCCTCTCTCTCTCTTCCCGCCGCTCTCTCTCTCTCTGGGGCGAG 120
QY	336 GGGGCT 395
Db	

FEATURES
source

Location/Qualifiers
1. .735

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/notes="Organ: ovary; Vector: pTV3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'] TGTACCAATCTGAAGTGGAGCGCGCCGCGACATTTTITTTTTTTT 3'] double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 159 a 233 c 204 g 137 t 2 others

Query Match 14.3%; Score 667.2; DB 10; Length 735;
Best Local Similarity 97.0%; Pred. No. 1.3e-116;
Matches 689; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 804 GCGCGCGCCACCTACGTCGAGNACCAGAGGAGGACTGCTGTACCTCAACCTCTACGTG 863
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QY 864 CCCACCGAGGACGGTCCGCTCACAACAAAACGTCGAGGCGAGCGTCAATCCGCGAGAC 923
Db 61 CCCACCGAGGACGGTCCGCTCACAACAAAACGTCGAGGCGAGCGTCAATCCGCGAGAC 120
QY 924 ACAGATATCGTGACCTCGGAGAGACCTGTGATGCTGTTTCTCATGCGGCTCTCTAC 983
Db 121 ACAGATATCGTGACCTCGGAGAGACCTGTGATGCTGTTTCTCATGCGGCTCTCTAC 180
QY 984 ATGAGGGGACCGAACAATGTCATGGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1043
Db 181 ATGAGGGGACCGAACAATGTCATGGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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QY 1104 GCAAAAGGCAACTATGGCTCCTGGACCATCCAGGCTGCTGCTGCTGCTGCTGCTGCTG 1163
Db 301 GCAAAAGGCAACTATGGCTCCTGGACCATCCAGGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 1164 ATCGCCCACTTTGGGGGCGACCCCGAGCGTATCACCATCTTTGGTTCCGGGGCAGGGGC 1223
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Db 421 TCCTGGTCAACCTCTGATCTCTCCACCATTCAGAGGGTGTTCAGAGGGCCATC 480
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QY 1464 ATCGCTTTTGGGCGCGGTGGTGGAGCGAGCTGGTCCCGATGACCCCTGA 1513
Db 661 ATCGCTTTTGGGCGCGGTGGTGGAGCGAGCTGGTCCCGATGACCCCTGA 709

RESULT 13

BF529926

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF529926 1073 bp mRNA linear EST 11-DEC-2000
602042317F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179748
5', mRNA sequence.
BF529926
BF529926.1 GI:11617289
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
1 (bases 1 to 1073)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9490 row: b column: 05
High quality sequence stop: 635.
Location/Qualifiers
1. .1073
/organism="Homo sapiens"
/mol_type="mRNA"
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/clones="IMAGE:4179748"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Brn67"
/notes="Organ: brain; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 279 a 296 c 316 g 181 t 1 others

FEATURES
source

Query Match 14.3%; Score 665.8; DB 10; Length 1073;
Best Local Similarity 92.7%; Pred. No. 2.6e-116;
Matches 733; Conservative 0; Mismatches 52; Indels 6; Gaps 3;

QY 3866 CTTGTCTCCCGAGTTGGGGGAGGGGGTGTGGCAACGTGCCCCCGCAGAGGCCACGCAT 3925
Db 2 CTTGTCTCCCGAGTTGGGGGAGGGGGTGTGGCAACGTGCCCCCGCAGAGGCCACGCAT 61
QY 3926 GTTTGACCAAGCCCTCATTTGTGTCGAGGACAGCCCTTTTCCCGAGCCCTCAGAGATT 3985
Db 62 GTTTGACCAAGCCCTCATTTGTGTCGAGGACAGCCCTTTTCCCGAGCCCTCAGAGATT 121
QY 3986 GCTCATCGTCCCAAACTGGGTAGTGTGATTTAGCGGAAAGACTCCCAAAATGTGCCAA 4045
Db 122 GCTCATCGTCCCAAACTGGGTAGTGTGATTTAGCGGAAAGACTCCCAAAATGTGCCAA 181
QY 4046 GAATTTCCAGTCCCGAGGAGGGGAGGAGGAACTAAGGGCAAGCAGGATACAGGGCGAGG 4105
Db 182 GAATTTCCCGTCCCGAGGAGGGGAGGAGGAACTAAGGGCAAGCAGGATACAGGGCGAGG 241
QY 4106 GATGTGGCAGGTGAGGGGCTCCCGCTGTGCGCTTCTCTCCTACCATGTCTCCCGCCACC 4165
Db 242 GATGTGGCAGGTGAGGGGCTCCCGCTGTGCGCTTCTCTCCTACCATGTCTCCCGCCACC 301
QY 4166 CTGGCTCAGTTTCTCCGTTCCCTTTTCATCTCGTCCCTCTTTTGAAGCTGTCCCGCATCTC 4225
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 16:42:38 ; Search time 1126.58 Seconds
(without alignments)
11182.718 Million cell updates/sec

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Perfect score: 4667
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4667	100.0	4667	ABA95199	Human carboxyleste
2	4332.4	92.8	4763	AAD40569	Human drug metabol
3	4245.6	91.0	4622	ABN59628	Novel human coding
4	2508	53.7	2508	ABA55200	Human carboxyleste
5	2452.6	52.6	2523	AAF82996	Human MBSP4 polype
6	2383.4	51.1	2663	ABA94727	Human drug metabol
7	1618.2	34.7	1969	AAI05198	Human reproductive
8	1618.2	34.7	1969	ABL98083	Human testicular a

9	1092	23.4	1446	19	AAV59639	Human secreted pro
10	1092	23.4	1446	24	ABN73626	Human cDNA #1 for
11	1014.2	21.7	2865	24	ABO61047	3 isoform protein
12	1011.2	21.7	4933	21	AAZ45600	cDNA sequence of h
13	930.4	19.9	4975	23	AA574457	DNA encoding novel
14	924	19.8	924	21	AAZ74943	Human ORFX ORF498
15	912.2	19.5	3112	21	AAZ58592	Human PRO701 prote
16	912.2	19.5	3113	20	AAZ34209	Human PRO701 nucle
17	912.2	19.5	3113	21	AAZ78552	Human PRO701 (UNQ3
18	912.2	19.5	3113	25	ABX92581	cDNA encoding huma
19	886.2	19.0	5454	25	ABZ24056	CES2 related polyn
20	884.6	19.0	3751	25	ABZ24059	CES2 related polyn
21	871	18.7	4436	21	AAZ45601	cDNA sequence of h
22	870.2	18.6	3502	24	ABA97533	Human neuroilignin
23	751.8	16.1	4365	25	ABZ24057	CES2 related polyn
24	751.2	16.1	815	23	AAZ74453	DNA encoding novel
25	724.6	15.5	1764	21	AAZ45598	cDNA sequence of h
26	721.8	15.0	2183	23	AAZ74451	DNA encoding novel
27	700.4	15.0	2818	21	AAZ45599	cDNA sequence of h
28	697.4	14.9	2362	22	AAH15864	Human cDNA sequenc
29	697.4	14.9	2362	25	ABZ24058	CES2 related polyn
30	501.4	10.7	1189	23	ABX43603	DNA encoding novel
31	494.8	10.6	5454	21	AAZ45596	DNA sequence of th
32	486.8	10.4	856	22	AAH05453	Human cDNA clone (
33	484	10.4	496	23	AAZ74456	DNA encoding novel
34	455.8	9.8	1792	22	AAK94113	Human full-length
35	449	9.6	802	23	AAZ68309	DNA encoding novel
36	449	9.6	940	23	AAZ68306	DNA encoding novel
37	438	9.4	941	23	AAZ79638	DNA encoding novel
38	414.4	8.9	697	21	AAZ79890	Human secreted pro
39	384.4	8.2	17869	24	ABK39920	Human chemically p
40	384.4	8.2	17869	24	ABL32104	Human immune syste
41	365.6	7.8	2222	22	AAK94265	Human full-length
42	360.2	7.7	17869	24	ABK39921	Human chemically p
43	360.2	7.7	17869	24	ABL32105	Human immune syste
44	358.4	7.7	848	22	AAK91579	Human cDNA 5'-end
45	358.4	7.7	848	22	AAK93152	Human cDNA clone r

ALIGNMENTS

RESULT 1
ABA95199
ID ABA95199 standard; cDNA; 4667 BP.
XX ABA95199;
AC ABA95199;
XX
DT 10-JUN-2002 (first entry)
XX Human carboxylesterase family member, 33410 cDNA sequence.

XX Carboxylesterase; 33410; cytosolic; cardiac; dermatological; human;
KW antidiabetic; anirrhematic; antiarthritic; antiarrhythmic; vasotropic;
KW vulnerary; neuroprotective; antiinflammatory; antitumor; antischismic;
KW antiallergic; antiviral; hepatotropic; nephrotropic; anti-Hiv; gene;
KW antiparkinsonian; tuberculostatic; hypotensive; antiatherosclerotic;
KW neurotropic; antisense therapy; angiogenesis; gene therapy; ss.

OS Homo sapiens.

Key	Location/Qualifiers
5'UTR	1..419
FT	/*tag= a
FT	420..2927
CDS	/*tag= b
FT	/product= "33410 polypeptide"
FT	2928..4667
5'UTR	/*tag= c

WO200216616-A2.

28-FEB-2002.

1501 CCGATGACCTGAGATCCTCATGTCAGCAGGAGAAATTCCTCAACTAGCACATGCTCATCG 1560
1561 GCGTCAACACAGGAGAGGCGCTCAAGTTCTGTTGGAGACTCTGACAGAGCAGACCGGTG 1620
1561 GCGTCAACACAGGAGAGGCGCTCAAGTTCTGTTGGAGACTCTGACAGAGCAGACCGGTG 1620
1621 TGCTGCGAGGCGCTTTGACTCTGACTGCTCCAACTTTGTGGAACAACCTGATGCTTACC 1680
1621 TGCTGCGAGGCGCTTTGACTCTGACTGCTCCAACTTTGTGGAACAACCTGATGCTTACC 1680
1681 CGGAAGGCAAGATGCTCTCGGAGAGCAATCAAGTTTATATACACAGACTGCGGCGAAC 1740
1681 CGGAAGGCAAGATGCTCTCGGAGAGCAATCAAGTTTATATACACAGACTGCGGCGAAC 1740
1741 GGGACAATGGGAAATGGCGCGAAACCTGCTGGGCGCTCTTTACTGACCAATGGG 1800
1741 GGGACAATGGGAAATGGCGCGAAACCTGCTGGGCGCTCTTTACTGACCAATGGG 1800
1801 TGGCACAGCTGTGCGCACTGCGCAAGCTGACGCGGACTACAGTCTCCCGTCTACTTTT 1860
1801 TGGCACAGCTGTGCGCACTGCGCAAGCTGACGCGGACTACAGTCTCCCGTCTACTTTT 1860
1861 ACACCTTCTACCACTGCGCAGGCGGAGGCGCGGCTGAGTGGCGAGATGCGGCGCACG 1920
1861 ACACCTTCTACCACTGCGCAGGCGGAGGCGCGGCTGAGTGGCGAGATGCGGCGCACG 1920
1921 GGGATGAATGCTTCTGCGTGGCGCAAACTCTGCTGGCGCTCTTTACTGACCAAAATGGG 1980
1921 GGGATGAATGCTTCTGCGTGGCGCAAACTCTGCTGGCGCTCTTTACTGACCAAAATGGG 1980
1981 GTAACCTCTCAAGAAATGACGTCTGCTGAGTGGCGGCTGAGTGGCGAGATGCGGCGCACG 2040
1981 GTAACCTCTCAAGAAATGACGTCTGCTGAGTGGCGGCTGAGTGGCGAGATGCGGCGCACG 2040
2041 TCGCCAAAGACTGGGAGCCCCAACAGCGGCTGCGGAGGATACCAAGTTCAATCCACCA 2100
2041 TCGCCAAAGACTGGGAGCCCCAACAGCGGCTGCGGAGGATACCAAGTTCAATCCACCA 2100
2101 AGCCCAATCGCTTGAGAGAGTGGTGGAGCAAAATTCACAGCAAGGAGAGCAGTATC 2160
2101 AGCCCAATCGCTTGAGAGAGTGGTGGAGCAAAATTCACAGCAAGGAGAGCAGTATC 2160
2161 TGACATAGGCGCTGAAGCAGCGTGGCTGACAACTACCGCGCCAAAGAGTGGCGCTTCT 2220
2161 TGACATAGGCGCTGAAGCAGCGTGGCTGACAACTACCGCGCCAAAGAGTGGCGCTTCT 2220
2221 GGTGAGCTGCTGCGCCCACTGCAACCTGCGACAGGAGCTTTCACACACACACG 2280
2221 GGTGAGCTGCTGCGCCCACTGCAACCTGCGACAGGAGCTTTCACACACACACG 2280
2281 GCCTGCTTCCCTACGCCACGCGTGGCGGCTCTGTCGCCCGCGCTGGCGCCCGGCGAC 2340
2281 GCCTGCTTCCCTACGCCACGCGTGGCGGCTCTGTCGCCCGCGCTGGCGCCCGGCGAC 2340
2341 GCGGCGCCCGCGCTGCGCACTGCTCCGAGCGGAGCGGCGGCGGCGGCGGCGGCGG 2400
2341 GCGGCGCCCGCGCTGCGCACTGCTCCGAGCGGAGCGGCGGCGGCGGCGGCGGCGG 2400
2401 CCTATGACCGCTTCCCGGAGCTACAGGAGTACTCCACGAGCTGAGCTGACCGTGG 2460
2401 CCTATGACCGCTTCCCGGAGCTACAGGAGTACTCCACGAGCTGAGCTGACCGTGG 2460
2461 CCGTGGGTGCTTCCCTCTCTTCTCAACATCTGCGGCTTTGCTGCCCTCTACTTACAGC 2520
2461 CCGTGGGTGCTTCCCTCTCTTCTCAACATCTGCGGCTTTGCTGCCCTCTACTTACAGC 2520
2521 GGGACCGGCGGAGAGCTGCGGTGAGCGCGCTTAGCCACCTGCGGCGCTCAGGCTCTG 2580
2521 GGGACCGGCGGAGAGCTGCGGTGAGCGCGCTTAGCCACCTGCGGCGCTCAGGCTCTG 2580
2581 GCGTCCCTGCTGGGGCGGCTGCTCCCGCGCGGCGGCTGAGCTGCCACAGAGAGG 2640
2581 GCGTCCCTGCTGGGGCGGCTGCTCCCGCGCGGCGGCTGAGCTGCCACAGAGAGG 2640

2641 AGCTGTGTCACTGACGCTGAAGCGGGGTGGCGTTCGGGGCGGACCCCTGCGAGGCTC 2700
2641 AGCTGTGTCACTGACGCTGAAGCGGGGTGGCGTTCGGGGCGGACCCCTGCGAGGCTC 2700
2701 TCGCCCTGCTGCTGCGCGCGGACTACACCTGCGCCTGCGCGCGGACACCGAGTGTGC 2760
2701 TCGCCCTGCTGCTGCGCGCGGACTACACCTGCGCCTGCGCGCGGACACCGAGTGTGC 2760
2761 CTCTCTTGGCGCGCGGCGGCTGACCTGCTGCGCAGTGGCTGCGGCGGACACCGACCC 2820
2761 CTCTCTTGGCGCGCGGCGGCTGACCTGCTGCGCAGTGGCTGCGGCGGACACCGACCC 2820
2821 CACCGCGCGCGCTTCTGCGGCGGCTTCCCGCGCGGCTTCCCGCGCGGCTTCCCGCGG 2880
2821 CACCGCGCGCGCTTCTGCGGCGGCTTCCCGCGCGGCTTCCCGCGCGGCTTCCCGCGG 2880
2881 GCGACAACACAGCTTACCCGACCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 2940
2881 GCGACAACACAGCTTACCCGACCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 2940
2941 AGCCCTTCTGCGCGCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 3000
2941 AGCCCTTCTGCGCGCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 3000
3001 CAACTGGCTTCTGCTGAGTGTGTCTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCC 3060
3001 CAACTGGCTTCTGCTGAGTGTGTCTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCC 3060
3061 GATTCCTGCTGCGGCTTCTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 3120
3061 GATTCCTGCTGCGGCTTCTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 3120
3121 TCTGGGCTTCTGAAACAACTGGGCGGCTTCTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 3180
3121 TCTGGGCTTCTGAAACAACTGGGCGGCTTCTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 3180
3181 TGTGGAATGTTATTTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCC 3240
3181 TGTGGAATGTTATTTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCCCGCGGCTTCC 3240
3241 CCAATGTGAGGCTGAGGTTTTTTTGGCACCCCTGGGACACATGTTGGCGGCTTCCAAAGA 3300
3241 CCAATGTGAGGCTGAGGTTTTTTTGGCACCCCTGGGACACATGTTGGCGGCTTCCAAAGA 3300
3301 ATTTCTGCGGATTTGTACCCAGAACTCTGTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 3360
3301 ATTTCTGCGGATTTGTACCCAGAACTCTGTTCCCGCGGCTTCCCGCGGCTTCCCGCGG 3360
3361 CTTCTCCCTCCCGCTGGAGACCTGGAAGTGTGTTCACATACAGTACAGTACAGTACAG 3420
3361 CTTCTCCCTCCCGCTGGAGACCTGGAAGTGTGTTCACATACAGTACAGTACAGTACAG 3420
3421 CAGACCAACAGAGATGAGGCTTGGGAGAGCAGGAGGAAATCAGAGCGGCTTCCCGCGG 3480
3421 CAGACCAACAGAGATGAGGCTTGGGAGAGCAGGAGGAAATCAGAGCGGCTTCCCGCGG 3480
3481 CTTCCCTTCCCGCTACCCCGGAGAGTGTTCGCCCGGAGCGGCTTGGGACAGTGC 3540
3481 CTTCCCTTCCCGCTACCCCGGAGAGTGTTCGCCCGGAGCGGCTTGGGACAGTGC 3540
3541 AGATGAAGCACTTCTGCGGCGGAGGCTTCCCGCGGAGGCTTCCCGCGGAGGACAGATTC 3600
3541 AGATGAAGCACTTCTGCGGCGGAGGCTTCCCGCGGAGGCTTCCCGCGGAGGACAGATTC 3600
3601 CTGCTGGGAGGAGGAGTCCACGATCTCTGCTGCTGAGTGTATTTTCCCGG 3660
3601 CTGCTGGGAGGAGGAGTCCACGATCTCTGCTGCTGAGTGTATTTTCCCGG 3660
3661 GCGAGGACCACTTCTCTGAGTGGAAACAGGTTCTTGCATGTGGATGTGTTCGCCAG 3720
3661 GCGAGGACCACTTCTCTGAGTGGAAACAGGTTCTTGCATGTGGATGTGTTCGCCAG 3720

analyse the proteome of a tissue or cell type. The invention is useful for creating knock-in humanised animals or transgenic animals to model human disease, in somatic or germline gene targeting. It creates a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion etc. among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. The present sequence is human DME-5 cDNA.

Sequence 4763 BP; 871 A; 1601 C; 1364 G; 927 T; 0 other;

Query Match	92.8%; Score 4332.4; DB 24; Length 4763;
1st Local Similarity	99.2%; Pred. No. 0;
Matches 4396; Conservative 0; Mismatches 26; Indels 8; Gaps 4	
238	GAGAGGAACAGACCCCTCTCTGTGTCAGCTTAAACCCAGGTCCCTCCCAACACCCCTCCCTC 297
1	GAGAGAAATAGACTCTCTCTTCTGTCTCTTCTTAAACCCAGGTCCCTTACCGTACCCCTCTCTC 60
298	CTTCTCTTTCCCCCGCCCT 357
61	CTTCTCTTTCCCCCGC-CCT 119
358	CCCTTCT 417
120	CCCTTCT 174
418	GCATGTGGCT 477
175	GCATGTGGCT 234
478	GTCCCGCGCGCGCGCCCG 537
235	GTCCCG 294
538	GCTTTCOCGGTGTGTAAACAGCGCTTACGGCGCAGTGCAGCGGTGTGCAGCGCGAGCTCAACA 597
295	GCTTTCOCGGTGTGTAAACAGCGCTTACGGCGCAGTGTGCAGCGCGAGCTCAACA 354
598	ACGAGATCTCTGGGCCCGGCTGTGTGAGTCTTTTGGCGTGCCTTACGCCACGCCCGCCCTGG 657
355	ACGAGATCTCTGGGCCCGGCTGTGTGAGTCTTTTGGCGTGCCTTACGCCACGCCCGCCCTGG 414
658	GCAGCGCGCGCTTTCAGCGCGCTGTAGGCGCGCGCGCTGTGTGCGCGCGCGCTGTGTGCGCG 717
415	GCAGCGCGCGCTTTCAGCGCGCTGTAGGCGCGCGCGCTGTGTGCGCGCGCGCTGTGTGCGCG 474
718	CCACCTTGCAGCGCGCGCTTGCAGCGAGACCTGTACAGCGCGCGCTGTGTGCGCGCTGTGTGCG 777
475	CCACCTTGCAGCGCGCGCTTGCAGCGAGACCTGTACAGCGCGCGCTGTGTGCGCGCTGTGTGCG 534
778	CTGTGTGGTTCACCGACAACTTTGAGGCGCGCGCGCACTTACGTGTGAGAACCGAGACGAGG 837
535	CTGTGTGGTTCACCGACAACTTTGAGGCGCGCGCGCACTTACGTGTGAGAACCGAGACGAGG 594
838	ACTGCGCTGTACTTCAACCTTACGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 897
595	ACTGCGCTGTACTTCAACCTTACGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 654
898	ACGAGCGCAGCGTCAATCCGCGCAGACACAGATATCCGTGACCCCTGGGAGAGAGCGCTGTGA 957
655	ACGAGCGCAGCGTCAATCCGCGCAGACACAGATATCCGTGACCCCTGGGAGAGAGCGCTGTGA 714
958	TGCTGTCTTCTCATGGCGGCTCTTACATGAGGAGGACCGGAAACATGTTCGATGTGCTCAG 1017
715	TGCTGTCTTCTCATGGCGGCTCTTACATGAGGAGGAGCGGAAACATGTTCGATGTGCTCAG 774
1018	TCTGTGCTGCCCTATGGCAAGTCAATTGTAGCCAGCTTCAACTACCGCTTTGGGGGTGCTCG 1077
775	TCTGTGCTGCCCTATGGCAAGTCAATTGTAGCCAGCTTCAACTACCGCTTTGGGGGTGCTCG 834
1078	GTCTTCTCAGCACCGCGGACCGAGGCTGCAAAAGCAACTATGTGGGCTCTGTGACCAAGATCC 1137

Db 4134 GAACAGATGGAGGGGAGTGGGACAGGGCTTGGGCAGACACAGCAGGAGTAATTTGA 4193
 QY 4438 AATGTGTAGTGACTCCCGAGGGCTTGGGCTTGGGCAATTTGGGAAAGATGATGT 4497
 Db 4194 AATGTGTAGTGACTCCCGAGGGCTTGGGCTTGGGCAATTTGGGAAAGATGATGT 4253
 QY 4498 CTGGAAGGGCTTAAGGGACACAGTGGACAGGGGAGAGTCCCTCATCTGTGGCAATTTGT 4557
 Db 4254 CTGGAAGGGCTTAAGGGACACAGTGGACAGGGGAGAGTCCCTCATCTGTGGCAATTTGT 4313
 QY 4558 GGGGTGTAGTGCCAACTTGAATAGGGCTTGGGCTTGGGCTTGGGCAATTTGGGAAAGATGATGT 4617
 Db 4314 GGGGTGTAGTGCCAACTTGAATAGGGCTTGGGCTTGGGCTTGGGCAATTTGGGAAAGATGATGT 4373
 QY 4618 CCAGAATCCCTGGTCTTGAAT-CCAGAACTTTGGCTTCTTGACTGTCCCT 4666
 Db 4374 CCAGAATCCCTGGTCTTGAAT-CCAGAACTTTGGCTTCTTGACTGTCCCT 4423

RESULT 3
 AEN59628
 ID AEN59628 standard; cDNA; 4622 BP.
 AC AEN59628;
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Novel human coding sequence SEQ ID NO: 39.
 XX
 KW Human; antianaemic; vulinary; antiinflammatory; immunomodulator;
 KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
 KW neuroprotective; antiparkinsonian; protein therapy; EST;
 KW expressed sequence tag; gene; ss.
 XX

OS Homo sapiens.
 XX
 PN WO200222660-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US26015.
 XX
 PR 11-SEP-2000; 2000US-0659671.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX
 DR WPI; 2002-292408/33.
 DR P-PSDB; ABB97215.
 XX

PT An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis -
 XX
 PS Claim 1; SEQ ID NO 39; 509pp; English.
 XX
 CC The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
 CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
 CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a coding sequence of the
 CC invention.

SQ Sequence 4622 BP; 850 A; 1540 C; 1344 G; 888 T; 0 other;
 Query Match 91.0%; Score 4246.6; DB 24; Length 4622;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4282; Conservative 0; Mismatches 4; Indels 3; Gaps 3;
 QY 380 GGGGGGGTCCCAAGGAGGAGGGGGGTCCCGCATGACATGTGCTCTCGGCGCTGTG 439
 Db 1 GGGGGGGTCCCAAGGAGGAGGGGGGTCCCGCATGACATGTGCTCTCGGCGCTGTG 60
 QY 440 TCTGGTGGGGCTGGGGGGGTCTCAACGGGGGGTCCCGGGTCCCGGGCGGCCCGGG 499
 Db 61 TCTGGTGGGGCTGGGGGGGTCTCAACGGGGGGTCCCGGGCGGCCCGGGCGGCC 120
 QY 500 CGGCCCCGGCTGGGGCTGGGCGAGCTCGGCGAGAGCGCTTCCCGGTGGTGAACACGGC 559
 Db 121 CGGCCCCGGCTGGGGCTCGGAGCTCGGCGAGAGCGCTTCCCGGTGGTGAACACGGC 180
 QY 560 CTACGGGGGAGTGGCGGTGGCGGGGAGTCAACACGAGATCCTTGGGCGGCCGTGT 619
 Db 181 CTACGGGGGAGTGGCGGTGGCGGGGAGTCAACACGAGATCCTTGGGCGGCCGTGT 240
 QY 620 GCAGTTCTTGGGGTGGCTTACGCCACCGCCCTTGGGGCGGCCCGCTTCCAGCCGCC 679
 Db 241 GCAGTTCTTGGGGTGGCTTACGCCACCGCCCTTGGGGCGGCCCGCTTCCAGCCGCC 300
 QY 680 TGAGGGGGCGGCTCGTGGCGGGGTGGGCGAAGCGCACACCTTGGCGGGCGGCCGCC 739
 Db 301 TGAGGGGGCGGCTCGTGGCGGGGTGGGCGAAGCGCACACCTTGGCGGGCGGCCGCC 360
 QY 740 GCAGAACTTGCACGGGGGTGGCGGCATATGCTGTGTGTGTGTGTGTGTGTGTGTGT 799
 Db 361 GCAGAACTTGCACGGGGGTGGCGGCATATGCTGTGTGTGTGTGTGTGTGTGTGTGT 420
 QY 800 GGAGGGGGCGGCACTTACGTGAGAACAGAGCGAGTGTGCTGTGTGTGTGTGTGTGTGT 859
 Db 421 GGAGGGGGCGGCACTTACGTGAGAACAGAGCGAGTGTGCTGTGTGTGTGTGTGTGTGT 480
 QY 860 CGTGGCCACCGAGGAGTGGCTTCAAAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 919
 Db 481 CGTGGCCACCGAGGAGTGGCTTCAAAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
 QY 920 AGACACAGATATCCGTGACCTTGGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 979
 Db 541 AGACACAGATATCCGTGACCTTGGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 QY 980 CTACATGGAGGGGACCGGAAACATGTTGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1039
 Db 601 CTACATGGAGGGGACCGGAAACATGTTGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 QY 1040 CATTTAGCCAGCTCAACTACCGTCTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1099
 Db 661 CATTTAGCCAGCTCAACTACCGTCTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
 QY 1100 GGCTGCAAAAGCACTATGGGCTCTGGACAGATCCAGGCCCTTGGCTGGCTCAGTGA 1159
 Db 721 GGCTGCAAAAGCACTATGGGCTCTGGACAGATCCAGGCCCTTGGCTGGCTCAGTGA 780
 QY 1160 AAACATCGCCCACTTTGGGGGCGACCCGAGCTATCACCATCTTGGTTCGGGGGAGG 1219
 Db 781 AAACATCGCCCACTTTGGGGGCGACCCGAGCTATCACCATCTTGGTTCGGGGGAGG 840
 QY 1220 GGCTTCTCGGTCAACTTGTGATCTCTCCCACTTCAAGAGGGCTGTTCAGAAAGC 1279
 Db 841 GGCTTCTCGGTCAACTTGTGATCTCTCCCACTTCAAGAGGGCTGTTCAGAAAGC 900
 QY 1280 CATCCGCCAGAGTGGCACCGGCATTTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1339
 Db 901 CATCCGCCAGAGTGGCACCGGCATTTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
 QY 1340 CACGGGGTGTGGCAGCAAGGTGGGCTGTGACCGAGAGGACAGTGTGTGAAGCTGTGGA 1399
 Db 961 CACGGGGTGTGGCAGCAAGGTGGGCTGTGACCGAGAGGACAGTGTGTGAAGCTGTGGA 1020
 QY 1400 GTGTCTGGCGGGAAGCCCTCCCGGAGCTGGTGGACCGAGACCTGTGAGCTGCCCGCTA 1459

Db 1021 GTGCTGGCCCGAAGCCCTCCCGGAGCTGGTGGACAGGACGTGAGCCTGCGCGCTA 1080
Qy 1460 CCATACGCTTTGGGCGCGTGGTGGATGGCGAGTGGTCCCGGATGACCCCTGAGATCCT 1519
Db 1081 CCATACGCTTTGGGCGCGTGGTGGATGGCGAGTGGTCCCGGATGACCCCTGAGATCCT 1140
Qy 1520 CATGACGAGGAGAAATTCCTCACTAGGACATGCTCATGGCGTCAACAGGAGAGGG 1579
Db 1141 CATGACGAGGAGAAATTCCTCACTAGGACATGCTCATGGCGTCAACAGGAGAGGG 1200
Qy 1580 CCTCAAGTTCGTGAGGACTCTGACAGAGAGGAGAGCGGTGTGCTGCCAGCGCTTTGA 1639
Db 1201 CCTCAAGTTCGTGAGGACTCTGACAGAGAGGAGAGCGGTGTGCTGCCAGCGCTTTGA 1260
Qy 1640 CTTACATGCTCTCAACTTTGTGGACAACTGTATGGCTAACCGGAGGCAAGATGTCT 1699
Db 1261 CTTACATGCTCTCAACTTTGTGGACAACTGTATGGCTAACCGGAGGCAAGATGTCT 1320
Qy 1700 TCGGAGAGCACTCAAGTTTATGATACAGACTGGGCGGACCGGAGCAATGGCGAATGCG 1759
Db 1321 TCGGAGAGCACTCAAGTTTATGATACAGACTGGGCGGACCGGAGCAATGGCGAATGCG 1380
Qy 1760 CCGCAAAACCCCTGTGGCGCTCTTTACTGACCAACCAATGGGTGGCAACAGCTGTGCCAC 1819
Db 1381 CCGCAAAACCCCTGTGGCGCTCTTTACTGACCAACCAATGGGTGGCAACAGCTGTGCCAC 1440
Qy 1820 TGCCAAAGTGCACCGGACTACAGTCTCCGCTCTACTTTTACCTTTACCAACACTG 1879
Db 1441 TGCCAAAGTGCACCGGACTACAGTCTCCGCTCTACTTTTACCACTTTACCAACACTG 1500
Qy 1880 CCAGCGAGGCGCGGCTGAGTGGGAGATGCGGCGCACGGGATGAATGCGCCCTATGT 1939
Db 1501 CCAGCGAGGCGCGGCTGAGTGGGAGATGCGGCGCACGGGATGAATGCGCCCTATGT 1560
Qy 1940 CTTTGGGCTGCCATGTGGTGCCACCGGACTCTTCCCTGTAACTTCTCAGAAATGA 1999
Db 1561 CTTTGGGCTGCCATGTGGTGCCACCGGACTCTTCCCTGTAACTTCTCAGAAATGA 1620
Qy 2000 CGTCATGCTCAGTCCGCTGGTCACTAGCTACTGAGCAACTTCGCCAAGACTGGGACCC 2059
Db 1621 CGTCATGCTCAGTCCGCTGGTCACTAGCTACTGAGCAACTTCGCCAAGACTGGGACCC 1680
Qy 2060 CAACAGCGGTGCGGAGGATCAAGTTCACTCACCACCAAGCCCAATCGCTTCGAGGA 2119
Db 1681 CAACAGCGGTGCGGAGGATCAAGTTCACTCACCACCAAGCCCAATCGCTTCGAGGA 1740
Qy 2120 GETGCTGGAGCAATTCACAGCAAGGAGAGCAGTATCTGCATAGGCTGGAGCC 2179
Db 1741 GGTGGTGGAGCAATTCACAGCAAGGAGAGCAGTATCTGCATAGGCTGGAGCC 1800
Qy 2180 ACGGCTGCTGACAACTACCGCGCCAAACAAGGTGGCCTTCTGGCTGGAGCTCGTGCCCA 2239
Db 1801 ACGGCTGCTGACAACTACCGCGCCAAACAAGGTGGCCTTCTGGCTGGAGCTCGTGCCCA 1860
Qy 2240 CTTGCAAACTGACAGGAGCTTTCACGACCAACGCGGCTGCTCCCTACGCGCAC 2299
Db 1861 CTTGCAAACTGACAGGAGCTTTCACGACCAACGCGGCTGCTCCCTACGCGCAC 1920
Qy 2300 GCGCTGGCGGCTGCTCCCGCGCTGGCGCCCGGGCACAGCGGCGCCCGCGCGCTGC 2359
Db 1921 GCGCTGGCGGCTGCTCCCGCGCTGGCGCCCGGGCACAGCGGCGCCCGCGCGCTGC 1980
Qy 2360 CACCTGCTCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGGCTATGAACGCTTCCCGG 2419
Db 1981 CACCTGCTCCGAGCCGAGCCGAGCCGAGCCGAGGCTATGAACGCTTCCCGG 2040
Qy 2420 GGACTCAGGAGCTACTCAGAGGCTGAGCTACCGTGCGGCTGGGTGCTCCCTCT 2479
Db 2041 GGACTCAGGAGCTACTCAGAGGCTGAGCTACCGTGCGGCTGGGTGCTCCCTCT 2100
Qy 2480 CTTCTCAACATCTGCGCTTTGTGCTCTACTACAGCGGAGCGGCGGAGGAGCT 2539
Db 2101 CTTCTCAACATCTGCGCTTTGTGCTCTACTACAGCGGAGCGGCGGAGGAGCT 2160

Qy 2540 GCGGTGCAGGCGGCTTAGCCACCTGGCGGCTCAGGCTCTGCGTGTGCTGGGCGCC 2599
Db 2161 GCGGTGCAGGCGGCTTAGCCACCTGGCGGCTCAGGCTCTGCGTGTGCTGGGCGCC 2220
Qy 2600 CTTGCTCCCGCGCGGCGGCTGAGCTGCACACAGAGAGAGCTGGTGTCACTGCAGCT 2659
Db 2221 CTTGCTCCCGCGCGGCGGCTGAGCTGCACACAGAGAGAGCTGGTGTCACTGCAGCT 2280
Qy 2660 GAAAGCGGCTGTGCTGCGGCGGAGACCTTGCAGGCTCTGCGCCCTGCTGCGCCG 2719
Db 2281 GAAAGCGGCTGTGCTGCGGCGGAGACCTTGCAGGCTCTGCGCCCTGCTGCGCCG 2340
Qy 2720 CGACTACACCTTGGCCCTTGGCGCGGCGACCGAGACGATGTGCTCTTGTGGCCCCCGGG 2779
Db 2341 CGACTACACCTTGGCCCTTGGCGCGGCGACCGAGACGATGTGCTCTTGTGGCCCCCGGG 2400
Qy 2780 CTTGACCTGTGCTGCGGCTGGGCGGACCGGCGGCTGGGCGGCTGGGCGGCTGGGCGG 2839
Db 2401 CTTGACCTGTGCTGCGGCTGGGCGGACCGGCGGCTGGGCGGCTGGGCGGCTGGGCGG 2460
Qy 2840 TCCCTTGGGCGGCTTTCGCCCGGCGGCTTCCACCGGCGGCGGCGGCGGCGGCGGCGG 2899
Db 2461 TCCCTTGGGCGGCTTTCGCCCGGCGGCTTCCACCGGCGGCGGCGGCGGCGGCGGCGG 2520
Qy 2900 CCACCGGCGGCTTTCGCCCGGCGGCTTTCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 2959
Db 2521 CCACCGGCGGCTTTCGCCCGGCGGCTTTCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 2580
Qy 2960 TCCCTTGGGCGGCTTTCGCCCGGCGGCTTTCGCCCGGCGGCGGCGGCGGCGGCGGCGG 3019
Db 2581 TCCCTTGGGCGGCTTTCGCCCGGCGGCTTTCGCCCGGCGGCGGCGGCGGCGGCGGCGG 2640
Qy 3020 GGAGTGTGTACACGCGCATCAGAGCGCTAAGGTGGACATGGGATTCCTCCCTGGGATGC 3079
Db 2641 GGAGTGTGTACACGCGCATCAGAGCGCTAAGGTGGACATGGGATTCCTCCCTGGGATGC 2700
Qy 3080 GTGCTTTTCCACGCGAGAGAGCGGCTTTCCTTCTTGGGCTTGGGCGGCTTGGGCGGCT 3139
Db 2701 GTGCTTTTCCACGCGAGAGAG - CCGAGTCTTCTTCTGATCTGGGCTTGGGCGGCTTGGGCGGCT 2759
Qy 3140 GGGGCGGCTTTTCTCCCGGCGGCTTTCGCCCGGCGGCTTTCGCCCGGCGGCTTTCGCCCGGCT 3199
Db 2760 GGGGCGGCTTTTCTCCCGGCGGCTTTCGCCCGGCGGCTTTCGCCCGGCGGCTTTCGCCCGGCT 2819
Qy 3200 TCCCGGCTGGAGGTGTGCTTTCACACGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3259
Db 2820 TCCCGGCTGGAGGTGTGCTTTCACACGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 2879
Qy 3260 TTTTCTTTCGCCCGGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3319
Db 2880 TTTTCTTTCGCCCGGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 2939
Qy 3320 CCGGAGATCTGTTTCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3379
Db 2940 CCGGAGATCTGTTTCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 2999
Qy 3380 ACCCTGGAAGTGTGTTTTCACATACAGTACCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3438
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Qy 3439 AGCTTGGAGAGGAGGAGAAATCAGAGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3498
Db 3060 AGCTTGGAGAGGAGGAGAAATCAGAGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3119
Qy 3499 CGGCGAGGAGTGTTCGCCCGGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3558
Db 3120 CGGCGAGGAGTGTTCGCCCGGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3179
Qy 3559 CGGCGAGGAGTGTTCGCCCGGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3618
Db 3180 CGGCGAGGAGTGTTCGCCCGGCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCTTTCGCCCGGCT 3239

Qy	2640	GAGCTGGTGTCACTGCAAGCTGAACGCGGGGTGGCTCGGGCGGACCTTCGCGAGGCT	2699
Db	2221	GAGCTGGTGTCACTGCAAGCTGAACGCGGGGTGGCTCGGGCGGACCTTCGCGAGGCT	2280
Qy	2700	CTGGGCCCTGCTGCGCCGCGCGACTACACCTGGCCCTGCGCGGGACCGGACAGATGTG	2759
Db	2281	CTGGGCCCTGCTGCGCCGCGCGACTACACCTGGCCCTGCGCGGGACCGGACAGATGTG	2340
Qy	2760	CCTCTCTTGGCCCCCGGGGCGCTGAACCTGCTGCCAGTGGCTTGGGGCCACCGCACCC	2819
Db	2341	CCTCTCTTGGCCCCCGGGGCGCTGACCTCTGCTGCCAGTGGCTTGGGGCCACCGCACCC	2400
Qy	2820	CCACCGGCCCTCCCTTCATCCCTTCGGGACCTTCGCCCGGCCCTCCACCGGCACC	2879
Db	2401	CCACCGGCCCTCCCTTCATCCCTTCGGGACCTTCGCCCGGCCCTCCACCGGCACC	2460
Qy	2880	AGCCACAACACGCTACCCCAACCCCACTCCACCACTCGGTATAG	2927
Db	2461	AGCCACAACACGCTACCCCAACCCCACTCCACCACTCGGTATAG	2508

RESULT 5
AAF82996
ID AAF82996 standard; cDNA; 2523 BP.
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XX AAF82996;
XX
XX 29-JUN-2001 (first entry)
DT

DE Human MBSP4 polypeptide encoding cDNA (clone 21417374.0.9).

MBSPX; cancer; preclampsia; immune system; neurological; cytostatic; gynecological; antiinflammatory; neuroprotective; inotropic; relaxant; cardiant; dermatological; gene therapy; human; MBSP4; ss

OS Homo sapiens.

	Key	Location/Qualifiers
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PN WO200127277-A2.

19-APR-2001.

XX
PF 13-OCT-2000: 2000WO-US28480.

13-OCT-1999: 99MS-0159231

PR 13-OCT-1999; 99US-0159231.
PR 12-JAN-2000; 2000US-0175670

PR 12-JAN-2000; 2000US-0175670.
PR 12-OCT-2000; 2000US-0159231.

PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Lichenstein H. Boldog ET.

XX
DR WPI: 2001-282030/29.

DR WPI; 2001-282030/29.
DR P-PSDB; AAB62400.

xx Novel human polynucleotide sequences and the membrane bound or secreted
PT polypeptides encoded by these sequences, designated MBSPX -
PT

PS Claim 9; Page 26-29; 157pp; English.

The invention relates to novel polypeptides, termed MBSPX and polynucleotides encoding the MBSPX polypeptides. The MBSPX polypeptide, nucleic acid and an MBSPX antibody are useful for treating or preventing a pathology associated with the protein especially in humans. The MBSPX nucleic acid can be used to express MBSPX protein (e.g. via a recombinant expression vector in a host cell in gene therapy applications), an to detect MBSPX mRNA in a biological sample or a genetic lesion in a MBSPX gene. Disorders associated with insufficient or excessive production of MBSPX protein include cancer, preclampsia, immune system disorders and

Db 901 AACTACAGCGCTCAAGTACACGCGCTGTGGAGCAAGGTGGGCTGTGACCGAGAG 960
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 Db 1321 CGGACATGCGGAATGCGCGGCAAAACCTGTGGGCTCTTTACTGACCAACCAATGG 1380
 QY 1800 GTGCAACAGCTGTGGGCACTGCAAGCTGCAAGCGGCACTACCAAGTCTCCCGCTCTACTTT 1859
 Db 1381 GTGCAACAGCTGTGGGCACTGCAAGCTGCAAGCGGCACTACCAAGTCTCCCGCTCTACTTT 1440
 QY 1860 TACACCTTTACACCACTGCGAGCGAGGCGCGGCTGAGTGGGAGATGGCGGCGAC 1919
 Db 1441 TACACCTTTACACCACTGCGAGCGAGGCGCGGCTGAGTGGGAGATGGCGGCGAC 1500
 QY 1920 GGGATGAACCTGCCCTATGCTTTGGGCTGCGCATGGTGGTGCCACCGACCTCTTCCCC 1979
 Db 1501 GGGATGAACCTGCCCTATGCTTTGGGCTGCGCATGGTGGTGCCACCGACCTCTTCCCC 1560
 QY 1980 TGTAACTTCTCAAGATGACGTATGCTCATGTCGCTGTGATGACCTACTGGACCAAC 2039
 Db 1561 TGTAACTTCTCAAGATGACGTATGCTCATGTCGCTGTGATGACCTACTGGACCAAC 1620
 QY 2040 TTCGCCAGCTGGGACCCCAACAGCGGTGCGGAGATACCAAGTTCATCCACAC 2099
 Db 1621 TTCGCCAGCTGGGACCCCAACAGCGGTGCGGAGATACCAAGTTCATCCACAC 1680
 QY 2100 AAGCCCAATCGCTTCGAGGAGTGTGTGGAGCAAAATCAACAGCAAGGAGAGAGTAT 2159
 Db 1681 AAGCCCAATCGCTTCGAGGAGTGTGTGGAGCAAAATCAACAGCAAGGAGAGAGTAT 1740
 QY 2160 CTGACATAGCTGAGAGCAAGCTGCTGAGCAACTACCGGCAACAAAGTGTGGCTTC 2219
 Db 1741 CTGACATAGCTGAGAGCAAGCTGCTGAGCAACTACCGGCAACAAAGTGTGGCTTC 1800
 QY 2220 TGGCTGGAGCTGCTGCCCCCACTGCACAACTGACACAGGAGTCTTTCACCAACCAACG 2279
 Db 1801 TGGCTGGAGCTGCTGCCCCCACTGCACAACTGACACAGGAGTCTTTCACCAACCAACG 1860
 QY 2280 CGCTGCTGCTTACGCAAGCTGCTGCGGCTGTGCTCCCC--CGCTGCGCGCCCGGGC 2336
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 Db 1921 ACAGCGGCGCCCGCGCTGCGCACTGCTCCCGAGCCCGAGCCCGAGCCCGGCCA 1980
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 QY 2517 AAGCGGACCGCGGAGAGCTGGGTGAGGCGGCTTAGCCCACTTGGCGGCTCAGGC 2576
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 QY 2577 TCTGGGCTGCTGGTGGGCGCCCTGCTCCCGCGCGGCGCTGAGTGCACACAGAG 2636
 Db 2161 TCTGGGCTGCTGGTGGGCGCCCTGCTCCCGCGCGGCGCTGAGTGCACACAGAG 2220
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 Db 2221 GAGGAGCTGGTGTCTACTGAGCTGAAGCGGCTGTGGGTGCGGCGGAGACCTTCCCGAG 2280
 QY 2697 GCTCTGGGCGCTGCTGCGCGGCGGCTGAGTGCACACAGCTGAGTGCACACAGAG 2756
 Db 2281 GCTCTGGGCGCTGCTGCGCGGCGGCTGAGTGCACACAGCTGAGTGCACACAGAG 2340
 QY 2757 GTGCTCTTGTGGCGCCCTGCGCGGCGGCTGAGTGCACACAGCTGAGTGCACACAGAG 2816
 Db 2341 GTGCTCTTGTGGCGCCCTGCGCGGCGGCTGAGTGCACACAGCTGAGTGCACACAGAG 2400
 QY 2817 CCGGCAACCGCGCGGCTGCGCGGCGGCTGAGTGCACACAGCTGAGTGCACACAGAG 2873
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 QY 2874 GCGACAGCCCAACAAACAGCTACCCCGGCGGCTGAGTGCACACAGCTGAGTGCACAG 2933
 Db 2461 GCGACAGCCCAACAAACAGCTACCCCGGCGGCTGAGTGCACACAGCTGAGTGCACAG 2520
 QY 2934 GGT 2936
 Db 2521 GGT 2523

RESULT 6
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 ID ABA94727 standard; cDNA; 2663 BP.
 XX ABA94727;
 AC AC
 XX AC
 DT 23-APR-2002 (first entry)
 XX
 DE Human drug metabolizing enzyme (DME) cDNA (ID: 7473875CBI).
 XX
 KW Drug metabolizing enzyme; DME; antiallergic; antianemic; antiaesthetic;
 KW osteopathic; antirheumatic; antiarthritic; dermatological; nephrotropic;
 KW antineoplastic; antitumor; antiparasitic; antiparasitic;
 KW protozoacide; fungicide; antihelminthic; cytostatic; ophthalmological;
 KW antiarteriosclerotic; hepatotropic; antidiabetic; anorectic; human;
 KW thrombolytic; metabolic; anticoagulant; antithyroid; gynecological;
 KW antianginal; antiulcer; antidiarrhoeic; laxative; enzyme; ss.
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 OS Homo sapiens.
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 FH Key
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 FT 177..2582
 FT /tsa= a
 FT /product= "DME"
 FT /transl_except= "(pos: 475..477, aa: Xaa)"
 FT /note= "Xaa = unknown"
 XX
 PN WO200204612-A2.
 PD 17-JAN-2002.
 XX
 PF 05-JUL-2001; 2001WO-US21324.
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 PR 07-JUL-2000; 2000US-216804P.

Db 1435 ACCCGAAGGCAAGATGTGCTTCGGGAGACATCAAGTTTATGTACAGACTGGGCGG 1494
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Db 1615 TTATACCTTTACACCACTGCCAGGCGGAGGCGGCGCTGAGTGGGCGAGATCGGCGC 1674
QY 1918 ACGGGGATGAATGCGCTATGCTTTGGCGTGCCCATGGTGGGTGGCCACCGACCTCTTC 1977
Db 1675 ACGGGGATGAATGCGCTATGCTTTGGCGTGCCCATGGTGGGTGGCCACCGACCTCTTC 1734
QY 1978 CCGTAACTTCTCCAAAGATGACGTGCTGCTGAGTGGCGGTGCTGATGACCTTACTGGACCA 2037
Db 1735 CCGTAACTTCTCCAAAGATGACGTGCTGCTGAGTGGCGGTGCTGATGACCTTACTGGACCA 1794
QY 2038 ACTTGCCAAAGCTGGGACCCCAACAGCGGTGCGCAGATACCAAGTTTATCCACA 2097
Db 1795 ACTTGCCAAAGCTGGGACCCCAACAGCGGTGCGCAGATACCAAGTTTATCCACA 1854
QY 2098 CCAAGCCCAATCGCTTCGAGAGGTGTGTGAGCAATTCACAGCAAGGAGAGCAGT 2157
Db 1855 CCAAGCCCAATCGCTTCGAGAGGTGTGTGAGCAATTCACAGCAAGGAGAGCAGT 1914
QY 2158 ATGTGCAATAGGCTGAAGCCAGCGGTGCTGAGCAACTACCGGCGCAACAAAGTGGCGCT 2217
Db 1915 ATGTGCAATAGGCTGAAGCCAGCGGTGCTGAGCAACTACCGGCGCAACAAAGTGGCGCT 1974
QY 2218 TCTGGCTGAGCTGTGCGCCACCTGACACCTGACACAGGAGCTTTTACACCAACCA 2277
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RESULT 7

AA05198

ID AA05198 standard; DNA; 1969 BP.

XX

AC AA05198;

XX

DT 21-NOV-2001 (first entry)
XX Human reproductive system related antigen DNA SEQ ID NO: 7886.
XX Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
XX Homo sapiens.
XX WO200155320-A2.
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
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 PR 21-SEP-2000; 2000US-0234223.
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 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.

PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254037.
 PR 03-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-465570/50.
 DR Isolated nucleic acid molecule encoding a reproductive system antigen
 XX is used in preventing, treating or ameliorating a medical condition -
 PT Disclosure; SEQ ID NO 7886; 1297bp + Sequence Listing; English.
 XX
 PS The present invention provides the protein and coding sequences of a
 XX number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
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 SQ Sequence 1969 BP; 396 A; 594 C; 537 G; 442 T; 0 other;
 Query Match 34.7%; Score 1618.2; DB 22; Length 1969;
 Best Local Similarity 99.7%; Pred. No. 7.4e-278;
 Matches 1642; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
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 DB 1 GAGTCGTACACGCGCATCCAGCAGCGCTAAGTGTGACATGGGATTCCTCCCTGGCATGG 60
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 DB 61 TGTCTTTCCACGACGAGAG-CCGAGTCTTCTCTGTAICTGGGCTTTGAAACAATG 119
 YQ 3141 GGGGGCGTTTCTCCGCCCATTTGGGACACCATCTTGGTGTGTGGATGGTATTTT 3200
 DB 120 GGGGGCGTTTCTCCGCCCATTTGGGACACCATCTTGGTGTGTGGATGGTATTTT 179
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 YQ 3321 CCAGAACTCTTCTCCCGCATCCCTTCTCCACCTCTCCCTCCCTCCCTCCCTCCCTCC 3380
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 DB 360 CCCTGGAAGTGTGTGTTCACATACAGTGACCTTGGCCACAGACACAGAGGATGAG 419
 YQ 3441 CCTGGGAAGCAGGAGGAATCAAGCCCTCGCCCTCGCCCTCGCCCTCGCCCTACCCCG 3500
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 DB 480 GCGAAGCATGTTCCCGCGAGCGCCCTTGGCAAGTCAAGTGAAGCAGGCTTCTGCGG 539
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PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 12-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251858.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483232/52.
XX
XX Nucleic acids encoding 973 human testicular antigen polypeptides,
PT useful for preventing, diagnosing and/or treating testicular cancer
PT
XX
PS Disclosure; SEQ ID NO 2735; 765pp; English.
XX
XX The present invention provides the protein and coding sequences of 973
CC human testicular antigens, and fragments of their genomic sequences. The
CC sequences can be used in the treatment of cardiovascular, urinary system,
CC reproductive system, immune, respiratory, neurological and
CC gastrointestinal disorders, infections, and particularly cancer,
CC especially testicular cancers. The present sequence is a DNA encoding a
CC protein fragment of the invention.
XX
SQ Sequence 1969 BP; 396 A; 594 C; 537 G; 442 T; 0 other;

Query Match 34.7%; Score 1618.2; DB 23; Length 1969;
Best Local Similarity 99.7%; Pred. No. 7.4e-278; Indels 2; Gaps 2;
Matches 1642; Conservative 0; Mismatches 3;

QY 3021 GAGTCGTACACGCCATCCAGCAGCGCTAAGGTGACATGGGATTCCTCCCTGCGATGCG 3080
DB 1 GAGTCGTACACGCCATCCAGCAGCGCTAAGGTGACATGGGATTCCTCCCTGCGATGCG 60
QY 3081 TGTCTTTCCACGACGAGAGCCAGTCTCTCTCTGATCTGGGCTTGGCAACTG 3140
DB 61 TGTCTTTCCACGACGAGAG-CCAGTCTCTCTCTGATCTGGGCTTGGCAACTG 119
QY 3141 GGGGGGTTTTCTCCGCCCATTTGGACACCACTCTTGGTGTGGATGGTATTTT 3200
DB 120 GGGGGGTTTTCTCCGCCCATTTGGACACCACTCTTGGTGTGGATGGTATTTT 179
QY 3201 CCCGGTGGAGGTGTCTTTCTCAACGCGGTGTGTTCCTCCATGTGAGGTGAGTT 3260
DB 180 CCCGGTGGAGGTGTCTTTCTCAACGCGGTGTGTTCCTCCATGTGAGGTGAGTT 239
QY 3261 TTTTGTGCGCCCTGGACACATGTTGGCCCTCAAGAATTTCTGTGGGATTTGTAC 3320
DB 240 TTTTGTGCGCCCTGGACACATGTTGGCCCTCAAGAATTTCTGTGGGATTTGTAC 299
QY 3321 CCAGAAATCTGTTCCTCCATCCCTTCTCCACCTCTCCCTCTCCCTCCCTCCCTGAGA 3380
DB 300 CCAGAAATCTGTTCCTCCATCCCTTCTCCACCTCTCCCTCTCCCTCCCTGAGA 359
QY 3381 CCTGGAAGTGTGTGTTTCAATACATGACGACCTTGGCCACCAAGAGGATGGAG 3440
DB 360 CCTGGAAGTGTGTGTTTCAATACATGACGACCTTGGCCACCAAGAGGATGGAG 419
QY 3441 CCTGGAAGCAGCAGGAAATCAGAGCCCTCTGCGCCCTCTCCCTCTCCCTACCCCG 3500
DB 420 CCTGGAAGCAGCAGGAAATCAGAGCCCTCTGCGCCCTCTCCCTCTCCCTACCCCG 479
QY 3501 GCGAAGCATGTTCCCTCCGACGCCCTCTGCGCAAGTCAATGAGCACTTCTGCGG 3560
DB 480 GCGAAGCATGTTCCCTCCGACGCCCTCTGCGCAAGTCAATGAGCACTTCTGCGG 539
QY 3561 GGGAGGCCCTCACCTTCCAGAGGACACACATTTCTGTGGGGAGGAGGAGT 3620
DB |||||

```

RESULT 9	
AAV59639	
ID	AAV59639 standard; DNA; 1446 BP.
XX	
AC	AAV59639;
XX	
DT	19-JAN-1999 (first entry)
DE	
DE	Human secreted protein gene 129 clone HHSCV65.
XX	
XX	Human; secreted protein; fusion protein; gene
KW	diagnosis; tissue; cancer; tumour; neurodegene
KW	developmental abnormality; foetal deficiency;
KW	immune system; asthma; lymphocytic disease; Br
KW	cognitive disorder; ischaemic shock; Alzheimer's dis
KW	osteoporosis; arthritis; testis; lung; thyroid
XX	endocrine; metabolism; regulation; malabsorpti
OS	Homo sapiens.
XX	
PN	WO9839448-A2.
XX	
PD	11-SEP-1998.
XX	
PF	06-MAR-1998; 98WO-US04493.
XX	
XX	02-OCT-1997; 97US-0061060.
PR	07-MAR-1997; 97US-0038621.
PR	07-MAR-1997; 97US-0040161.
PR	07-MAR-1997; 97US-0040162.
PR	07-MAR-1997; 97US-0040163.
PR	07-MAR-1997; 97US-0040333.
PR	07-MAR-1997; 97US-0040334.
PR	07-MAR-1997; 97US-0040336.
PR	07-MAR-1997; 97US-0040826.
PR	11-APR-1997; 97US-0043311.
PR	11-APR-1997; 97US-0043312.
PR	11-APR-1997; 97US-0043313.
PR	11-APR-1997; 97US-0043314.
PR	11-APR-1997; 97US-0043568.
PR	11-APR-1997; 97US-0043569.
PR	11-APR-1997; 97US-0043670.
PR	11-APR-1997; 97US-0043671.
PR	11-APR-1997; 97US-0043672.
PR	11-APR-1997; 97US-0043674.
PR	11-APR-1997; 97US-0043576.
PR	11-APR-1997; 97US-0043578.
PR	11-APR-1997; 97US-0043580.
PR	11-APR-1997; 97US-0043569.
PR	11-APR-1997; 97US-0043670.
PR	11-APR-1997; 97US-0043671.
PR	11-APR-1997; 97US-0043672.
PR	11-APR-1997; 97US-0043674.
PR	23-MAY-1997; 97US-0047492.
PR	23-MAY-1997; 97US-0047500.
PR	23-MAY-1997; 97US-0047501.
PR	23-MAY-1997; 97US-0047502.
PR	23-MAY-1997; 97US-0047503.
PR	23-MAY-1997; 97US-0047581.
PR	23-MAY-1997; 97US-0047582.
PR	23-MAY-1997; 97US-0047583.
PR	23-MAY-1997; 97US-0047585.
PR	23-MAY-1997; 97US-0047586.
PR	23-MAY-1997; 97US-0047587.
PR	23-MAY-1997; 97US-0047588.
PR	23-MAY-1997; 97US-0047589.
PR	23-MAY-1997; 97US-0047590.
PR	23-MAY-1997; 97US-0047592.
PR	23-MAY-1997; 97US-0047593.
PR	23-MAY-1997; 97US-0047594.
PR	23-MAY-1997; 97US-0047595.
PR	23-MAY-1997; 97US-0047596.
PR	23-MAY-1997; 97US-0047597.

Qy	4304	TGAATGGTGGAGGAGGACAGTGGGGAGAAAGGTCTCACCGGACAGGTTCGGAGAAATGAGG	4363	PR	11-APR-1997;	97US-043580P.
Db	781	TGAATGGTGGAGGAGGACAGTGGGGAGAAAGGTCTCACCGGACAGGTTCGGAGAAATGAGG	840	PR	11-APR-1997;	97US-043669P.
Qy	4364	TCAGCGGTGCTGGGACACATGGAGGGGACAGTGGGACAGGCTTGGGACACACCG	4423	PR	11-APR-1997;	97US-043672P.
Db	841	TCAGCGGTGCTGGGAGAACACATGGAGGGGACAGTGGGACAGGCTTGGGACACACCG	900	PR	11-APR-1997;	97US-043674P.
Qy	4424	CAGGAATAATTTGAAATGTGTGAGGTGACTCCCGGAGGGCCCTTGGGCAATTTGG	4483	PR	23-MAY-1997;	97US-047500P.
Db	901	CAGGAATAATTTGAAATGTGTGAGGTGACTCCCGGAGGGCCCTTGGGCAATTTGG	959	PR	23-MAY-1997;	97US-047501P.
Qy	4484	GAAAGAAATGATGCTGGAGGGCTTAAGGGACACAGTGGACAGGGAGAGTCTTCATC	4543	PR	23-MAY-1997;	97US-047503P.
Db	960	GAAAGAAATGATGCTGGAGGGCTTAAGGGACACAGTGGACAGGGAGAGTCTTCATC	1019	PR	23-MAY-1997;	97US-047508P.
Qy	4544	TGCTGGCAATTTTGGGGTGTAGTGCCAAACTTGAATAGGGCTGGGGTGTCTTCTCC	4603	PR	23-MAY-1997;	97US-047581P.
Db	1020	TGCTGGCAATTTTGGGGTGTAGTGCCAAACTTGAATAGGGCTGGGGTGTCTTCTCC	1079	PR	23-MAY-1997;	97US-047582P.
Qy	4604	ACTGACACCCAAATCCAGAAATCCCTGTCTTGAGT-CCGAGAACTTTGCCCTCTTGACTGT	4662	PR	23-MAY-1997;	97US-047583P.
Db	1080	ACTGACACCCAAATCCAGAAATCCCTGTCTTGAGT-CCGAGAACTTTGCCCTCTTGACTGT	1139	PR	23-MAY-1997;	97US-047584P.
Qy	4663	CCCT 4666		PR	23-MAY-1997;	97US-047585P.
Db	1140	CCCT 1143		PR	23-MAY-1997;	97US-047586P.
RESULT 10						
ABS73626						
ID	ABS73626 standard; cDNA; 1446 BP.					
AC	ABS73626;					
DT	15-JAN-2003 (first entry)					
DE	Human cDNA #1 for novel secreted protein gene 129.					
KW	Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;					
KW	rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;					
KW	liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;					
KW	cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;					
KW	nervous system disorders; Alzheimer's disease; infection;					
KW	ocular disorder; corneal infection; wound healing; tissue regeneration;					
KW	epithelial cell proliferation; organ transplantation; food additive;					
OS	Preservative; nutritional.					
XX	Homo sapiens.					
XX	US6420526-B1.					
XX	16-JUL-2002.					
XX	08-SEP-1998;					
XX	98US-0149476.					
XX	07-MAR-1997;					
XX	97US-038621P.					
PR	07-MAR-1997;					
PR	97US-040161P.					
PR	07-MAR-1997;					
PR	97US-040162P.					
PR	07-MAR-1997;					
PR	97US-040163P.					
PR	07-MAR-1997;					
PR	97US-040333P.					
PR	07-MAR-1997;					
PR	97US-040334P.					
PR	07-MAR-1997;					
PR	97US-040336P.					
PR	07-MAR-1997;					
PR	97US-040626P.					
PR	11-APR-1997;					
PR	97US-043311P.					
PR	11-APR-1997;					
PR	97US-043312P.					
PR	11-APR-1997;					
PR	97US-043313P.					
PR	11-APR-1997;					
PR	97US-043314P.					
PR	11-APR-1997;					
PR	97US-043315P.					
PR	11-APR-1997;					
PR	97US-043568P.					
PR	11-APR-1997;					
PR	97US-043569P.					
PR	11-APR-1997;					
PR	97US-043576P.					
PR	11-APR-1997;					
PR	97US-043578P.					

XX		3 isoform protein encoding sequence.
DE	XX	Cytoprotective; immunomodulatory; cancer; chromosome Xq13.1;
DE	XX	Neurostatic; anti-inflammatory; gene therapy; nutritional supplement;
KW	KW	wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
KW	KW	amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
KW	KW	vulnerary; gene; ss.
OS	XX	Homo sapiens.
OS	XX	WO200231111-A2.
PN	XX	18-APR-2002.
PD	XX	11-OCT-2001; 2001WO-US7760.
PF	XX	12-OCT-2000; 2000US-0687527.
PR	XX	(HYSE-) HYSEQ INC.
PA	XX	Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI	PI	Xue AJ, Yang Y, Wehrman T, Drmanac RT;
PI	XX	WPI: 2002-426278/45.
DR	DR	N-PSDB; ABP43803.
XX	XX	New polypeptides and their encoded proteins, useful as nutritional
PPT	PPT	sources or supplements, or in gene therapy, particularly for treating
PPT	PPT	wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PPT	PPT	inflammation -
PS	XX	Claim 1; SEQ ID # 260; 357pp + sequence listing; English.
XX	XX	The invention relates to 446 newly isolated polynucleotide sequences.
CC	CC	The activity of polynucleotides of the invention may be described as,
CC	CC	vulnerable, neuroprotective, immunomodulator, cytostatic and
CC	CC	anti-inflammatory. Compositions comprising nucleic acids of the invention
CC	CC	are useful for treating a mammalian subject, or as nutritional sources or
CC	CC	supplements. These are useful in gene therapy, particularly for treating
CC	CC	wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC	CC	amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC	CC	inflammation. The nucleic acids and polypeptides are also useful in
CC	CC	diagnostic and research methods. The sequences given in records
CC	CC	ABQ60788-ABQ61233 represent polynucleotides of the invention.
CC	CC	NOTE: The sequence data for this patent did not form part of the printed
CC	CC	specification, but was obtained in electronic format directly from WIPO
CC	CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	XX	Sequence 2865 BP; 593 A; 906 C; 772 G; 594 T; 0 other;
SQ		
		Query Match 21.7%; Score 1014.2; DB 24; Length 2865;
		Best Local Similarity 65.3%; Pred. No. 9.8e-171;
		Matches 1584; Conservative 0; Mismatches 778; Indels 63; Gaps 4
QY	417	AGCATGTGCTCTCGCGCTGTGTCGTGGGCTGC GGCGCTCAACGCCGGGAGGG 476
Db	329	AACATGTGCTCGCGCTTGGCGCGCCTCGCTGTCCCTGAGCCCCAAGCCCACGGTTGCG 388
QY	477	GGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGCGAGCTTCGGCGAGAG 536
Db	389	AGAGAGCTGTGCTCACCTGTGGTTCCTCAGTTTGCGCTGAGGGCGAGTACCAGGCC 448
QY	537	CGCTTCCCGGTGGTGAACACGCCCTACCGGGCGAGTGC CGGTGTGCGCGCGAGCTCAAC 596
Db	449	CCAGCACCCACAGTCAACTCACCTTTGGGAAGCTTAAGGGGTGCCCGAGTACCACCTGCC 508
QY	597	AACGAGATCTGGGCCCGCTGTGCAGATTCTGG3CGTGGCCCTACGCACGCCGCCCGCTG 656
Db	509	AGTGAGATCTGGGGCGCTGTGACCAATACTTGGGGTGCCTACGAGCTCCCGCGATC 568
QY	657	GGCGCCCGCGCTTCCAGCGCGCTGAGCGCGCGCGCTGTGGCCCGCGTGCACAACGCC 716

1788 GACCAACATGGTGGCAGCAGTGTGGCCACTGCCAAGCTGCAGCGGACTACCACTCT 1847
 1709 GACCAACATGGTGGCAGCAGTGTGGCCACTGCCAAGCTGCAGCGGACTACCACTCT 1768
 1848 CCGTCTACTTTTACACCTTTTACCACTACTGCCAGCGGAGCGGCGCTGAGTGGCA 1907
 1769 CTTACCTACTTTTACCGCTTTTATCATCTACTGCCAGAGCCTCATGAAGCCTGCTTGTCA 1828
 1908 GATCGCGGCGCAGGAGATGAATCGCCCTATGCTTTGGCGTGCCTCATGCTGGTGCAC 1967
 1829 GATCGAGCTCATGGGATGAAGTACCTATGTTTGGGGTTCCTATGATGAGCCCACT 1888
 1968 GACCTCTTCCCTGTAACTTCTCCAAAGATGAGTCACTGCTCAGTGCCTGCTGATGACC 2027
 1889 GACCTTTTCCCTGTAACTTCTCCAAAGATGAGTCACTGCTCAGTGCCTGCTGATGACC 1948
 2028 TACTGACCAACTTCGCGAAGCTGGGACCCCAACACCGGTCGCGAGATACCAAG 2087
 1949 TATTGACCAACTTTGCCAAGCTGGGATCCCAACAGCCGCTCCCGCAGGACCAAG 2008
 2088 TTTATCCACACCAAGCCCAATCTCTCGAGGAGTGTGTGGAGCAAAATTCACAGCAAG 2147
 2009 TTTATTTACACCAAGGCAACCGCTTTGAGGAGTGTGTGGAGTGTGTCCAAATACATCCCGA 2068
 2148 GAGAAGCAGTATCTGCACATAGCTGTGAAGCAGCGCTGCTGACAACTACCGGCGCAAC 2207
 2069 GACCACTCTTACCTTTCATCTCGGCTGAAACCAAGGCTCCGAGATCATTTACCGGCGCACT 2128
 2208 AAGGTGGCTTCTGGTGGAGCTGCTGCCCCACCTGCACAACTGCACACGAGGCT--- 2264
 2129 AAGGTGGCTTCTGGTGGAGCTGCTGCCCCACCTGCACAACTGCACACGAGGCT--- 2188
 2265 -----TTACACCAACCAAGCGCTGCTTCCCTACGCCAGCGTGGCGCTCGTCCC 2318
 2189 TATACGTTCACCAACCAAGGCTGCTGCGATACCAACCGCTCCACATCAC 2248
 2319 CCGCTGGCGCCCGGGGACACCGCGCGCGCGCGCTGCGACCTGCTCGGAGCC 2378
 2249 CGCAGGCGCAATGCGAAGCTGCGGACCAAGCGCGCGCGCTGCGACCTGCTGAGC 2308
 2379 GAGCGCGAGCGC-----GGCCCAAGGCGCTTATGACCGCTTCCCGCG 2420
 2309 AACGAGATCCCGAGGGTCTCGAAGCGGACGAGATCGAGGCGCATCTCTGTTGAG 2368
 2421 GACTCAGCGGACTTCTCAGGAGTGAAGTCAACCGTGGCGCTGCTGCTGCTCTC 2480
 2369 AACCTCGTACTACTCACTGAATTAAGTGTACCATCGCGCTGGGCGCTTCCCTCTG 2428
 2481 TTCTCAACATCTGCGCTTGTGCGCTTCTACTACAAAGCGGACCGGCGGAGGCTG 2540
 2429 TTCTTTAACGTTCTGCGCTTGTGCGCTTCTACTACGTAAGACAAACGCGCGGAGG 2488
 2541 CGGTGAGGCGGCTTACCCCACTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 2600
 2489 CCGCTGCGGAGCTAGC-----CCTCAGCGGCGGAGCC 2521
 2601 CTGCTCCCGCGCGCGCTGAGTCTCCACAGAGAGAGTGTGTCTACGCTGAGCTG 2660
 2522 GGGCGCCCGAGTGTGGAGTGTCTCAGAGGAGAGCTGCGACATTAACATTCAGGCGCC 2581
 2661 AAGCGGGGTGTGCGCTGCGGCGGAGCTTCCGAGGCTCTGCGCGCTGCTGCTGCTGCTG 2720
 2582 ACCACACAGAGTGTGAGCGCGGCTTCCCGCCATGACAGCTGCGCTCACTGATTTGCC 2641
 2721 GACTACACCTTGGCGCTTGGCGGCGGACCGGACGATGTGCTTCTTGGCGCGCGGCG 2780
 2642 GACTACACCTTGGCGCTTGGCGGCGGCTTCCCGGATGACATCCATCTGATGACCCCAAC 2801
 2781 CTGACCTTGTGCGCACTGGCGCTG 2805
 2702 ATCACTATGATCCCACTCCCTGG 2726

RESULT 12
 AA45600
 ID AA45600 standard; cDNA; 4233 BP.
 XX
 AC AA45600;
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE cDNA sequence of human neuroigin-3 (NL-3) gene clone #4.
 XX
 KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;
 KW mental retardation; autism; depression; bipolar affective disorder;
 KW hypothyroidism; OPA gene; neuropsychiatric disorder; neuroigin-3;
 KW NL-3; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9955915-A2.
 XX
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-US09365.
 XX
 PR 29-APR-1998; 98US-0083465.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Philibert RA, Gimms EI;
 XX
 DR WPI; 2000-126357/11.
 XX
 PT Identification of polymorphisms in the PCTG4 region of Xq13 for
 PT diagnosing mental retardation or autism -
 XX
 PS Example 7; Page 74-76; 100pp; English.
 XX
 CC The present sequence represents the cDNA sequence of a human
 CC neuroigin-3 (NL-3) clone, isolated from heart. The NL-3 gene is
 CC derived from the human PCTG4 region of chromosome Xq13. Polymorphisms
 CC in this region are associated with mental retardation, autism,
 CC depression, bipolar affective disorder or hypothyroidism. One 12 bp
 CC insertion polymorphism occurs within the coding region of the human
 CC OPA gene, and introduces a 4 amino acid insertion in a putative OPA
 CC domain. This domain has been shown to be involved in tissue specific
 CC expression. Another polymorphism consists of a pentanucleotide
 CC repeat approximately 7 kb upstream of the 12 bp polymorphism. Another
 CC polymorphism consists of a dinucleotide repeat approximately 4.5 kb
 CC downstream of the 12 bp polymorphism. The specification describes a
 CC method for screening for polymorphisms in a PCTG4 nucleic acid sequence
 CC obtained from a subject. The PCTG4 related sequences within the q13
 CC region of the X chromosome have polymorphisms associated with
 CC neuropsychiatric disorders. The methods can be used to screen for the
 CC presence of a heritably linked form of mental retardation, autism,
 CC depression, bipolar affective disorder or hypothyroidism.
 XX
 SQ Sequence 4233 BP; 945 A; 1279 C; 1097 G; 906 T; 6 other;
 Query Match 21.7%; Score 1011.2; DB 21; Length 4233;
 Best Local Similarity 65.5%; Pred. No. 3.5e-170;
 Matches 1589; Conservative 0; Mismatches 773; Indels 64; Gaps 5;
 QY 417 AGCATGTGGCTCTGCTGGCGCTGTGTCTGTGGGGTGGCGGGGTCTCAACGCGGGGAGGG 476
 DB 404 AACATGTGGCTGGCTTGGCGCGCTGTGTCTGTGGCGCGCGCGCGCGCGCGCGCGCG 463
 QY 477 GGTCCCG 536
 DB 464 AGGAGCTGTGCTTCCCTGCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 523
 QY 537 CGCTTCCCGGTGGTGAACACCGCGCTACCGGCGAGTGGCGGTGTGCGGCGCGAGCTCAAC 596

Db 524 CCAGCACCCACAGTCAACACTCACTTTGGGAAGCTAAGGGGTGCGCGAGTACCACCTGCCC 583
 Qy 597 AACGAGATCCTGGGCGCCCGCTGTCAGATTCTTTGGGCGTGCCTTAGCGCACGCGCCCTG 656
 Db 584 AGTGAGATCTGGGGCTGTGGACCAATACCTTGGGGTGCCTACGACGTCGCCCGATC 643
 Qy 657 GGGCGCGCGCTTCAGCGCGCTGAGGGCGCGCTGTCGCGCGCGCGTGGCGAACGCC 716
 Db 644 GGGGAGAAAGTTCTGCGCCCTGAAACACCCCCATCCTGTGCGGCATCCGGAACGCC 703
 Qy 717 ACCACCTCGCGCGCTGCGCGCAGAACCTTGACGGGGCGTGCCTCCGCTCATGTGTG 776
 Db 704 ACACATTTCCCGAGTGTGCGCGCAGAACATCCACAGCTGTGCCGAGTCACTGTG 763
 Qy 777 CTTGTGTGTTACCGACAACTTTGGAGGGCGCGCCACCTACGTGAGAACACAGAGCGAG 836
 Db 764 CCGGTCTGGTTCACTGCGCAACTTGGATATCGTCGCTACTTATACATCCAGAGGCCAACGAA 823
 Qy 837 GACTGCTGTACCTCAACCTTACGTCGCGCCACCGAGCGGTCCGCTCACAAAAACGCT 896
 Db 824 GACTGTCTACCTGAACGTCATGTGCGCAGCGAGATGGATCCGGCGCTAAGAAACAG 883
 Qy 897 GACGA-----GGCGACGCTCAATCCGCCAGACACAGATATCCGTGACCCCTGGGAAG 947
 Db 884 GCGGAGACTTAGCGGATATGACGGGATGAAGATGAAGACATCCGGGACAGTGTGCT 943
 Qy 948 AAGCTGTGATGCTGTTCTCCATGGCGGCTCCTACATGAGGGGACCGGAACATGTTT 1007
 Db 944 AAACCCGCTATGCTTACATCCACGGAGGCTCTTACATGAGGAGACAGCAACATGAT 1003
 Qy 1008 GATGGCTCAGTCTGGGTGCTATGACCAAGCTCAATGTAGCCACGCTCAACTACCGTCTT 1067
 Db 1004 GATGGAGCATCTCGCCAGTTATGGCAATGTATAGTCACTACCCCTCAACTATCGGTT 1063
 Qy 1068 GGGGTGCTCGGTTTCTAGACACCGGGACAGGCTGCTCAAAAGGCAACTATGGGCTCTG 1127
 Db 1064 GGAAGTATAGTGTCTGAGTACTGAGATCAGGCTGCCAAGGGCAACTATGGGCTCCT 1123
 Qy 1128 GACAGATCCAGGCGCTGCGGTGCTCAGTGAAGCAATCGCCCACTTTGGGGGCGCACCCC 1187
 Db 1124 GACAGATCCAGGCGCTGCGGTGCTGAGCGAGATATGCTCTTTCGGGGGAGACCCC 1183
 Qy 1188 GAGCGTATCACCACTTTTGGTTCGGGGCAGGGGCTCTGCGTCAACCTTCTGATGCTC 1247
 Db 1184 CGCGGATCACTGTCTTTGGCTCGGCGATTTGGTGCATCTCGCTCAGCCCTCTCAGTTG 1243
 Qy 1248 TCCACCACTTCCAGAGGCTTTCAGAGGCGCATCGCCAGAGTGCGACCGCATTTCC 1307
 Db 1244 TCACATCACTCAGAGGGGACTTTTCCAGAGGCGCATTCACAGGCTGTGGCAGACAAAGTGGC 1303
 Qy 1308 AGCTGGTCTGTCAACTACAGCGCTCAAGTACACGCGGCTGTGGCAGCCAAAGTGGC 1367
 Db 1304 AGCTGGGCTGTGAATCAACCAAGTGAAGTACACCGCTGTGGCAGACAAAGTGGC 1363
 Qy 1368 TGTGACGAGAGGACAGTGTGAAGCTGTGAGTGTCTGCGCGAGAGCCCTCCCGGAG 1427
 Db 1364 TGTATGTGCTGGACACCGTGGATATGTGTGACTGTCTTGGCAAAAGAGTGCCAAAGAG 1423
 Qy 1428 CTGTGGACAGGACGTCAGCTGCGCGCTACACATCGCTTTGGGCGCGCTGGTGGAT 1487
 Db 1424 CTGTGAGAGGAGACATCCAGCGAGCGCTACCACTGCGTGGGCTTTGGCCCTGTGATTGAT 1483
 Qy 1488 GCGAGCTGTGCTCCGATGACCTGAGATCTCTATGACGAGGAGAAATCTCTCAACTAC 1547
 Db 1484 GGTGATGTCAITTCCTGATGACCTGAGATCTCTATGAGAGGCGAGTTCCTCAACTAT 1543
 Qy 1548 GACATGCTCATCGGCGTCAACACAGGAGAGGCGCTCAAGTTCTGTGGAGGACTCTGACAG 1607
 Db 1544 GACATCATGCTAGTGTCAACCGAGGCGAGGGTCTCAAGTTTGTGGAAGGGTGTGTGAC 1603
 Qy 1608 AGCGAGGAGCGGTGTGCTCTGCCAGCGCTTTGACTTCACTGTCTCAACTTTGTGGACAAC 1667
 Db 1604 CTTGAGGATGGTGTCTCTGGCACTGACTTTGACTATTCCGTCTCCAAATTTGTGGACAAT 1663

Qy 1668 CTGTATGGCTTACCGGAAGGAGGATGTCTTCGGAGACCATCAAGTTTATGTATACACA 1727
 Db 1664 CTGTATGGCTTATCTTGGGTAAGGACACCTTCGGAGAGACCATCAAGTTCAATATACA 1723
 Qy 1728 GACTGGCGCCAGCGGAGCAATGCGGAATGCGCGCAAAACCTGTGTGGGCTCTTTACT 1787
 Db 1724 GACTGGGACAGCGTGACAACTGAGACCGCGCGTAAACACTGGTGGCACTCTTCACT 1783
 Qy 1788 GACACCAATATGGGTGGACACAGCTGTGGCCACTGCCAAGCTGCACGCGACTACCACTCT 1847
 Db 1784 GACCACAGTGGGTGGAGCCCTCAGTGGTGACAGCCGATCTGATGCGCGCTACGCTCG 1843
 Qy 1848 CCGCTCTACTTTTACACTTCTACCACTGCGCAGCGGAGGCGCGCTGTAGTGGCA 1907
 Db 1844 CTTACCTTACTTCTACGCTTCTATCATCTGCGCAGAGCCTCATGAAGCCTGTGTGTCA 1903
 Qy 1908 GATCGGCGACCGGGATGAATGCTCCCTATGTCTTTGGCGTGCCTAGTGGGTGGCCACC 1967
 Db 1904 GATGAGCTCATGGGATGAAGTACCTATGTATTTTGGGGTTCCTATGGTAGGCCCCACT 1963
 Qy 1968 GACTCTTCCCTGTAACTTCTCCAGAATGAAGTCAATGTCTCAGTGCCTGTGTCAAGC 2027
 Db 1964 GACTTTTCCCTGCACTTCTCCAGAATGAATGTATGTCTCAGTGTCTGTGTCAAGC 2023
 Qy 2028 TACTGGACCAACTTGGCAAGACTGGGGAACCCCAACAGCGCGTGCAGGATACCAAG 2087
 Db 2024 TATTGGACCAACTTGGCAAGACTGGGGAACCCCAACAGCGGTCCCCCAGGACCAAG 2083
 Qy 2088 TTCACTCCACACCAAGCCCAATCGCTTCGAGGAGTGTGTGGAGCAAAATCAACAGCAAG 2147
 Db 2084 TTCACTCCACCAAGCCCAACCGCTTTGAGGAATGAGTGTGCTGCTCAATCAATCAATCCCGA 2143
 Qy 2148 GAGAAGCAGTATCTGCAATAGGCTTGAAGCCACGCTGTGTGAGCAACTACTACCGCGCAAC 2207
 Db 2144 GACAGCTCTTACCTTCACTCGGCTGAACCAAGGTCGAGATCATTTACCGGCGCACT 2203
 Qy 2208 AAGTGGGCTTCTGGCTGAGCTCGTCCCGCTGCTGACACCTGACACCGTGCACCGAGCTC --- 2264
 Db 2204 AAGTGGGCTTCTGGGAAACATCTGGTGGCGCCACCTATACAACTGATGATGATGTTCCAC 2263
 Qy 2265 -----TTCACACCAACCAACGCGCTGCTCCCTACGCGACGCGTGGCGCGCTGCTGCC 2318
 Db 2264 TATAGTCCACCAACCAAGTCCGCTCGGATACCAACAGCTCCACATCACTCACC 2323
 Qy 2319 CCGCTGCGCGCGCGGACACGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCGAGCGC 2378
 Db 2324 CGCAGCGCGCAATGGCAAGACCTGGAGCACCAAGCGCGCGCGCTCTCACCTGCTTACAGC 2383
 Qy 2379 GAG-----CCGAGCGCGCGCGCGCGCGCTATGACCGCTTC---CCCGG 2419
 Db 2384 AACGAGATGCCAGGGGTCTTGGAACGGGACCCAGGATGCCAGGCGCACCTCTGTTGA 2443
 Qy 2420 GGACTCAGCGGACTACTCCACGAGCTGAGCGTCAACGCTGCGCTGGTGGTCTCTCTCT 2479
 Db 2444 GAACCTCGTGACTACTCTCACTGAATTAAGTGTCAACATCGCGTGGGGGCTCTCTCTCT 2503
 Qy 2480 CTTCTCTCAACATCTGCGCTTGTCTGCGCTCTTACTTACAAAGCGGACCGCGCGGAGGCT 2539
 Db 2504 GTTCTCTAACGTTCTGGCGCTTCTGCTGCGCTCTTACTTACCGTAAGGACAAACCGCGCAGGA 2563
 Qy 2540 GCGGTGCGAGCGGCTTAGCCCACTTGGCGGCTCAGGCTCTGCGGTGCTGTTGGGGGCGC 2599
 Db 2564 GCCCTTGGCGAGCTAGC-----CCTCAGCGGGGAGC 2596
 Qy 2600 CTGTCTCCCGCGCGCGCGCTGAGCTGCCACAGAGGAGGAGTGTGCTCACTCAGCT 2659
 Db 2597 CGGGCGCGCGGAGTGTGGAGCTGCTCCAGAGAGGAGCTGGCAGCATTTACAACTGGGCGC 2656
 Qy 2660 GAAGCGGGTGTGTGCGTTCGGGGCGGACCTTCGCGAGGCTCTGCGCGCTGCTGCGCGC 2719
 Db 2657 CACCCACACAGTGTGAGGCGCGCTCCCCCATGACACGCTGCGCTCACTGCTGCTGCTG 2716

QY 2500 TTGCTGCTCTACTACAGCGGACCGCGCGGAGGAGCTCGCTGAGAGCGGCTTAGCC 2559
Db 1305 TTGCTGCTCTACTACAGCGGACCGCGCGGAGGAGCTCGCTGAGAGCGGCTTAGCC 1364
QY 2560 CACCTGGCGGCTCAGGCTCTGGCGTGGCTGG 2590
Db 1365 CACCTGGCGGCTCAGGCTCTGGCGTGGCTGG 1395

RESULT 14

AACT4943
ID RAC74943 standard; cDNA; 924 BP.

XX AAC74943;

XX AAC74943;

XX 08-FEB-2001 (first entry)

DE Human ORFX ORF498 polynucleotide sequence SEQ ID NO:995.

XX Human; open reading frame; ORFX; detection; cytotatic; hepatotropic;
KW human; antipsoriatic; antiparkinsonian; nontropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CUFA-) CUPAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2000-602362/57.

XX P-PSDB; AAB40734.

XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -

XX Claim 5; Page 969-970; 5507pp; English.

XX AACT74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytotatic; hepatotropic; vulnary;
CC antipsoriatic; antiparkinsonian; nontropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy

CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX SQ Sequence 924 BP; 189 A; 306 C; 261 G; 168 T; 0 other;

Query Match 19.8%; Score 924; DB 21; Length 924;

Best Local Similarity 100.0%; Pred. No. 8.8e-155;

Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1422 CGGAGCTGTGTGACAGGACGTGACGCTGCCGCTTACCATCGCTTTGGGCCCGTG 1481

Db 1 CGGAGCTGTGTGACAGGACGTGACGCTGCCGCTTACCATCGCTTTGGGCCCGTG 60

QY 1482 GTGGATGGCGACGTGTCCCGGATGACCTGAGATCCTCATGACAGGAGAAATTCCTC 1541

Db 61 GTGGATGGCGACGTGTCCCGGATGACCTGAGATCCTCATGACAGGAGAAATTCCTC 120

QY 1542 AACTACGACATGCTCATCGCGGTCAACAGGAGAGGGCTCAAGTTCGTGGAGGACTCT 1601

Db 121 AACTACGACATGCTCATCGCGGTCAACAGGAGAGGGCTCAAGTTCGTGGAGGACTCT 180

QY 1602 GCAGAGAGCGAGAGCGGTGTCTGCGAGCGCTTTGACTTCACTGTCTCCAACTTTGTG 1661

Db 181 GCAGAGAGCGAGAGCGGTGTCTGCGAGCGCTTTGACTTCACTGTCTCCAACTTTGTG 240

QY 1662 GACAACTGTATGGCTACCCGGAAGGAGATGTGCTTCGGGAGACCATCAAGTTTATG 1721

Db 241 GACAACTGTATGGCTACCCGGAAGGAGATGTGCTTCGGGAGACCATCAAGTTTATG 300

QY 1722 TACACAGACTGGGCGGACCGGCAATGGCGAAATGGCGGCAAAACCTGTGGGGCTC 1781

Db 301 TACACAGACTGGGCGGACCGGCAATGGCGAAATGGCGGCAAAACCTGTGGGGCTC 360

QY 1782 TTTACTGACCACTAATGGGTGGGACAGAGTGTGGCCACTGCGCAAGCTGACGCGGACTAC 1841

Db 361 TTTACTGACCACTAATGGGTGGGACAGAGTGTGGCCACTGCGCAAGCTGACGCGGACTAC 420

QY 1842 CAGTCTCCCGTCTACTTTTACACCTTCTACACACTGCGAGCGGAGGCGCGCTGAG 1901

Db 421 CAGTCTCCCGTCTACTTTTACACCTTCTACACACTGCGAGCGGAGGCGCGCTGAG 480

QY 1902 TGGGACAGTGGGCGGACGCGGATGAATGCTTCTTTGGCGTGGCCCATGTTGGGT 1961

Db 481 TGGGACAGTGGGCGGACGCGGATGAATGCTTCTTTGGCGTGGCCCATGTTGGGT 540

QY 1962 GCCACCGACTCTTCCCGCTGTAATCTTCCAGAAATGAGTCTAGTGGCGTGGGT 2021

Db 541 GCCACCGACTCTTCCCGCTGTAATCTTCCAGAAATGAGTCTAGTGGCGTGGGT 600

QY 2022 ATGACCTACTGGACCACTTTCGCCAAGACTGGGAGACCCCAACAGCGGTGGCAGAGAT 2081

Db 601 ATGACCTACTGGACCACTTTCGCCAAGACTGGGAGACCCCAACAGCGGTGGCAGAGAT 660

QY 2082 ACCAAGTTTCACTCACACCAACCAAGCCCAATCGCTCGAGAGGCTGTGGAGCAAAATTCAC 2141

Db 661 ACCAAGTTTCACTCACACCAACCAAGCCCAATCGCTCGAGAGGCTGTGGAGCAAAATTCAC 720

QY 2142 AGCAAGAGAGAGGAGTATCTGCAATAGCGCTGAAGCCACGGGTGGTGGACAACTACCGC 2201

Db 721 AGCAAGAGAGAGGAGTATCTGCAATAGCGCTGAAGCCACGGGTGGTGGACAACTACCGC 780

QY 2202 GCCAACAAGGTGGCTTCTGGCTGGAGGCTGTGCCCCCACTGCAAACTGACACGAG 2261

Db 781 GCCAACAAGGTGGCTTCTGGCTGGAGGCTGTGCCCCCACTGCAAACTGACACGAG 840

QY 2262 CTCTTTCACACCAACCAAGCGGCTGTGCTTCCCTAGCCACGCGGTGGCGCTGTCCCCC 2321

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Db      841  CTTCTTACCACACACGCGCTCCTCCCTACGCCACGCGGTGGCGCTGCGCCCTCGCCGCC 900
Qy      2322  GCTGGCGCGCGCGGACACGCGCG 2345
Db      901  GCTGGCGCGCGCGGACACGCGCG 924

RESULT 15
AAC58592
ID  AAC58592 standard; cDNA, 3112 BP.
XX
AC  AAC58592;
XX
DT  29-JAN-2001 (first entry)
DE  Human PRO701 protein UNQ365 encoding cDNA SEQ ID NO:66.
XX
KW  Human; immune related disease; diagnosis; antinflammatory; cardiant;
KW  dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW  haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW  antianemic; hepatotropic; viricide; antipsoriatic; antiallergic;
KW  antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW  osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW  idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW  systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW  autoimmune thrombocytopaenia; immune-mediated renal disease;
KW  demyelinating disease; hepatobiliary disease; Whipple's disease;
KW  inflammatory bowel disease; gluten-sensitive enteropathy;
KW  autoimmune disease; immune-mediated skin disease; allergic disease;
KW  immunological disease; transplantation associated disease;
KW  graft rejection; graft-versus-host-disease; ss.
XX
OS  Homo sapiens.
XX
FN  WO200053758-A2.
XX
PD  14-SEP-2000.
XX
PF  02-MAR-2000; 200WO-US05841.
XX
PR  08-MAR-1999; 99WO-US05028.
PR  10-MAR-1999; 99US-0123618.
PR  12-MAR-1999; 99US-0123957.
PR  13-MAR-1999; 99US-0125775.
PR  12-APR-1999; 99US-0128849.
PR  20-APR-1999; 99WO-US08615.
PR  28-APR-1999; 99US-0131445.
PR  04-MAY-1999; 99US-0132371.
PR  14-MAY-1999; 99US-0134287.
PR  02-JUN-1999; 99WO-US12252.
PR  23-JUN-1999; 99US-0141037.
PR  20-JUL-1999; 99US-0144758.
PR  26-JUL-1999; 99US-0145698.
PR  28-JUL-1999; 99US-0146222.
PR  01-SEP-1999; 99WO-US20111.
PR  08-SEP-1999; 99WO-US20594.
PR  13-SEP-1999; 99WO-US20944.
PR  15-SEP-1999; 99WO-US21090.
PR  15-SEP-1999; 99WO-US21547.
PR  05-OCT-1999; 99WO-US23089.
PR  29-OCT-1999; 99US-0162506.
PR  29-NOV-1999; 99WO-US28214.
PR  30-NOV-1999; 99WO-US28313.
PR  30-NOV-1999; 99WO-US28409.
PR  01-DEC-1999; 99WO-US28301.
PR  01-DEC-1999; 99WO-US28634.
PR  02-DEC-1999; 99WO-US28551.
PR  02-DEC-1999; 99WO-US28564.
PR  16-DEC-1999; 99WO-US28565.
PR  20-DEC-1999; 99WO-US30095.
PR  20-DEC-1999; 99WO-US30999.
PR  30-DEC-1999; 99WO-US31274.

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05-JAN-2000; 200WO-US00219.
06-JAN-2000; 200WO-US00277.
06-JAN-2000; 200WO-US00376.
11-FEB-2000; 200WO-US03565.
18-FEB-2000; 200WO-US04341.
18-FEB-2000; 200WO-US04342.
22-FEB-2000; 200WO-US04414.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI  Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI  Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR  WPI; 2000-572271/53.
DR  P-PSDB; AAB33427.
XX
XX  Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX  immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX  arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
PS  Claim 23; Fig 27; 309pp; English.
XX
XX  The present invention describes sixty four human PRO proteins which can
XX  be used in the treatment of immune related diseases. The human PRO
XX  proteins, anti-PRO antibodies, agonists and antagonists are useful for
XX  treating and diagnosing immune related disorders. The disorders are
XX  selected from systemic lupus erythematosus, rheumatoid arthritis,
XX  osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX  systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX  syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX  anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
XX  immune-mediated renal disease, demyelinating diseases of the central
XX  and peripheral nervous systems, hepatobiliary diseases, inflammatory
XX  bowel disease, gluten-sensitive enteropathy and Whipple's disease,
XX  autoimmune or immune-mediated skin diseases, allergic diseases,
XX  immunological diseases of the lung, and transplantation associated
XX  diseases including graft rejection and graft-versus-host-disease.
XX  AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
XX  in the isolation of human PRO sequences. AAC58579 to AAC58642 and
XX  AAB33414 to AAB33477 represent human PRO polynucleotide and protein
XX  sequences given in the exemplification of the present invention.
SQ  Sequence 3112 BP; 853 A; 867 C; 712 G; 680 T; 0 other;

Query Match      19.5%; Score 912.2; DB 21; Length 3112;
Best Local Similarity 64.7%; Pred. No. 1.2e-152;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

Qy      527  CGCGGAGGAGCGCTTCCCGGTGGTGAACACGCGCTACGGGCGAGTCCGCGGTGCGCGG 586
Db      112  CAGCCAAGCACAGTATCCAGTTGTCAACACAAATATGCAAAATCCGGGGGCTAAGAAC 171
Qy      587  CGAGCTCAACAACGAGATCCTGGGCGCGCTGTCAGATTCTTTGGGCGTCCCTACGCCAC 646
Db      172  ACCGTTACCAATGAGATCTTGGTCCAGTGAGGAGAGTACTTAGGGTCCCTATGCTTC 231
Qy      647  GCGCGCCCTGGGCGCGCGCTTTCAGCGGCTGAGGCGCGCGCTCTGTCGCGCGCT 706
Db      232  ACCGCCCACTGGAGAGAGGCGGTTTCAGCGCGCGAGAACCCCGCTCTCTCTGAGATGGCAT 291
Qy      707  GCGCAACGCCACACCCCTGCGCGCGCTGCGCGCGAGACCTGTCAGCAGCAGC 763
Db      292  CGAAATACTACTCAGTTTGTGTCGTGTGTCGCGCGCGAGACCTGGATGAGATCTTACT 351
Qy      764  CGCCATCATGCTGCTGTGTGTGTTTCCCGACAACCTTGGAGGCGCGCGCGCACCTAGTGA 823
Db      352  GCATGACATGCTGCCCATCTGTGTTTACCGCAATTTGGATACTTTGATGACCTATGTTCA 411
Qy      824  GAAACGAGCGAGGAGTGTCTGTACTCTCACTTACCTGTCGCGCGCGCGCGCGCGCGCT 883
Db      412  AGATCAAAATAGAGACTGCTTCTTACTTAAACATCTACGTGCCCGCGAGAGTGGAGCCAA 471

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884 CACAAAAAAGCGTACGAGGCG-----ACGCTCAATCGCCAGACACAGATATCCG 934
472 CACAAAAAAGCGAGATATACAGATATACCGTGTGAGACGAGATATCA 531
935 TGACCCCTG---GGAAGAACCTGTGATGCTGTTCTCCATGCGGCTCTACATGGAGG 991
532 TGATCAGAAACAGTAAGAACCCGTCATGGTCTATATCCATGGGGATCTTACATGGAGG 591
992 GACCGGAAACATGTTCCGATGGCTCAGTCTCGCTGCTGCTATGCGAACGTCATGTCAC 1051
592 CACCGCAACATGATGACGCGAGCATTTTGGAACTACGAAACGTCATGTCATCAC 651
1052 GCTCAACTACCGCTTTGGGGTGTCTGGTTTCTCAGACCGGGGACAGGCTGCAAAAG 1111
652 CATTAACACTACCGCTCTGGGAATACTAGGGTTTTAAAGTACCGGTGACCGAGGCAAAAG 711
1112 CAACTATGGCTCTCGGACACAGATCCAGCCCTGCGCTCACTGAAACATCGCCCA 1171
712 CAACTATGGCTCTCGGACACAGATCCAGCACTGCGGTGGATGAGGAGATGTTGGAGC 771
1172 CTTTGGGGGCGACCCCGAGCGTATACCAATCTTTGGTTCCGGGCGAGGGCTCTCTGCGT 1231
772 CTTTGGCGGGGACCCCAAGAGAGTACCAATCTTTGGCTCGGGGCTTGGGGCTCTCTGCT 831
1232 CAACTTCTGATCTCTCCCAACATTCAGAGGCTGTTCCAGAGGCGCATCGCCAGAG 1291
832 CAGCCTGTTGACCTGTCCCACTACTCAGAGGCTCTTCCAGAGGCGCATCTTCAGAG 891
1292 TGGCACCGCCATTTCCAGCTGTCTCTCACTACAGCCGCTCAAGTACACCGGCTGCT 1351
892 CGCACCGCCCTGTCCAGCTGGGCACTGAATACCAAGCGGCGCAAGTACACTCGGATAT 951
1352 GGCAGCAAGGCTGGCTGTGACCGAGGACAGTGTGAGCTGTGAGTGTGCGGCG 1411
952 GGCAGCAAGGCTGGCTGTGACCGAGACAGTGTGAGCTGTGAGTGTGCGGAA 1011
1412 GAAGCCCTCCCGGAGCTGTGTGACAGGACGTCAGCTGCGCGCTACCACTCGCCTT 1471
1012 CAAGAACTACAGAGCTCATCCAGAGACCATCACCCCGGCGCACTACCATAGCTT 1071
1472 TGGGCCCGTGGTGGAGCGAGCTGTGTCGGGATGACCTGTGAGATCTCATGAGAGG 1531
1072 CGGGCCCGTGTATCGACCGGCGCTCATCCAGAGACGACCCCGGAGATCTGATGAGCAAG 1131
1532 AGATTCCTCAACTAGACATGTCTACGSCGTCAACAGGAGAGGCGCTCAAGTTGCT 1591
1132 CGAGTTCCTCAACTAGACATGTCTGCGGCTCAACAGGAGAGGCTGAGTTGCT 1191
1592 GGAGGACTCTGCAGAGAGCGAGACGCTGTGTCTGCGAGCGCTTTGACTTCACTGTCTC 1651
1192 GGACGGCATCTGTGATTAACAGAGACGCTGTGTGACGCGCAACGACTTTGACTTCTCCGTGC 1251
1652 CAACCTTGTGACCAACTGTATGGCTACCGGAGGCAAGGATGCTTTCGGGAGACCAT 1711
1252 CAACCTTGTGACCAACTTTACGGCTACCTGAGGGAAGAGACACTTTGGGGAGACTAT 1311
1712 CAAGTTTGTACACAGACTGGGCGGACCGGAGCAATGGGAAATGCGCGCAAAACCTT 1771
1312 CAAGTTTGTACACAGACTGGGCGGATAGGAAACCCCGAGACGCGGCGGAAACCTT 1371
1772 GCTGGCGCTCTTTACTGACCAACCATGGGTGGGACAGCTGTGGCCACTGCCAAGCTGCA 1831
1372 GGTGGCTCTCTTTACTGACCAACCATGGGTGGGCGGCGGCTGGCC---GCCAGCTGCA 1428
1832 CGCGGACTACAGCTCTCCGCTACTTTTACACCTTTTACACCTTACACCTTGCAGGCGGAGG 1891
1429 CGCGGAGTACGGCTCCCGCACTTACTTCTATGCTTCTATCATCACTGCCAAAGCGAAT 1488
1892 CCGGCTGTAGTGGGAGATCGGCGGACGGGAGTGAATCGCCCTATGCTTTTGGCGTGCC 1951
1489 GAAAGCCAGCTGGGAGATTCGGGCCCATGGGTGATGAGGTCCTCTATGCTTTCGGCATCCC 1548
1952 CATGGTGGTGGCCCGGACCTTCTCCCTGTGTAACCTTCTCCAGAAATGACGTCATGCTCAG 2011

1549 CATGATCGGTCCACGAGCTCTTCAGTTGTAACTTTTCCAAAGACGAGTCATGCTCAG 1608
2012 TGCCTGTGTTCAATCACTACTTGGACCAACTTTCGCAAGACTTGGGAGCCCAACAGCGGT 2071
1609 CGCGTGTGTTCAATCACTACTTGGACGAACTTTCGCAAAACTGGTGTATCCAAATCAACAGT 1668
2072 GCGCAGGATACCAAGTTTATCCACCAAGCCCATCGCTTCGAGGAGTGGTGGAG 2131
1669 TCTCAGGATACCAAGTTTATCCACCAAAACCCAAACCGCTTTGAAGAAGTGGCTGGTC 1728
2132 CAAATTCACAGCAAGAGAGAGTATCTGCACATAGGCTGAAGCCACGCTGGTGA 2191
1729 CAAGTATATCCCAAGACCCAGCTCTATCTGCATATTTGGCTTGAACCCAGAGTGAGAGA 1788
2192 CAATACCGGCGCAACAGGTCCTTCTGGCTGGAGCTGTGCGCCCACTGACACACCT 2251
1789 TCACTACCGGCGCAACAGGTCCTTCTGGTTGGAAGTGTCTTCCCTCATTTTGCACAACTT 1848
2252 GCA-----CAGGAGCTCTTCCACCAACGCGCTGCTCTCCCTACGCCACGG 2302
1849 GAAGAGATATTCAGTATGTTTCAACACCAACAAAGTTCTCCACACAGATGACATC 1908
2303 CTGSCCGCTCTGTCCTCCCGCTGGCGGCGACAGCGCGGCGCGCGGCTGAC 2362
1909 ATTTCCCTATGGCACCGCGGATCTCCCGCAAGATATGCGCAACCAACGCGCAGC 1968
2363 CTTGCTTCCGAGCGCGGCGGCGGCG-----CCGCGCCCAAGGCG 2401
1969 AATCACTCTCTGCGCAACATCCCAACCACTTAAGGACCTCAACAAACAGGCGCTGAGGA 2028
2402 CTATGACCGCTTCCCGGCGGACTCAAGGACTACTCCACGAGCTGAGCGTCAACCGTGC 2461
2029 CACAACTGTCTCTCATTTGAACCAACAGAGATTTTCCACCGAATTAAGTGTCAACATTC 2088
2462 CGTGGGTGCTCTCTCTCTCTCTCAACATCTGCGCTTGTGCTGCTCTACTACAAGCG 2521
2089 CGTGGGCGGCTGCTCTCTCTCTCTCAACATCTTGTGCTTGTGCGGCTGTACTACAAA 2148
2522 GGACCGGCGGAGAGCTGCGGTGCGAGCGGCTTAGCCACCTGCGGCGCTCAGGCTCTGG 2581
2149 GGAACAGAGGCGGCTATGAGACTCAAGCGCGCGCGCGCGAGAGAAACCAACAAATGA 2208
2582 CGTGGCTGTGGGGGCGGCTGCTCTCCCGCGGCGGCGGCTGAGTGTGCAACAGAGGAGGA 2641
2209 TATCGCTCACAATCCAGAAACGAGAGATCATGTCTCTGCAATGAAGCAGCTGGAAACGGA 2268
2642 GCTGTGTCTACTGAGCTGAAGCGGCTGAGTGTGCGGTGCGGCGGAGCCCTGCGGAGGCTCT 2701
2269 TCACAGTGTGAGTGTGCTGAG-----GCACACGACACACT 2304
2702 GCGCGCTGCTGCGCGCGGCGGCTACACCTGCGCTTGGCGGCGGCGGCGGAGCTGTC 2761
2305 GAGGCTCACCTGCGCGCGGAGACTACACCTCAGCGCTGCGCGGCTGCGGAGATGACATCCC 2364
2762 TCTTGTGGCGCGGCGGCGGCTGAGCTGCTGCGCGGAGTGGCTG 2804
2365 ACTTATGAGCGGCAACACCATCATCATGATTCACAAACACTG 2407

Search completed: February 19, 2004, 00:51:30
Job time : 1135.58 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 16:45:36 ; Search time 243.269 Seconds
(without alignments)
8467.711 Million cell updates/sec

Title: US-09-934-323-1

Perfect score: 4667

Sequence: 1 ggcacgggaacttggtct.....ttgcctcttgactgtccctc 4667

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
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- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	871	18.7	4436	4	US-09-491-356C-6
4	724.6	15.5	1764	4	US-09-491-356C-3
5	700.4	15.0	2818	4	US-09-491-356C-4
6	494.8	10.6	5298	4	US-09-491-356C-1
7	145.6	3.1	1905	4	US-09-347-878-33
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ALIGNMENTS

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; Sequence 139, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23

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; Patent No. 6566061				
; GENERAL INFORMATION:				
; APPLICANT: Philibert, Robert A.				
; APPLICANT: Ginns, Edward I.				
; APPLICANT: Delisi, Lynn				
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XOL3				
; FILE REFERENCE: 9465.60S11				
; CURRENT APPLICATION NUMBER: US/09/491.356C				
; CURRENT FILING DATE: 2000-01-26				
; PRIOR APPLICATION NUMBER: PCT/US99/09365				
; PRIOR FILING DATE: 1999-04-29				
; PRIOR APPLICATION NUMBER: 60/083,465				
; PRIOR FILING DATE: 1998-04-29				
; NUMBER OF SEQ ID NOS: 24				
; SOFTWARE: Patentin version 3.1				
; SEQ ID NO 3				
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; TYPE: DNA				
; ORGANISM: Homo sapiens				
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; Sequence 1, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465-6US-1
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1

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Query Match
10.6%; Score 494.8; DB 4; Length 55298;

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Dd	49835	GCTGGTAGAGCAGGACATCCAGCCAGCCGCTACCAACGTTGGSCCTTTGGCCCTGTGATTGA	49894	
Qy	1487	TGGCGACGTGGTCCCCGATGACCCCTGAGATCTCTCATGACGACGGAGAGAATTCCTCAACTA	1546	
Dd	49895	TGGTGAATGTCATCTCTGATGACCCCTGAGATCTCATGGAGCAGGCGGAGTTCCTCAACTA	49954	
Qy	1547	CGACATGCTCATCGGCGTCAACACGAGGAGAGGGCCCTCAAGTTCGTGGAGGACTCTGCGAGA	1606	
Dd	49955	TGACATCATGCTAGGTGTCAACACAGGGCGAGGCTCTCAAGTTGTGGAAAGGGGTGGTGA	50014	
Qy	1607	GAGCGAGGACGDTGTGTCTGCGCAGCGCCTTTGACATTCATGTCCTCAAACCTTTGTGGACAA	1666	
Dd	50015	CCCTGAGATGGTGTCTCTGGCACATGACTTTGACTATTTCGGTCTCCAATTTGTGGACAA	50074	
Qy	1667	CTGTATGCTACCCCGAAGGCAAGATGTGTCTCGGAGAGACCATCAAGTTTATGTATAC	1726	
Dd	50075	TCTGTATGCTATCTCTGAGGGTAAGAACACCCCTCGAGAGACCATCAAGTTATGTATATAC	50134	
Qy	1727	AGACTGGGCGCACCGGGACAATGGGGGAAATGCGCGCAAAAACCTGCTGGGGCTCTTAC	1786	
Dd	50135	AGACTGGGCGACCGGTGACAACCCCTGAGACCCCGTAAAAACACTGGTGGCCTCTTCCAC	50194	
Qy	1787	TGACCAACCAATGGGTGGCACACAGCTGTGGCCACTGCCAAGCTGCACGCGGACTACCACTC	1846	
Dd	50195	TGACCAACCAATGGGTGGACCCCTCAGTGGTGNACGCCGATCTGCATGCGCGTACGGCTC	50254	
Qy	1847	TCCCGTCTACTTTTATACA CTTTCTTACA CCA CCA CTGCGCAGCGGAGGGCCCGCCCTGAGTGGGC	1906	
Dd	50255	GCTACTACTTCTTAGCGCCTCTATCATCATCTGCCAGAGCCCTCATGAAGCCTGCTTGGTC	50314	
Qy	1907	AGATGGGCGCACCGGGATGAACCTGCCCTATGCTCTTTGGCGGTGCCCATGTGGGGTGGCCAC	1966	
Dd	50315	AGATGCAGCTCATGGGATGAAGTACCCTATGTTTTTGGGGTTCCTATGGTAGGCCCCAC	50374	
Qy	1967	CGACCTTTCCTCCCTGACTTCTCAAGAANTGACGTCTATGCTCAGTCCGCTGGTCTATGAC	2026	
Dd	50375	TGACCTTTTCCCCTGCAACTCTCCAGAANTGATGTTATGCTCAGTGTCTGCTGCTATGAC	50434	
Qy	2027	CTACTGGACCAACTTCGCCAAGACTGGGGA	2056	
Dd	50435	CTATTGGACCAACTTTGGCAAGACTGGGTA	50464	

RESULT 7

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US-09/347-878-33
RESOLUTION
; Sequence 33, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1653
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33

```

LENGTH: 1905
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
OTHER INFORMATION: Bovine pancreatic cholesterol esterase cDNA
PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: 08/462,884
PATENT FILING DATE: 1995-06-05
PUBLICATION DATE: 1997-04-29
US-09-347-878-33

Query Match 3.1%; Score 145.6; DB 4; Length 1905;
Best Local Similarity 53.0%; Pred. No. 1.2e-19;
Matches 335; Conservative 0; Mismatches 294; Indels 3; Gaps 1;

QY 1000 ACATGTTTCGATGGCTCAGTCTGGTGGCTATGCAACGTCATTGTAGCCACGCTCAACT 1059
DB 452 ACTCTACACGGGAGGAGATGCCACCGGGCAACGTCATGCTGGTCACTTCAACT 511
QY 1060 ACCGCTTGGGTGTCGGTTCCTTCAGCACCGGGACCGAGCTCCAACTGCAGTAACATG 1119
DB 512 ACCGGTTGGGCTTGGGCTTCTCAGCACCGGGACTCCAACTGCAGTAACATG 571
QY 1120 GGTCTCTGACAGATCCAGGCTTGGCTGGCTCAGTGAACATCGCCACTTTGGGG 1179
DB 572 GCTTTGGATCAGCATGAGGCTTGGTGGTGAAGAGAACATGAGGCTTCGGAG 631
QY 1180 GCGACCCGAGGATATCACTTCTTGGTTCGGGGCAGGGGCTCTCTGCTCAACTTC 1239
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QY 1240 TGATCTCTCCACCATTCAGAGGGCTTCCAGAGGCCATCCCGCAGAGTGGCACCG 1299
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QY 1300 CCAATTCAGCTGCTCTCAACTACAGCGCTCAAGTACACCGGCTCTGCTGACGCA 1359
DB 752 GTTTGCTGCTTGGGCTATCCAGCAGGACCCCTCTTCTGGGCTAAAAGGATTCGAGA 811
QY 1360 AGGTGGCTGTACCGAGAGACAGTGTGAAGTGTGGAGTGTCTGGCGGAGCCCT 1419
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DB 872 CCGTGCCTGACG--CTGGCTATAAGCTGCGCTTGGGAAGCAGCAATACCCCAAGC 928
QY 1480 TGTGTGATGGGACCTGTCCCGATGACCTGAGATCCTCATGCGACGAGAGATTC 1539
DB 929 TGCACTATCTGCTTCTGCTCCCGTCATCGATGAGACTTTCATCCCTGATGACCCGTC 988
QY 1540 TCAATACGACATGTCATCGCGCTCAACCGAGGAGGCGCTCAAGTTCGTGAGGACT 1599
DB 989 ACCTGTAGCCAAACCGCCGAGACGTCGACTACATAGCGGGCACCACATGACATGACG 1048
QY 1600 CTGACAGAGCAGACGCTGTGTGTCGACG 1631
DB 1049 ACCTTTTTCGGATGACGTCGCCGACATC 1080

RESULT 8

US-08-462-884A-2
Sequence 2, Application US/08462884A
Patent No. 5624836
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
TITLE OF INVENTION: Esterase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 10 South Wacker Drive

CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,884A
FILING DATE: Unknown
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1907 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 100..129
OTHER INFORMATION: /note= "complementary sequence to
OTHER INFORMATION: oligonucleotide probe"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1824
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1907
OTHER INFORMATION: /note= "Bovine pancreatic
OTHER INFORMATION: cholesterol esterase cDNA"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..30
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 31..1821
US-08-462-884A-2

Query Match 3.1%; Score 145.6; DB 1; Length 1907;

Best Local Similarity 53.0%; Pred. No. 1.2e-19;

Matches 335; Conservative 0; Mismatches 294; Indels 3; Gaps 1;

QY 1000 ACATGTTTCGATGGCTCAGTCTGGCTGGCTATGCAACGTCATTGTAGCCACGCTCAACT 1059
DB 452 ACTCTACACGGGAGGAGATTCACACCGGGCAACGTCATGCTGGTCACTTCAACT 511
QY 1060 ACCGCTTGGGGTCTCGTTCCTTCAGCACCGGGACCGAGGCTGCAAAAGGCAACTATG 1119
DB 512 ACCGGTTGGGCTTGGGCTTCTCAGCACCGGGACTCCAACTGCAGGTAACATG 571
QY 1120 GGTCTCTGACAGATCCAGGCTTGGCTGGCTCAGTGAACATCGCCACTTTGGGG 1179
DB 572 GCTTTGGATCAGCATGAGGCTTGGTGGTGAAGAGAACATGAGGCTTCGGAG 631
QY 1180 GCGACCCGAGGATATCACTTCTTGGTTCGGGGCAGGGGCTCTCTGCTCAACTTC 1239
DB 632 GAGACCCGAGCAACATCACCTCTTTGGGAGTTCGGCGGAGCGGCGAGCGTCTCTCTGC 691
QY 1240 TGATCTCTCCACCATTCAGAGGGCTGTTCAGAGGCGCATCGCCAGAGTGGCACCG 1299
DB 692 AGACCTCTCTCCCTACAAAGGSCCTCATCAAGCGAGCCATCAGCCAGAGTGGAGTG 751

QY 1300 CCATTTCAGCTGGTCTGCTCACTACCAAGCCGCTCAAGTACAGCGGCTCTGCGCAGCA 1359
 Db 752 GTTTGTGCTTGGCCATCCAGAGGACCCCTCTTCTGGCTTAAAGGATTTGCAGAGA 811
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 Db 872 CCGGAGAGCTGTGAGAGAGAGTGTGAGCTGTGCGGCTACCAATGCGCTTTGGGCGCG 928
 QY 1480 TGGTGTGAGGAG 1539
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 Db 989 ACCTGTAGCCCAACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048
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 Db 1049 ACCTCTTCTGCGGATGAGCTGCCAGCCATC 1080

RESULT 9

US-08-461-881B-2
 ; Sequence 2, Application US/08461881B
 ; Patent No. 5792832
 ; GENERAL INFORMATION:
 ; APPLICANT: Lange III, Louis G
 ; APPLICANT: Spilburg, Curtis A
 ; TITLE OF INVENTION: Mammalian Pancreatic
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive
 ; CITY: Chicago
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" hard disc
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/461,881B
 ; FILING DATE: June 5, 1995
 ; CLASSIFICATION: 435,
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: A. Blair Hughes
 ; REGISTRATION NUMBER: 32,901
 ; REFERENCE/DOCKET NUMBER: 89,852-J
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/913-0001
 ; TELEFAX: 312/913-0002
 ; TELEX: 910/221-5317
 ; INFORMATION FOR SEQ ID NO. 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1908 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 100..129
 ; OTHER INFORMATION: /note= "complementary sequence to
 ; OTHER INFORMATION: oligonucleotide probe"
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1824

Cholesterol Esterase

FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..1308
 ; OTHER INFORMATION: /note= "Bovine pancreatic
 ; OTHER INFORMATION: cholesterol esterase cDNA"
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 1..30
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 31..1821
 ; US-08-461-881B-2

Query Match 3.1%; Score 145.6; DB 1; Length 1908;

Best Local Similarity 53.0%; Pred. No. 1.2e-19;
 Matches 335; Conservative 0; Mismatches 294; Indels 3; Gaps 1;

QY 1000 ACATGTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1059
 Db 452 ACCTTACGACGGGAGGAGATTGCCACACGGGGCAACGTCACTGCTGCTGCTGCTGCTGCTGCT 511
 QY 1060 ACCGTCTTGGGGTGTCTGGTCTTCTCAGCACGGGGACAGGCTGCAAAAGGCAACTATG 1119
 Db 512 ACCGGTGTGGGGCTTCTGAGCACGGGGACTCCAACTGCGCAGGTAACTATG 571
 QY 1120 GGCTCTTGACACAGATCCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1179
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 QY 1180 GCGACCCCGAGCGTATCACCATCTTTTGGTTCGGGGGAGGGGCTCTCTGCTGCTCAACCTTC 1239
 Db 632 GAGACCCCGAGCAACATCACCTCTTTGGGAGTGGCCGAGGGGCGCAGGCTCTCTCTGTC 691
 QY 1240 TGATCTCTCCCAACATTCAGAGGGCTGTTCAGAGAGGCGCATCGCCAGAGTGGCACCG 1299
 Db 692 AGACCTCTCTCCCTACACAGAGGCTCTCATCAAGCGAGGCTATCAGCCAGAGTGGAGTGG 751
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 Db 752 GTTTGTGCTTGGGCTATCCAGAGGACCCCTCTTCTGGCTTAAAGGATTCAGAGA 811
 QY 1360 AGTGGGCTGTGACCGAGAGAGAGTGTGAGCTGTGAGTGTGCTGCGCGGAGAGCCCT 1419
 Db 812 AGTGGGCTGTGCGGCTGTGAGAGAGAGTGTGAGCTGTGAGTGTGCTGCGCGGAGAGCCCT 871
 QY 1420 CCGGAGAGCTGTGAGACAGAGAGAGTGTGAGCTGTGCGGCTACCATCGCTTTGGGCGCG 1479
 Db 872 CCGGTGCTTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 928
 QY 1480 TGGTGTGAG 1539
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 QY 1540 TCACTATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1599
 Db 989 ACCTGTAGCCCAACCGCGGAG 1048
 QY 1600 CTGCAG 1631
 Db 1049 ACCTCTTCTGCGGATGAGCTGCCAGCCATC 1080

RESULT 10

US-09-123-960-2
 ; Sequence 2, Application US/09123960
 ; Patent No. 5981299
 ; GENERAL INFORMATION:
 ; APPLICANT: Lange III, Louis G
 ; APPLICANT: Spilburg, Curtis A
 ; TITLE OF INVENTION: Mammalian Pancreatic
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff

TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2184 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: 82..2088
OTHER INFORMATION: /label= Variant_T
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 151..2085
FEATURE:
NAME/KEY: repeat.region
LOCATION: 1756..2052
FEATURE:
NAME/KEY: repeat.unit
LOCATION: 1756..1788
FEATURE:
NAME/KEY: repeat.unit
LOCATION: 1789..1821
FEATURE:
NAME/KEY: repeat.unit
LOCATION: 1822..1854
FEATURE:
NAME/KEY: repeat.unit
LOCATION: 1855..1887
FEATURE:
NAME/KEY: repeat.unit
LOCATION: 1889..1920
FEATURE:
NAME/KEY: repeat.unit
LOCATION: 1921..1953
FEATURE:
NAME/KEY: repeat.unit
LOCATION: 1954..1986
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NAME/KEY: repeat.unit
LOCATION: 1987..2019
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NAME/KEY: repeat.unit
LOCATION: 2020..2052
US-08-445-050-8
Query Match 2.8%; Score 132.4; DB 1; Length 2184;
Best Local Similarity 48.8%; Pred. No. 4.4e-17;
Matches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;
QY 1000 ACATGTCGATGGCTCAGTCCTGGCTGCTATGGCAAGTCATTGTAGCCACGCTCAACT 1059
DB 518 ACCTGATGACGGGAGGAGATCGCCACACGGGAAAGCTCATCGTGTCACTTCACT 577
QY 1060 ACCGTGTTGGGTGCTCGGTTTCTCAGCACCGGGACACAGGCTGCAAAAGGCAACTATG 1119
DB 578 ACCGTGTCGGCCCTTGGTTTCTCAGCACCTGGGGAGCCCAATCTGCCAGGTAACTATG 637
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QY 1240 TGATCTCTCCCACTTTCAGAAAGGCTGTTCCAGAAAGCCATCGCCCGAGAGTGCACCG 1299

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QY 1420 CCCGGAGCT---GGTGGACAGGACGTGACGCTGCCGCTACACATCGCCTTTGGGC 1476
DB 938 CCCGAGCCCTGACGCTGGCTATTAAGTGGCTGGCTGGCAGGCTGAGTACCCATGCTGC 997
QY 1477 CCGTGGTGGATGGCGACGTGTCTCCCGATGACCTGAGATCTCTCATGCGCAGGAGAT 1536
DB 998 ACTATGTGGCTTCTGCTCTCTCATTTGATGGAGCTTTCATCCCGCTGACCCGATCAACC 1057
QY 1537 TCCTCACTAGCATGCTCATCGGCTCAACAGGAGAGGGCTCAAGTTCTGTGGAGG 1596
DB 1058 TGTAGCCCAACGCCCGGACATGACTATATAGCAGGACCAACAACATGGACGCGCACA 1117
QY 1597 ACTCTGCAGAGAGGAGGACGCTGTGTGTGTCAGCGGCTTTGACTTCACTCTCTCCAACT 1656
DB 1118 TCTTCGCCAGCATCGACATGCTGCTCAACAAGGCAACAAGAAAGTCAAGGAGGAGG 1177
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DB 1178 ACTTCTCAAGCTGGTCACTGAGTTCAATCCAAAGGGCTCAGAGGCGCCAGAGCA 1237
QY 1711 TCAAGTTTATGTACACAGACTGGGCGGACCGGCAATGGCGAAATGGCGGCAAAACCC 1770
DB 1238 CTTTTGATGTCTACACCGAGCTCTGGGCGCCAGGACCCATCCAGGAGAAATAGAGAGA 1297
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DB 1298 CTGTGTGAGCTTTGAGACCGATGCTCTTCTGCTGGTCCCAACCGAGATGCGCTTAGGCC 1357
QY 1825 AGCTGACGCGGACTTACGAGTCTCC---GTCTACTTTTACACCTTCTACCACTGCTGCC 1881
DB 1358 AGCAGAGGCAATGCGAAGATGCGAAGACTTACGCTACCTGTTTCCCATCTCTCTC 1417
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DB 1418 GGATGCCGCTTACGCCAAATGGGTGGGGCGGACCATGCGATGACATTCAGTACGTTT 1477
QY 1942 TTGGGCTGCCATGTTGGTGGCCCGACCTCTTCCCTGTAACTTCTCAGAAATGAG 2001
DB 1478 TCGGGAAGCCCTTCGCCACCCCGGCTACCGGCTACCGGCCCCAAGACAGGACAGTCTTAAG 1537
QY 2002 TCATGCTCAGTCCGCTGCTCATGACTTCTGACCAACTTCCCAAGACTGGGGAGCCCA 2061
DB 1538 CCATGATCG-----CCTACTGGACCAACTTTGCCAAATTTGCCAAACAGGGAGCCCCA 1582
QY 2062 AC 2063
DB 1583 AC 1584

RESULT 12
US-08-204-691-8
; Sequence 8, Application US/08204691
; Patent No. 5827683
; GENERAL INFORMATION:
; APPLICANT: Blaeckberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Hennell, Olle
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stromqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5827683el Polypeptides

Db 1418 GATGCGCGTCTACCCCAATGGGTGGGGCCGACCATGCGAGATGACATTCACTAGCTTT 1477
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Db 1478 TCGGGAAGCCCTTTCGCCACCCCCACCGGCTACCGGCCCAAGACAGAGGACAGTCTCTAAG 1537
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QY 2062 AC 2063
Db 1583 AC 1584

RESULT 13
US-09-347-878-31
; Sequence 31, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 2344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(2252)
; FEATURE:
; OTHER INFORMATION: Human cholesterol esterase cDNA
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M85201/GenBank
US-09-347-878-31

Query Match 2.8%; Score 132.4; DB 4; Length 2344;
Best Local Similarity 48.8%; Pred. No. 4.5e-17;
Matches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;

QY 1000 ACATGTTTCGATGCTCAGTCCCTGGCTGCTATGGCAACGTCAATGTAGCAGCTCAACT 1059
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Db 925 ACTATGTGGCTTCTGCTCCCTGTCAATGATGGAGACTTCACTCCCGCTGACCCGATCAAC 984
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QY 1597 ACTCTCAGAGAGGAGGAGGCTGTCTGCGAGCGCTTTGACTTCACTGTCTCCAAT 1656
Db 1045 TCTTCGCGAGCATCGACATGCTGCTCCATCAACAGGGCAACAGAAATCAAGGAGG 1104
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RESULT 14
US-08-445-050-1
; Sequence 1, Application US/08445050
; Patent No. 5763739
; GENERAL INFORMATION:
; APPLICANT: Blaeckberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hanson, Lennart
; APPLICANT: Hernell, Oile
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stroemqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5763739el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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QY 2002 TCATGCTCAGTGGCTGTGATGCTGACCTGAGGACCACTTTCGCGGAGCTGGGAGCCCA 2061
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Db 1583 AC 1584

RESULT 15
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; Sequence 1, Application US/08204691
; Patent No. 5827683
; GENERAL INFORMATION:
; APPLICANT: Blaeckberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Harnell, Olle
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stromqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5827683el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,691
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300696-4
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300722-7
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner P.D., Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: mammary gland
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; OTHER INFORMATION: /product= "bile-salt-stimulated
; OTHER INFORMATION: lipase"
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US-08-204-691-1

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Query Match 2.8%; Score 132.4; DB 1; Length 2428;

Best Local Similarity 48.8%; Pred. No. 4.5e-17; Indels 33; Gaps 5;

Matches 528; Conservative 0; Mismatches 521;

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QY 2062 AC 2063
DB 1583 AC 1584

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